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(54) Title: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.

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METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

5 This application is related to USSN 60/302,814, filed July 3, 2001; USSN 60/310,099, filed August 3, 2001; USSN 60/343,705, filed November 8, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2001, each of which is incorporated herein by reference.

10 FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in bladder cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of bladder cancer. The invention further relates to methods for
15 identifying and using agents and/or targets that inhibit bladder cancer.

BACKGROUND OF THE INVENTION

In the United States, over 50,000 new cases of bladder cancer are diagnosed annually, and more than 10,000 deaths will be attributed to bladder cancer. Bladder cancer is now the
20 fourth most common cancer among American men and the ninth most common cancer among American women. It occurs three times more frequently in men than in women, and it occurs roughly twice more frequently in white versus black men.

Bladder cancer rarely occurs in people younger than 40 years of age, being primarily a disease of older men. Nonetheless, bladder cancer is a significant cause of illness and death
25 in the United States. The risk of bladder cancer increases steeply with age, with over half of all bladder cancer deaths occurring after age 70. In white men older than 65, the annual disease rate of bladder cancer is approximately 2 cases per 1,000 persons; this contrasts with a rate of 0.1 cases per 1,000 persons younger than 65.

Within the United States, bladder cancer rates are higher among people who reside in northern versus southern states, and is higher for people who live in urban versus rural areas. Although this difference suggests that environmental as well as genetic factors may contribute to the development and progression of the disease, other studies confirm that certain genes play a role in bladder cancer.. For example, expression of the tumor suppressor gene p53 has been associated with an adverse prognosis for patients with invasive bladder cancer. A retrospective study of 243 patients treated by radical cystectomy found that the presence of nuclear p53 was an independent predictor for recurrence among patients with mid to late stage tumors. Esrig, et al (1994) N.E.J. Med. 331:1259-64.

Urinary bladder cancers represent a spectrum of diseases that can be grouped into three general categories: superficial, invasive, and metastatic. The prognosis for treatment is highly dependent on the stage at which the tumor is first diagnosed. A unique aspect of bladder cancer treatment is that repeated surgical biopsy is an integral part of routine patient management. This has permitted the conduct of molecular genetic studies of tumors from specific stages of the disease. The results of these studies suggest that bladder cancers develop and progress along at least two discrete pathways, which may account for differences in invasiveness and metastatic potential. Incorporating molecular genetic factors into the current paradigm for diagnosis and treatment will optimize the probability of cure and allow the quality of life for bladder cancer patients to be maintained.

Early detection and treatment can prevent reoccurrence and progression of the disease to an incurable stage. Thus, the identification of novel diagnostic markers and therapeutic targets will improve the current treatment of bladder cancer patients. While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences in disease states. The elucidation of a role for novel proteins and compounds in disease states for identification of diagnostic markers and therapeutic targets is essential for improving the current treatment of bladder cancer patients. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of bladder cancer. Additionally, provided herein are molecular targets for therapeutic intervention in bladder cancer and other related bladder diseases.. Further provided are

methods that can be used to screen candidate bioactive agents for the ability to modulate bladder cancer.

SUMMARY OF THE INVENTION

5 The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in bladder cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate bladder cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

10 In one aspect, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

15 In one embodiment, the present invention provides a method of determining the level of a bladder cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

20 In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-13.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

25 In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat bladder cancer. In another embodiment, the patient is suspected of having metastatic bladder cancer.

In one embodiment, the patient is a human.

In one embodiment, the bladder cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of bladder cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a bladder cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic bladder cancer. In a further embodiment, the patient has a drug resistant form of bladder cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the bladder cancer-associated transcript to a level of the bladder cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1A-13.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a bladder cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to bladder cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1A-13.

In another aspect, the present invention provides a method for identifying a compound that modulates a bladder cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a bladder cancer-associated cell to treat bladder cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having bladder cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence

as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

5 In one embodiment, the control is a mammal with bladder cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time
10 periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 are individually compared to their respective levels in a control cell sample or mammal. In a
15 preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having bladder cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for
20 treating a mammal having bladder cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a bladder cancer. In one embodiment, a gene is selected from Tables 1A-13. The method further includes
25 adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary
30 when present, and wherein the comparison can occur after addition or removal of the drug

candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the bladder cancer modulatory protein, or an animal lacking the bladder cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1A-13, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with bladder cancer is provided. The method comprises determining the expression of a gene of Tables 1A-13 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with bladder cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in bladder cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a bladder cancer modulating protein (bladder cancer modulatory protein) or a fragment thereof and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a bladder cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. The method further includes determining the binding of said bladder cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits bladder cancer.

Also provided herein are methods of eliciting an immune response in an individual.

In one embodiment a method provided herein comprises administering to an individual a

composition comprising a bladder cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a bladder cancer modulating protein, preferably encoded by a nucleic acid of Tables 1A-13 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a bladder cancer modulating protein, preferably selected from the nucleic acids of Tables 1A-13, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a bladder cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

In another aspect of the invention, a method of treating an individual for bladder cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a bladder cancer modulating protein. In another embodiment, the method comprises administering to a patient having bladder cancer an antibody to a bladder cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for bladder disease (BD), e.g., cancer, including metastatic bladder cancer, as well as methods for screening for compositions which modulate bladder diseases. Also provided are methods and compositions for treating bladder disease. Various related conditions where these markers may be useful also, include, e.g., carcinoma in situ, various stages of papillary carcinomas; and such conditions in different stages, layers, structural portions, etc.

Recent advances in molecular medicine, generally, have increased the interest in tumor-specific cell surface antigens that could serve as diagnostic or prognostic markers, or as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in other, e.g., normal, adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, as a physiological consequence of such expression would be limited. Examples of such antigens in cancers other than bladder cancer include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer.

Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; and Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

15 Definitions

The term "bladder cancer protein" or "bladder cancer polynucleotide" or "bladder cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1A-13; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-13 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least

about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A

5 "bladder cancer polypeptide" and a "bladder cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" bladder cancer protein or nucleic acid refers to a bladder cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type bladder cancer

10 polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of splicing, including alternative splicing, or post-translation processing.

"Biological sample" as used herein is a sample of biological tissue or fluid, e.g., that contains nucleic acids or polypeptides of a bladder cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g.,

15 humans, or rodents, e.g., mice and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, urine, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most

20 preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, or mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g.,

25 isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same

30 or have a specified percentage of amino acid residues or nucleotides that are the same (e.g.,

about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, substitutions, naturally occurring variants, e.g., polymorphic or allelic, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison computer algorithm, test and reference sequences, subsequence coordinates, and sequence algorithm program parameters are typically designated. Default or alternative program parameters can be selected. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from about 20-600, usually about 50-200, more usually about 100-150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, by, e.g., the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444-448, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred algorithms suitable for determining percent sequence identity and sequence
 5 similarity include the BLAST and BLAST 2.0 algorithms. See Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402; and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information
 10 (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for
 15 initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to
 20 calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN
 25 program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of
 30 both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between
 5 two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another
 15 indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an
 20 expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a
 30 preparation is substantially purified. In particular, an isolated nucleic acid is separated from

some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments typically denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95%
5 pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which
10 at least one amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and a non-naturally occurring amino acid polymer.

The term "amino acid" embraces naturally occurring or synthetic amino acids, amino acid analogs, and amino acid mimetics. Naturally occurring amino acids are those encoded
15 by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs include compounds that share a basic chemical structure with a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, or an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have
20 modified R groups (e.g., norleucine) or modified peptide backbones, but share some basic chemical structure with a naturally occurring amino acid. Amino acid mimetics include chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by their commonly known three letter symbols
25 or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to amino acid or nucleic acid sequences.

With respect to particular nucleic acid sequences, conservatively modified variants refers to
30 those nucleic acids which encode identical or essentially identical amino acid sequences, or

where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Each nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another include: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M). See, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman.

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. See, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The

Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, which are portions of a polypeptide that often form a compact unit of the polypeptide, and are typically about 25-500 amino acids long. Typical domains are made of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds. In some cases, nucleic acid analogs are included that may have alternate backbones, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149); phosphorothioate (Mag, et al. (1991), Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048); phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-322); O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207. Other analog nucleic acids include those with positively charged backbones (Denpocy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101); non-ionic backbones (U.S. Patent Nos. 5,386,023; 5,637,684; 5,602,240; 5,216,141; and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426;

- Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2-3 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx); and non-ribose backbones (see U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6-7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also contemplated. See Jenkins and Turner (1995) Chem. Soc. Rev. 24:169-176. Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News. Modifications of the ribose-phosphate backbone may be made, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.
- Particularly preferred are peptide nucleic acids (PNA) which include peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. The PNA backbone typically exhibits improved hybridization kinetics, exhibiting larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs.
- DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. And due to their non-ionic nature, hybridization of the polymers is relatively insensitive to salt concentration. In addition, PNAs are not as easily degraded by cellular enzymes, and can be more stable.

- The nucleic acids may be single stranded or double stranded, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine, hypoxanthine,

isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures.

5 Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. Direct or indirect methods are contemplated. For example, useful labels include ^{32}P , fluorescent
10 dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the bladder cancer nucleic acids, proteins, and antibodies. Methods are well known for conjugating the antibody to the label,
15 including those methods described by Hunter, et al. (1962) Nature 144:945-946; David, et al. (1974) Biochemistry 13:1014-021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or
20 noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to a target, e.g., an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds; fluorescent compounds; an enzyme or substrate; tags such as epitope tags; a toxin; activatable moieties; a chemotherapeutic agent; a lipase; an antibiotic; a radioisotope emitting "hard", e.g., beta radiation; or an attracting moiety.

25 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding
30 partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which streptavidin linked label may bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operable linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced

recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

- 5 The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a
- 10 coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

- A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid
- 15 sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is
- 20 active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

- 25 An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

- 5 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview
- 10 of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Techniques in Biochemistry and Molecular Biology; vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which
- 15 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g.,
- 20 about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least about two times background, preferably about 10 times background hybridization.
- Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC,
- 25 and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-

- 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press NY.

- Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least about twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. Current Protocols in Molecular Biology Lippincott.

- The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a bladder cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the bladder cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease bladder cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cell viability, cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

- By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a bladder cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects.

Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the bladder cancer protein;

5 measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation or metabolism. Determination of the functional effect of a compound on bladder cancer can also be performed using bladder cancer assays, such as, in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or

10 serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. Functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for bladder

15 cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of bladder cancer polynucleotide and

20 polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of bladder cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of bladder cancer proteins, e.g., antagonists. Antisense nucleic acids

25 may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate bladder cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of bladder cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small

30 chemical molecules and the like. Such assays for inhibitors and activators include, e.g.,

expressing the bladder cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of bladder cancer can also be identified by incubating bladder cancer cells with the test compound and determining increases or decreases in the expression of 1 or more bladder cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more bladder cancer proteins, such as bladder cancer proteins encoded by the sequences set out in Tables 1A-13.

Samples or assays comprising bladder cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably about 50%, more preferably about 25-0%. Activation of a bladder cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably about 150%, more preferably about 200-500% (e.g., two to five fold higher relative to the control), more preferably about 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 of Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene.

Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using

recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

- For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques can be used. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

- A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of bladder cancer-associated sequences

- In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal bladder or other

tissue) may be distinguished from cancerous or metastatic cancerous tissue of the bladder, or bladder cancer tissue or metastatic bladder cancerous tissue can be compared with tissue samples of bladder and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different bladder cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in bladder cancer versus non-bladder cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate bladder cancer, and thus tumor growth or recurrence, in a particular patient; or does chemotherapy or radiation therapy induce expression of particular targets. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of bladder cancer in the tissue or origin of a primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the bladder cancer expression profile. This may be done by making biochips comprising sets of important bladder cancer genes, which can then be used in these screens. These methods can also be applied on the protein basis; that is, protein expression levels of the bladder cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the bladder cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or inhibitory nucleic acids, or the bladder cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in bladder disease or cancer relative to normal tissues and/or non-malignant bladder tissue, herein termed "bladder cancer sequences." As outlined below, bladder cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in bladder cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the bladder cancer sequences are from humans; however,

as will be appreciated by those in the art, bladder cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other bladder cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Bladder cancer sequences from other organisms may be obtained using the techniques outlined below.

Bladder cancer sequences can include both nucleic acid and amino acid sequences. Bladder cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications. Biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the bladder cancer sequences can be generated.

A bladder cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying bladder cancer-associated sequences, the bladder cancer screen typically includes comparing genes identified in different tissues, e.g., normal, non-malignant, or cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing bladder cancer samples with metastatic cancer samples from other cancers, such as lung, bladder, gastrointestinal cancers, ovarian, etc. Samples of different stages of bladder cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal bladder, but also including, and not limited to lung, heart, brain, liver, bladder, kidney,

muscle, colon, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the bladder cancer screen that are expressed in a significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable
5 that the target be disease specific, e.g., not be expressed on critical organs.

In a preferred embodiment, bladder cancer sequences are those that are up-regulated in bladder cancer; that is, the expression of these genes is higher in the bladder cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about
10 five-fold or higher being preferred. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and sequences of accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL)
15 and DNA Database of Japan (DDBJ).

In another preferred embodiment, bladder cancer sequences are those that are down-regulated in the bladder cancer; that is, the expression of these genes is lower in bladder cancer tissue as compared to non-cancerous tissue (see, e.g., Tables 1A-13). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least
20 about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in bladder cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas
25 of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with bladder cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation. See Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference,
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Coronado, CA. Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on an electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing bladder cancer, e.g., the identification of bladder cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be

catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity

5 between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis

10 described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as

15 the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxeavanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler

20 (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Oxford Univ. Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to

25 Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g.,

with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for bladder cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention
5 in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at
10 least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) comprising a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem,
15 ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result
20 obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data
25 file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of
30 the query target and results are output via an I/O device. For example, a central processor

can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of bladder cancer-associated proteins

Bladder cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the bladder cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in proteins of one or more structural motifs for which defined functions have been attributed. In

addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the bladder cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases

and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain

5 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors

10 include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved

15 motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example,

20 growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or

25 may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Bladder cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful

30 in imaging modalities. Antibodies may be used to label such readily accessible proteins in

situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods.

Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the bladder cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Bladder cancer proteins that are secreted or released proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or urine tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of bladder cancer nucleic acids

As described above, bladder cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The bladder cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-13, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the bladder cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a bladder cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire bladder cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant bladder cancer nucleic acid can be further-used as a probe to identify and isolate other bladder cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant bladder cancer nucleic acids and proteins.

The bladder cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the bladder cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense/inhibition applications. Alternatively, the bladder cancer nucleic acids that include coding regions of bladder cancer proteins can be put into expression vectors for the expression of bladder cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to bladder cancer nucleic acids (both the nucleic acid sequences outlined in the tables and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the bladder cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that

hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be a number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical

equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon[®], etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 00/55627.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being

particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of bladder cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a bladder cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of bladder cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative

PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification. See, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com.

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1080; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, and linker adapter PCR, etc.

Expression of bladder cancer proteins from nucleic acids

In a preferred embodiment, bladder cancer nucleic acids, e.g., encoding bladder cancer proteins, are used to make a variety of expression vectors to express bladder cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the bladder cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a

promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; two sequences may be operably linked if they are physically linked on a single polynucleotide. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the bladder cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are useful in the present invention.

In addition, an expression vector may comprise additional elements. The expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and replication. For integrating expression vectors, the expression vector may contain at least one sequence homologous to the host cell genome, and preferably two homologous sequences

which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known (e.g., Fernandez and Hoeffler, supra).

5 In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The bladder cancer proteins of the present invention may be produced by culturing a host cell transformed with an expression vector under the appropriate conditions to induce or
10 cause expression of the bladder cancer protein. Conditions appropriate for bladder cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will typically require optimizing the growth and proliferation of the host cell, while the use of an
15 inducible promoter typically requires identifying the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, insect, and
20 animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the bladder cancer proteins are expressed in mammalian
25 cells. Mammalian expression systems include retroviral and adenoviral systems. Retroviral vector systems are described in PCT/US97/01019 and PCT/US97/01048. Of particular use are promoters from mammalian viral genes, since viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the
30 CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription

termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian and other hosts are well known, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In another embodiment, bladder cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. Synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. A bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. Often an efficient ribosome binding site is desirable. The expression vector may include a signal peptide sequence that provides for secretion of the bladder cancer protein. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs, e.g., ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline, or biosynthetic genes, e.g., those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using, e.g., calcium chloride treatment, electroporation, and other methods.

Bladder cancer proteins can also be produced in insect cells. See, e.g., Miller, et al. (1997) Baculovirus Expression Vectors: A Laboratory Manual Oxford Books; ISBN: 0716770172; and Makrides (1999) Prot. Expr. Purif. 17:183-202.

Bladder cancer protein may be produced in yeast cells. Yeast expression systems exist with expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*. See, e.g., Jones, et al. (eds. 5 1993) The Molecular and Cellular Biology of the Yeast Saccharomyces: Gene Expression CSH Press; ISBN: 0879693657.

The bladder cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the bladder cancer protein may be fused to a carrier protein to form an 10 immunogen. Alternatively, the bladder cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the bladder cancer protein is a bladder cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression or purification purposes.

The bladder cancer protein is typically purified or isolated after expression. Bladder 15 cancer proteins may be isolated or purified in a variety of ways, depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, reverse-phase HPLC chromatography, and chromatofocusing. The bladder cancer protein may be purified using a standard anti-bladder cancer protein antibody 20 affinity column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see, e.g., Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the bladder cancer protein. In some instances no purification will be necessary, which may depend on the intended use.

25 Once expressed and purified, if necessary, the bladder cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of bladder cancer proteins

In one embodiment, the bladder cancer proteins are derivative or variant bladder cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative bladder cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most residues within the bladder cancer peptide.

Certain embodiments of bladder cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the bladder cancer protein, using cassette or PCR, mutagenesis, or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant bladder cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are often characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the bladder cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. To optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed bladder cancer variants screened for the optimal combination of desired activities. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is performed using assays of bladder cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be

tolerated. Deletions range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combinations thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the bladder cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the bladder cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the bladder cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. Substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, e.g., the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic acid or aspartic acid; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Covalent modifications of bladder cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a bladder cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a bladder cancer polypeptide. Derivatization with bifunctional agents is useful, e.g., for crosslinking bladder

cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-bladder cancer polypeptide antibodies or screening assays. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-(p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamic and aspartic residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (pp. 79-86, Creighton (1984) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the bladder cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence bladder cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence bladder cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express bladder cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to bladder cancer polypeptides may also be accomplished by-altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence bladder cancer polypeptide (for O-linked glycosylation sites). The bladder cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the bladder cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the bladder cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

Such methods are described in the art, e.g., in WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the bladder cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art. See, e.g., Hakimuddin, et al. (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of bladder cancer comprises linking the bladder cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Bladder cancer polypeptides of the present invention may also be modified to form chimeric molecules comprising a bladder cancer polypeptide fused to a heterologous polypeptide or amino acid sequence. In one embodiment, a chimeric molecule comprises a fusion of a bladder cancer polypeptide with an epitope tag. The epitope tag is generally placed at the amino- or carboxyl-terminus of the bladder cancer polypeptide. The presence of such epitope-tagged forms of a bladder cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the bladder cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a bladder cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616);

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other bladder cancer proteins of the bladder cancer family, and bladder cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related bladder cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the bladder cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known. See, e.g., Innis (1990) PCR Protocols, supra.

Antibodies to bladder cancer proteins

In a preferred embodiment, when the bladder cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the bladder cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller bladder cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known (see, e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a

nucleic acid of the tables or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor.

- 5 Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected as appropriate.

- The antibodies may be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975)
- 10 Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1A-13 or fragment
- 15 thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (pp. 59-103, Goding (1986) Monoclonal Antibodies: Principles and Practice
- 20 Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme
- 25 hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

- In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding
- 30 specificities for at least two different antigens or that have binding specificities for two

epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1A-13 or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to bladder cancer protein are capable of reducing or eliminating a biological function of a bladder cancer protein, as is described below. That is, the addition of anti-bladder cancer protein antibodies (either polyclonal or preferably monoclonal) to bladder cancer tissue (or cells containing bladder cancer) may reduce or eliminate the bladder cancer. Generally, at least about 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred, and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the bladder cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

- immunoglobulin. See Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596. Humanization can be performed, e.g., following the method of Winter and co-workers (see Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.
- 10 Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or of human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human
- 15 antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos.
- 20 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.
- 25 By immunotherapy is meant treatment of bladder cancer with an antibody raised against bladder cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient), which may be used to target a label or toxin. Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response
- 30 is the result of providing the recipient with an antigen to which antibodies are raised. As

appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

- 5 In a preferred embodiment the bladder cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted bladder cancer protein.

- 10 In another preferred embodiment, the bladder cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the bladder cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane bladder cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the bladder cancer protein. The antibody is also an antagonist of the bladder cancer protein. Further, the antibody prevents activation of the transmembrane bladder cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the bladder cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or
- 20 sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, bladder cancer is
- 25 treated by administering to a patient antibodies directed against the transmembrane bladder cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

- In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be a number of molecules, including labelling moieties such as
- 30 radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the

therapeutic moiety is a small molecule that modulates the activity of the bladder cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the bladder cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with bladder cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to bladder cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with bladder cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against bladder cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane bladder cancer proteins not only serves to increase the local concentration of therapeutic moiety in the bladder cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the bladder cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the bladder cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The bladder cancer antibodies of the invention specifically bind to bladder cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of bladder cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the bladder cancer phenotype. Expression levels of genes in normal tissue (e.g., not experiencing bladder cancer) and in bladder cancer tissue (and in some cases, for varying severities of bladder cancer that relate to prognosis, as outlined below), or in non-malignant disease, are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus bladder cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See Lockhart (1996) Nature Biotechnology 14:1675-1680.

Other techniques include, but are not limited to, quantitative reverse transcriptase PCR,

northern analysis and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from about 300-1000% being especially preferred.

5 Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the bladder cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass
10 spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to bladder cancer genes, e.g., those identified as being important in a bladder cancer or disease phenotype, can be evaluated in a bladder cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.
15 Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

20 In a preferred embodiment nucleic acids encoding the bladder cancer protein are detected. Although DNA or RNA encoding the bladder cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a bladder cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to,
25 oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method
30 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid

probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example, a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a bladder cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, bladder cancer proteins, including intracellular, transmembrane or secreted proteins, find use as diagnostic or prognostic markers of bladder cancer, or to assist in selecting therapy based on expression profile and archival data. Detection of these proteins in putative bladder cancer tissue allows for detection or diagnosis of bladder cancer. In one embodiment, antibodies are used to detect bladder cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the bladder cancer protein is detected, e.g., by immunoblotting with antibodies raised against the bladder cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the bladder cancer protein find use in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) "Antibodies in Cell Biology" Methods in Cell Biology (vol. 37). In this method cells are contacted with from one to many antibodies to the bladder cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable

label. In another method the primary antibody to the bladder cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of bladder cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing bladder cancer from blood, serum, plasma, stool, urine, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of bladder cancer proteins. Antibodies can be used to detect a bladder cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous bladder cancer protein.

In a preferred embodiment, in situ hybridization of labeled bladder cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including bladder cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to bladder cancer, clinical, pathological, or other information, e.g., in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, bladder cancer probes may

be attached to biochips for the detection and quantification of bladder cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR methods may provide more sensitive and accurate quantification.

5 Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression
10 profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids,
15 modified proteins and cells containing the native or modified bladder cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the bladder cancer phenotype or an identified physiological function of a bladder cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred
20 embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein
25 level. That is, having identified a particular gene as up regulated in bladder cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the bladder cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing bladder cancer, with changes of at least
30 about 10%, preferably about 50%, more preferably about 100-300%, and in some

embodiments about 300-1000% or greater. Thus, if a gene exhibits about 4-fold increase in bladder cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, about 10-fold decrease in bladder cancer tissue compared to normal tissue often provides a target value of about 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the bladder cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more bladder cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1A-13. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate bladder cancer, modulate bladder cancer proteins, bind to a bladder cancer protein, or interfere with the binding of a bladder cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the bladder cancer phenotype or the expression of a bladder cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter

expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a bladder cancer phenotype, e.g., to a normal tissue or non-malignant fingerprint. In another embodiment, a modulator induced a bladder cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than about 100 and less than about 2,500 daltons. Preferred small molecules are less than about 2000, or less than about 1500 or less than about 1000 or less than about 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl, or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a bladder cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a bladder cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88); peptoids (PCT Publication No WO 91/19735); encoded peptides (PCT Publication WO 93/20242); random bio-oligomers (PCT Publication WO 92/00091); benzodiazepines (U.S. Pat. No. 5,288,514); diversomers such as hydantoins, benzodiazepines, and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-6913); vinyllogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-6570); nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218); analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-2662); oligocarbamates (Cho, et al. (1993) Science 261:1303-1305); and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Strategene, Corp.); peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083); antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314, and PCT/US96/10287);

carbohydrate libraries (Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853); and small organic molecule libraries (see, e.g., benzodiazepines, Baum (p. 33, Jan 18, 1993) C&E News); isoprenoid (U.S. Patent No. 5,569,588); thiazolidinones and metathiazanones (U.S. Patent No. 5,549,974); pyrrolidines (U.S. Patent Nos. 5,525,735 and 5,519,134); morpholino compounds (U.S. Patent No. 5,506,337); benzodiazepines (U.S. Patent No. 5,288,514); and the like.

Devices for the preparation of combinatorial libraries are commercially available. See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; and 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Ru; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of bladder cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in

arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate nucleotide or amino acid substitutions. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the

length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of bladder cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag

or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the bladder cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a bladder cancer expression pattern leading to a normal expression pattern, or to modulate a single bladder cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated bladder cancer tissue reveals genes that are not expressed in normal tissue or bladder cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for bladder cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated bladder cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of bladder cancer cells, that have an associated bladder cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or

retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., bladder cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the bladder cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on bladder cancer activity. By defining such a signature for the bladder cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins" or a "bladder cancer modulatory protein". The bladder cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables 1A-13. Preferably, the bladder cancer modulatory protein is a fragment. In a preferred embodiment, the bladder cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the bladder cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has

an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the bladder cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the bladder cancer protein is conjugated to BSA.

Measurements of bladder cancer polypeptide activity, or of bladder cancer or the bladder cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the bladder cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of bladder cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian bladder cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a bladder cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the bladder cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the bladder cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the bladder cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein,

CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual
5 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins." The bladder cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown
10 herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate
15 differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products,
20 and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the bladder cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a bladder cancer protein and a candidate compound, and determining the binding of the compound to the bladder cancer protein. Preferred embodiments utilize the human bladder cancer protein,
25 although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative bladder cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the bladder cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated
30 sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the bladder cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the bladder cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the bladder cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the bladder cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., a bladder cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the bladder cancer protein and thus is capable of binding to, and potentially modulating, the activity of the bladder cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the bladder cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the bladder cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the bladder cancer proteins. In this embodiment, the methods comprise combining a bladder cancer protein and a competitor in a first sample. A second sample comprises a test compound, a bladder cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the bladder cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the bladder cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native bladder cancer protein, but cannot bind to modified bladder cancer proteins. The structure of the bladder cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a bladder cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a bladder cancer protein. The methods

comprise adding a test compound, as defined above, to a cell comprising bladder cancer proteins. Many different cell types may be transfected to contain a recombinant nucleic acid that encodes a bladder cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

5 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, and pharmacological agents including, e.g., chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In one example, the determinations are determined at different stages of the cell cycle process.

10 In this way, compounds that modulate bladder cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the bladder cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting bladder cancer cell division is provided. 15 The method comprises administration of a bladder cancer inhibitor. In another embodiment, a method of inhibiting bladder cancer is provided. The method comprises administration of a bladder cancer inhibitor. In a further embodiment, methods of treating cells or individuals with bladder cancer are provided. The method comprises administration of a bladder cancer inhibitor. In one embodiment, a bladder cancer inhibitor is an antibody as discussed above. 20 In another embodiment, the bladder cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are 25 transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify 30 modulators of bladder cancer sequences, which when expressed in host cells, inhibit

abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a bladder cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; Freshney (1994), *supra*). This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells. See, e.g., "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. See also, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer, Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate bladder cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1984), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (2000), supra.

Tumor growth in vivo

Effects of bladder cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the bladder cancer gene is disrupted or in which a bladder cancer gene is inserted. Knock-out

transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous bladder cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous bladder cancer gene with a mutated version of the bladder cancer gene, or by mutating the endogenous bladder cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be made. See Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a bladder cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of bladder cancer

Antisense and RNAi Polynucleotides

- In certain embodiments, the activity of a bladder cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a bladder cancer protein mRNA, or a subsequence thereof.
- 5 Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the bladder cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

- Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for bladder cancer molecules. A preferred antisense molecule is for a bladder cancer sequences in Tables 1A-13, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999)

Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of bladder cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes. See, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes.

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of bladder cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of bladder cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating bladder cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-bladder cancer antibody that reduces or eliminates the biological activity of an endogenous bladder cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a bladder cancer protein. This may be accomplished in many ways. In a preferred embodiment, e.g., when the bladder cancer sequence is down-regulated in bladder cancer, such state may be reversed by increasing the amount of bladder cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous bladder cancer gene or administering a gene encoding the bladder cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the bladder cancer sequence is up-regulated in bladder cancer, the activity of the endogenous bladder cancer gene is decreased, e.g., by the administration of a bladder cancer antisense nucleic acid.

In one embodiment, the bladder cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to bladder cancer proteins. Similarly, the bladder cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify bladder cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a bladder cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The bladder cancer antibodies may be coupled to standard affinity chromatography columns and used to purify bladder cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the bladder cancer protein.

Methods of identifying variant bladder cancer-associated sequences

Without being bound by theory, expression of various bladder cancer sequences is correlated with bladder cancer. Accordingly, disorders based on mutant or variant bladder cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant bladder cancer genes, e.g., determining all or part of the sequence of at least one endogenous bladder cancer genes in a cell. This may be accomplished using many sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the bladder cancer genotype of an individual, e.g.,

5 determining all or part of the sequence of at least one bladder cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced bladder cancer gene to a known bladder cancer gene, e.g., a wild-type gene.

- 10 The sequence of all or part of the bladder cancer gene can then be compared to the sequence of a known bladder cancer gene to determine if differences exist. This can be done using many known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the bladder cancer gene of the patient and the known bladder cancer gene correlates with a disease state or a propensity for a disease
- 15 state, as outlined herein.

In a preferred embodiment, the bladder cancer genes are used as probes to determine the number of copies of the bladder cancer gene in the genome.

- In another preferred embodiment, the bladder cancer genes are used as probes to determine the chromosomal localization of the bladder cancer genes. Information such as
- 20 chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the bladder cancer gene locus.

Administration of pharmaceutical and vaccine compositions

- 25 In one embodiment, a therapeutically effective dose of a bladder cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug
- 30 Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker,

ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharma. Assn.; and Pickar (1999) Dosage Calculations Thomson. As is known in the art, adjustments for bladder cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. USSN 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in bladder cancer and is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the bladder cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the bladder cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a bladder cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that bladder cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a bladder cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary

widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics McGraw-Hill.

5 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1-10 mg per patient per day. Dosages from about 0.1-100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
10 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman: The Pharmacological Basis of Therapeutics, supra.

The compositions containing modulators of bladder cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications,
15 compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered
20 depending on the dosage and frequency as required and tolerated by the patient. The composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition
25 and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies
30 may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present bladder cancer protein-modulating compounds can be administered alone or in combination with additional bladder cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1A-13, such as antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of bladder cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols in Molecular Biology Lippincott; and Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, bladder cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, bladder cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the bladder cancer coding regions) can be administered in a gene therapy application. These bladder cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Bladder cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (Vitiello, et al. (1995) J. Clin. Invest. 95:341-349); peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres

- (Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681); peptide compositions contained in immune stimulating complexes (ISCOMS) (Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243); multiple antigen peptide systems (MAPs) (Tam 5 (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32); peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-547; Kieny, et al. (1986) AIDS 10 BioTechnology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle 15 absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, 20 also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc., Needham, MA, may also be used.

- Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or 25 *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated 30 tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et al. (1990) Science 247:1465-1468 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode bladder cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a bladder cancer gene or portion of a bladder cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a bladder cancer patient. The bladder cancer gene used for DNA vaccines can encode full-length bladder cancer proteins, but more preferably encodes portions of the bladder cancer proteins including peptides derived from the bladder cancer protein. In one embodiment, a patient is immunized with a

DNA vaccine comprising a plurality of nucleotide sequences derived from a bladder cancer gene. For example, bladder cancer-associated genes or sequence encoding subfragments of a bladder cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the bladder cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment bladder cancer genes find use in generating animal models of bladder cancer. When the bladder cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the bladder cancer gene will also diminish or repress expression of the gene. Animal models of bladder cancer find use in screening for modulators of a bladder cancer-associated sequence or modulators of bladder cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the bladder cancer protein. When desired, tissue-specific expression or knockout of the bladder cancer protein may be necessary.

It is also possible that the bladder cancer protein is overexpressed in bladder cancer. As such, transgenic animals can be generated that overexpress the bladder cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of bladder cancer and are additionally useful in screening for modulators to treat bladder cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include one or more of the following: assay reagents, buffers, bladder cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense or inhibitory polynucleotides, ribozymes, dominant negative bladder cancer polypeptides or polynucleotides, small molecules inhibitors of bladder cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of bladder cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a bladder cancer-associated polypeptide or polynucleotide, control positive or negative samples, reaction tubes, and instructions for testing bladder cancer-associated activity. Optionally, the kit contains biologically active bladder cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described

- 5 (Glynn, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE DESCRIPTIONS

- 10 Table 1A shows about 3413 that exhibit increased or decreased expression in bladder cancer samples. See USSN 60/302,814.

Table 2A shows about 485 genes overexpressed in bladder tumors relative to normal tissues as analyzed using the Affymetrix/Eos Hu03 GeneChip array. See USSN 60/343,705.

- 15 Table 3A shows about 414 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as small molecule, antibody, DNA vaccine targets for the therapy of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the
20 relative level of mRNA expression.

- Table 4A shows about 129 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as diagnostics of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for
25 each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

- Table 5A shows about 149 genes upregulated in bladder cancer relative to normal body tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03
30 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

- Table 6A shows about 199 genes upregulated in bladder cancer relative to normal bladder
35 tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

- 40 Table 7A shows about 63 genes downregulated in bladder tumors relative to normal bladder. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip

array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Table 8A shows about 1440 genes upregulated in Ta or T1 bladder tumors from patients who later presented with muscle-invasive bladder tumors (stage T2-T4). Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

10 Table 9A shows about 1200 genes upregulated in Ta or T1 tumors of patients who later presented with either more Ta tumors or no tumors at all. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Table 10A shows about 65 genes upregulated in non-invasive exophytic Ta bladder tumors relative to T2-T4 muscle-invasive tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

20 Table 11A shows about 106 genes upregulated in muscle-invasive T2-T4 bladder tumors relative to non-invasive exophytic Ta bladder tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

25 Table 12A shows the Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 13. Seq ID No. is used to link Table 12A to table 13.

30 Tables 1B-12B show the accession numbers for those Pkey's lacking UnigeneID's for tables 1A -12A, respectively. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Tables 1C-12C show genomic positioning for Pkey's lacking Unigene ID's and accession numbers for tables 1A -12A, respectively. For each predicted exon, is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

40 TABLE 1A:

45	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	please refer to original application
	R2:	please refer to original application
	Target Type:	downregulate stage if target is downregulated in bladder tumors relative to normal bladder or

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early stage if target is an earl stage (Ta) bladder tumor marker or
late stage if target is a late stage (T2-T4) bladder tumor marker or
T2-T4 grade 3 papiloma marker or T2-T4 grade 3 solid tumor marker or Upregulate stage

	Protein	Accession	UniProt ID	UniProt Title	R1	R2	Target Type
5	P18440	X83967	Hs.83370	nebulin	0.17	2.05	downregulate stage
	Q08888				0.24	1.87	downregulate stage
	Q01666				0.19	4.06	downregulate stage
	Q01669				0.2	2.05	downregulate stage
10	Q01691				0.04	10.13	downregulate stage
	Q01905				0.3	1.87	downregulate stage
	Q02076				0.06	6.51	downregulate stage
	Q02110				0.43	2.35	downregulate stage
15	Q02271	NM_002197	Hs.154721	acetylase 1, soluble	0.21	2.16	downregulate stage
	Q03362				0.18	4.44	downregulate stage
	Q03687				0.32	1.91	downregulate stage
	Q03692				0.14	2.27	downregulate stage
	Q04015				0.2	2.48	downregulate stage
	Q04059				0.36	1.84	downregulate stage
20	Q04152				0.32	1.85	downregulate stage
	Q04436				0.14	2.18	downregulate stage
	Q04819				0.19	5.25	downregulate stage
	Q05001	U58196	Hs.295281	Interleukin enhancer binding factor 1	0.16	2.92	downregulate stage
	Q05349				0.18	3.8	downregulate stage
25	Q05390				0.3	2.54	downregulate stage
	Q05735				0.13	2.44	downregulate stage
	Q05968				0.28	1.85	downregulate stage
	Q08017				0.32	2.28	downregulate stage
	Q06305	BE261320	Hs.297096	transcriptional adaptor 3 (ADA3, yeast)	0.42	1.83	downregulate stage
30	Q06320				0.37	2.01	downregulate stage
	Q06704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.3	2.04	downregulate stage
	Q06706	X00740	Hs.231581	myosin, heavy polypeptide 1, skeletal mus	0.14	7.4	downregulate stage
	Q06707	S73840	Hs.351	myosin, heavy polypeptide 2, skeletal mus	0.05	12.51	downregulate stage
35	Q07013	X13637		gelsolin nebulin m94A, partial cds	0.14	2.17	downregulate stage
	Q07245	X00693	Hs.172004	filin	0.02	15.21	downregulate stage
	Q07330	AA82807		glb1n1105.s1 MCLCGAP_Ki68 Homo sapiens	0.42	1.57	downregulate stage
	Q07571	AA446183	Hs.9572	ESTs	0.38	2.13	downregulate stage
	Q07682	AL033593	Hs.3807	FXVD domain-containing ion transport reg	0.34	2.56	downregulate stage
40	Q07815	AW373893	Hs.301718	ESTs	0.31	2.44	downregulate stage
	Q07834	AW984991	Hs.26100	ESTs	0.15	2.98	downregulate stage
	Q07991	AA496020	Hs.41135	endomucin-2	0.15	3.33	downregulate stage
	Q07906	AA369685	Hs.41185	Homo sapiens m94A; cDNA DKFp664C1252 (f	0.12	3.05	downregulate stage
	Q07936	AA369697	Hs.60600	phospholamban	0.08	8.77	downregulate stage
	Q07965	W21483	Hs.41707	heal shock 2740 protein 3	0.26	2.29	downregulate stage
45	Q08009	AF020498	Hs.41735	purinergic receptor P2X, ligand-gated io	0.49	1.91	downregulate stage
	Q08139	AA451986	Hs.43005	RA29A-like protein	0.41	1.88	downregulate stage
	Q08221	AA312183	Hs.47447	ESTs	0.04	24.1	downregulate stage
	Q08374	AW025453	Hs.155591	forkhead box F1	0.35	2.35	downregulate stage
50	Q08453	BE206854	Hs.69039	phosphoglycerate mutase 2 (muscle)	0.09	9.04	downregulate stage
	Q08508	A1806109	Hs.135736	KAA1580 protein	0.45	2.2	downregulate stage
	Q08614	AL137839	Hs.46531	Homo sapiens m94A; cDNA DKFp34C4C1915 (f	0.13	5.48	downregulate stage
	Q08652	R43409	Hs.9629	ESTs	0.33	2.5	downregulate stage
	Q08713	AA337192	Hs.47438	S/S domain binding glutamic acid-rich pr	0.05	6.94	downregulate stage
	Q08936	A1810447	Hs.42778	niban protein	0.39	2.01	downregulate stage
55	Q09227	T06558	Hs.156880	ESTs	0.18	2.75	downregulate stage
	Q10023	AB017169	Hs.57929	slt (Drosophila) homolog 3	0.07	27	downregulate stage
	Q10036	R57171	Hs.57975	calyculin 2, cardiac muscle	0.59	5.23	downregulate stage
	Q10132	NM_003480	Hs.58882	Microtubulin-associated glycoprotein-2	0.24	2.34	downregulate stage
	Q10168	AW834050	Hs.3973	tensin	0.39	2.17	downregulate stage
60	Q10243	D83402	Hs.289006	ESTs, Weakly similar to alternatively sp	0.11	2.02	downregulate stage
	Q10339	AB016499	Hs.290518	ESTs	0.15	2.16	downregulate stage
	Q10577	NM_003278	Hs.66424	tetranectin (plasminogen binding protein	0.22	2.65	downregulate stage
	Q10868	T06529	Hs.98518	Homo sapiens cDNA FLJ11490 fs, clone HE	0.2	2.74	downregulate stage
	Q11048	AK001742	Hs.67991	hypothetical protein DKFp34C4C0522	0.2	1.92	downregulate stage
65	Q11067	AB81006	Hs.301543	ESTs	0.11	3.41	downregulate stage
	Q11069	AL133032	Hs.68055	hypothetical protein DKFp34C4C0428	0.17	5.8	downregulate stage
	Q11644	H22064	Hs.301548	ESTs	0.06	13.8	downregulate stage
	Q11741	AW839650		gbr/RCO-CT0359-071299-011-d03 CT0358 Homo	0.35	2.5	downregulate stage
	Q12047	AA934589	Hs.49986	ESTs	0.18	3.57	downregulate stage
70	Q12095	AB024707	Hs.8521	Homo sapiens cDNA FLJ11592 fs, clone C	0.32	1.89	downregulate stage
	Q12389	AW947655		gbr/RCO-MTC003-040C0-031-b07 MTC003 Homo	0.38	2.6	downregulate stage
	Q12442	A983730	Hs.26530	serum deprivation response (phosphatidyl	0.12	3.67	downregulate stage
	Q12519	AA196241	Hs.73980	integrin T1, skeletal, slow	0.24	1.86	downregulate stage
	Q12622	AW864708	Hs.171869	ESTs	0.05	5.45	downregulate stage
75	Q12649	NM_002206	Hs.73469	integrin, alpha 7	0.29	2.96	downregulate stage
	Q12659	AW753965	Hs.74376	oligodendrocyte related ER localized protei	0.18	2.06	downregulate stage
	Q12758	Y07818	Hs.74566	dihydropyrimidinase-like 3	0.3	2.23	downregulate stage

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412802	U41518	Hs.74802	aquaporin 1 (channel-forming integral pr	0.11	2.71	downregulate stage
412975	T70556	Hs.75106	cleistrolin (complement lytic inhibitor, S	0.44	2.03	downregulate stage
413074	A071368	Hs.8417	ESTs	0.47	1.91	downregulate stage
413272	AA127923	Hs.293265	ESTs	0.06	4.44	downregulate stage
413276	ZW4775	Hs.75260	mlgag inducible 2	0.23	2.48	downregulate stage
413508	BE145354		gblc.LH0119-151099-125-e05 HIT0188	0.31	2.53	downregulate stage
413624	BE177019	Hs.75445	SPARC-like 1 (nestin, hevin)	0.33	2.17	downregulate stage
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	0.33	2.83	downregulate stage
414065	H27694	Hs.75745	apoptogenin D	0.42	1.85	downregulate stage
414241	AA423065	Hs.4007	Sarcolemmal-associated protein	0.16	2.22	downregulate stage
414290	AA568801	Hs.71721	ESTs	0.02	10	downregulate stage
414629	AA345824	Hs.78688	carboxylesterase 1 (monocyte/macrophage	0.13	4.14	downregulate stage
414657	AA424074	Hs.78750	protein phosphatase 1, regulatory (mito	0.33	2.14	downregulate stage
414712	N89859	Hs.77039	ribosomal protein S3A	0.4	2.5	downregulate stage
414903	AA451700	Hs.85835	Homo sapiens cDNA: FLJ22641 fa, clone K	0.3	3.3	downregulate stage
415165	AW867604	Hs.78065	complement component 7	0.04	3.41	downregulate stage
415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	0.32	3.29	downregulate stage
41547	ZPT711	Hs.74454	myosin, trabecular meshwork inducible	0.12	6.55	downregulate stage
415672	N53007	Hs.193679	ESTs	0.28	3.55	downregulate stage
415934	NVL_000928	Hs.992	phospholipase A2, group IB (pancreas)	0.34	2.64	downregulate stage
416127	N49843	Hs.79022	GTP-binding protein overexpressed in sks	0.3	1.98	downregulate stage
416349	XB0689	Hs.79277	myomesin (titin-protein) 2 (titin2)	0.41	1.96	downregulate stage
416555	X54162	Hs.79386	telomerase 1 (smooth muscle)	0.02	49.3	downregulate stage
416854	H40164	Hs.80296	Purkinje cell protein 4	0.02	76.5	downregulate stage
416941	BE000150	Hs.48778	citrate kinase, mitochondrial 2 (succinat	0.27	2.18	downregulate stage
416952	J05401	Hs.80691	alanine kinase, mitochondrial 2 (succinat	0.29	2.43	downregulate stage
417011	F08212	Hs.25498	ESTs	0.41	2.68	downregulate stage
417258	AW669539	Hs.37958	ESTs	0.27	3.7	downregulate stage
417501	AL041219	Hs.82222	sera domain, immunoglobulin domain (Ig)	0.39	2.08	downregulate stage
417553	L08190	Hs.82276	trichostatin	0.29	2.59	downregulate stage
417867	A1210272	Hs.50153	ESTs	0.22	2.09	downregulate stage
418257	R01254		gby94e12.1 Sources fetal liver spleen	0.28	1.9	downregulate stage
418332	R34976	Hs.78293	ESTs	0.2	3.9	downregulate stage
418391	NM_003281	Hs.84673	tropoin 1, skeletal, slow	0.35	2.02	downregulate stage
418495	AA115332	Hs.130669	ESTs, Weakly similar to AF062522 1 refi	0.21	3.9	downregulate stage
418421	R58200	Hs.85050	g-phosphatidyl	0.2	2.08	downregulate stage
418499	U79421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.05	21.55	downregulate stage
418533	NM_004333	Hs.85537	myosin-binding protein C, fast-type	0.42	1.95	downregulate stage
418787	AW286134	Hs.88999	ESTs	0.68	1.87	downregulate stage
419165	AW382937	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	0.26	2.43	downregulate stage
419547	W52990	Hs.22890	ESTs	0.13	7.18	downregulate stage
419307	R39995	Hs.7894	ESTs	0.27	2	downregulate stage
419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFp5881524 (f	0.19	5.25	downregulate stage
419555	AW139550	Hs.115173	ESTs	0.31	2.59	downregulate stage
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	0.28	3.38	downregulate stage
419685	W76063	Hs.173077	ESTs	0.4	2.21	downregulate stage
419703	AJ79257	Hs.128161	ESTs	0.09	3.62	downregulate stage
419942	U25138	Hs.93841	potassium large conductance calcium-act	0.28	2.96	downregulate stage
420056	AK001423	Hs.94494	Homo sapiens cDNA FLJ115961 fa, clone NT	0.3	2.09	downregulate stage
420165	N44348	Hs.300794	ESTs	0.22	2.79	downregulate stage
420261	AW206093	Hs.748	fibroblast growth factor receptor 1 (fms	0.35	1.96	downregulate stage
420274	NM_000055	Hs.1327	butyrylcholinesterase	0.29	3.5	downregulate stage
421296	NM_002666	Hs.100253	perlecan	0.36	2.11	downregulate stage
421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDN	0.13	4.3	downregulate stage
421763	AW163600	Hs.109080	cysteine and glycine-rich protein 1	0.26	3.49	downregulate stage
421855	AL117472	Hs.108524	DNF2P58BP1422 protein	0.14	5	downregulate stage
421953	AA094330	Hs.111878	protein kinase H11; small class protein	0.2	2.29	downregulate stage
422067	F16365	Hs.114348	cytochrome c oxidase subunit I/Va polype	0.27	2.58	downregulate stage
422320	A1745248	Hs.236550	ESTs, Weakly similar to AAB47496 NGS (H	0.24	2.95	downregulate stage
422533	AW56632	Hs.118904	enolase 3 (beta, muscle)	0.23	3.67	downregulate stage
422589	AB29287	Hs.173724	creatine kinase, brain	0.39	1.97	downregulate stage
423534	AF000006	Hs.127293	hypothetical protein FLJ11044	0.37	2.29	downregulate stage
423587	AA328074	Hs.284296	hypothetical protein FLJ14033 similar to	0.37	2.47	downregulate stage
423889	AL035447	Hs.134594	hypothetical protein LOC57158	0.24	2.43	downregulate stage
424181	AL039482	Hs.142577	Homo sapiens mRNA; cDNA DNF2p434F0810 (f	0.27	2.28	downregulate stage
424206	NM_003324	Hs.188241	androgen oxidase, copper containing 3 (vnc	0.3	2.58	downregulate stage
424479	AF064238	Hs.149038	smoothelin	0.26	3.29	downregulate stage
424580	AA446539	Hs.35092	ESTs	0.15	2.57	downregulate stage
424846	AU077324	Hs.1832	neuropilin-1, Y	0.4	2.84	downregulate stage
424938	NM102637	Hs.242323	ESTs	0.29	2.16	downregulate stage
424982	U94777	Hs.154084	phosphorylase, glycogen; muscle (McArdle	0.42	1.89	downregulate stage
425383	D83407	Hs.155007	Down syndrome critical region gene 1-like	0.14	1.86	downregulate stage
425545	N86529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	0.03	13.25	downregulate stage
425622	AW368847	Hs.13578	ESTs	0.3	1.9	downregulate stage
425751	T19239	Hs.1940	crystallin, alpha B	0.47	1.92	downregulate stage
425889	AA524547	Hs.190319	FXD domain-containing ion transport reg	0.45	1.85	downregulate stage
425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DNF2p588N020 (f	0.19	2.85	downregulate stage

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5	425932	M81650	Hs.1968	semenogelin I	0.02	15.3	downregulate stage
	425934	NM_004010	Hs.165470	dystrophin (muscular dystrophy, Duchenne)	0.27	2.52	downregulate stage
	425949	X73114	Hs.195849	myosin-binding protein C, slow-type	0.1	10.3	downregulate stage
	425752	X95490	Hs.172054	Rfa	0.03	31.3	downregulate stage
	425809	BE31114	Hs.787016	ESTs	0.34	2.85	downregulate stage
	427076	A0576062	Hs.111902	ESTs	0.22	2.11	downregulate stage
	427136	AL17415	Hs.173716	Homo sapiens mRNA; cDNA DKFZp434K0521 (f	0.37	2.33	downregulate stage
	427154	AB337271	Hs.173971	KUAF1300 protein	0.12	5.47	downregulate stage
	427165	AA398530	Hs.166274	ESTs	0.27	4.65	downregulate stage
	427373	AG070972	Hs.177533	Homo sapiens mRNA; cDNA DKFZp689N0316 (f	0.22	3.18	downregulate stage
15	427393	AB029018	Hs.177535	KUAF1095 protein	0.27	2.13	downregulate stage
	427565	AF134803	Hs.180141	cofilin 2 (muscle)	0.05	4	downregulate stage
	427575	AA394052	Hs.180266	tropomyosin 2 (beta)	0.45	1.57	downregulate stage
	427686	AA470398	Hs.137598	ESTs	0.38	2.04	downregulate stage
	427980	AA418305		glucy96g05.s1 Soares_NIHMPu_S1 Homo sapi	0.32	2.39	downregulate stage
	428087	AA100573	Hs.182421	ironicun C2, fast	0.17	4.37	downregulate stage
	428138	AA773842	Hs.253799	ESTs	0.45	2.2	downregulate stage
	428221	U97591	Hs.183576	ESTs, Highly similar to Ca2+-ATPase of f	0.29	3.26	downregulate stage
	428329	AA426091	Hs.98453	ESTs	0.21	2.09	downregulate stage
	428409	AW117207	Hs.98523	ESTs	0.1	7.63	downregulate stage
20	428491	AW291454	Hs.10338	potassium voltage-gated channel, subunit	0.32	1.98	downregulate stage
	428548	AF552728	Hs.180221		0.09	2.99	downregulate stage
	428549	AL045715	Hs.188228	Homo sapiens cDNA FLJ11003 f1, clone PL	0.11	2.07	downregulate stage
	428699	AA744610	Hs.194431	paladin	0.42	1.84	downregulate stage
	429350	AW54534	Hs.131987	ectonucleoside triphosphate diphosphohyd	0.06	4.73	downregulate stage
	429525	N92540	Hs.203353	lymphocyte antigen 5 complex, locus E	0.18	2.51	downregulate stage
	429545	AB241384	Hs.77657	myosin, light polypeptide kinase	0.31	2.07	downregulate stage
	429555	U49559	Hs.211582	myosin I (skelemin) (189kd)	0.33	2.18	downregulate stage
	429892	NM_003803	Hs.2504	myosin I (skelemin) (189kd)	0.35	2.17	downregulate stage
	429930	AI90809	Hs.99569	ESTs	0.15	5.5	downregulate stage
30	429956	A374951	Hs.22542	ESTs	0.22	4.45	downregulate stage
	430013	AA493833	Hs.151275	ESTs	0.21	3.03	downregulate stage
	430271	T08199	Hs.237505	heat shock cognate 40	0.47	1.55	downregulate stage
	430310	U30115	Hs.239059	four and a half LIM domains 1	0.18	3.44	downregulate stage
	430416	R08593	Hs.363059	heart and neural crest derivatives target	0.59	2.26	downregulate stage
	430589	AW698847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	0.15	2.52	downregulate stage
	430712	AW045457	Hs.199284	ESTs	0.29	1.94	downregulate stage
	430778	D90337	Hs.247916	neutrophil peptide precursor C	0.14	4.48	downregulate stage
	430998	AF125847	Hs.204038	Indolethylamine N-methyltransferase	0.35	1.87	downregulate stage
	432247	AAS31397	Hs.105905	ESTs	0.21	1.99	downregulate stage
40	432659	AB018320	Hs.278626	Auq/Abi-interacting protein ArgBP2	0.11	1.98	downregulate stage
	432792	AA448114	Hs.278550	procalcitonin beta 1	0.22	2.93	downregulate stage
	433142	AL120597	Hs.110540	ESTs	0.21	1.18	downregulate stage
	433533	AB065919	Hs.94530	ESTs	0.54	2.57	downregulate stage
	433588	AA528467	Hs.112572	Homo sapiens cDNA FLJ14130 f1, clone MA	0.35	2.27	downregulate stage
	433626	AA609938	Hs.144492	ESTs	0.24	1.91	downregulate stage
	434025	AF114254	Hs.216381	Homo sapiens clone FH409 unknown mRNA	0.07	3.46	downregulate stage
	434160	BE551195	Hs.114275	ESTs	0.5	2	downregulate stage
	434362	AF129505	Hs.91692	small muscle protein, X-linked	0.34	2.13	downregulate stage
	434361	AF129755	Hs.117772	ESTs	0.03	31.3	downregulate stage
50	435731	AA699581	Hs.188811	ESTs	0.31	3.25	downregulate stage
	435869	AF259910	Hs.94550	vascular endothelial junction-associated	0.21	3.73	downregulate stage
	435978	AF723899	Hs.135118	Homo sapiens PIV-domain zinc finger prote	0.55	2.25	downregulate stage
	436359	Z83505		gbr14.sapiens mRNA for ancestral dyx16	0.24	3.28	downregulate stage
	436638	A1271945	Hs.134984	ESTs	0.35	1.87	downregulate stage
	436953	AW959074	Hs.23548	Homo sapiens cDNA FLJ13097 f1, clone NT	0.14	6.35	downregulate stage
	437115	AW179809	Hs.42346	calcitonin-binding protein calcitonin-1	0.32	2.19	downregulate stage
	437233	D81449	Hs.153961	ARPI (actin-related protein 1, yeast)	0.27	2.58	downregulate stage
	438619	AB027273	Hs.8341	TUJ2B1-TY protein	0.19	2.69	downregulate stage
	438695	AW014493	Hs.129727	ESTs	0.15	1.98	downregulate stage
60	439231	AW591335	Hs.114480	ESTs	0.1	3.9	downregulate stage
	439673	A733308	Hs.124653	ESTs	0.15	6.2	downregulate stage
	440172	AA869584	Hs.126154	ESTs	0.24	2.34	downregulate stage
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.11	3.02	downregulate stage
	440637	AL080272	Hs.7058	hypothetical protein FLJ13110	0.19	2.95	downregulate stage
	440700	AW852281	Hs.169184	ESTs, Highly similar to GRP1_HUMAN GUAN	0.19	2.69	downregulate stage
	440737	A531757	Hs.133221	Homo sapiens cDNA FLJ12401 f1, clone MA	0.5	2	downregulate stage
	441805	AA285136	Hs.7974	neuronal specific transcription factor D	0.07	13.55	downregulate stage
	441959	A733385	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.38	1.86	downregulate stage
	442169	BE218975	Hs.272395	ESTs	0.24	2.86	downregulate stage
70	442985	A020994	Hs.154027	ESTs	0.19	2	downregulate stage
	443090	Z78674	Hs.8914	procollagen C-endopeptidase enhancer 2	0.09	3.66	downregulate stage
	443164	A038503	Hs.55780	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.2	1.86	downregulate stage
	443476	AW806594	Hs.133878	ESTs, Weakly similar to AF151891 I CG-1	0.11	2.79	downregulate stage
	443594	CD3577	Hs.9515	myosin regulatory light chain 2, smooth	0.24	3.4	downregulate stage
	443790	NM_003500	Hs.9795	acyl-CoA:cholesterol oxidase 2, branched chain	0.28	3.6	downregulate stage
	443932	AW888222	Hs.9973	brassin	0.32	2.57	downregulate stage

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5	444195	AB002351	Hs.10567	KIA0353 protein	0.19	4.04	downregulate stage
	444484	AK002126	Hs.11760	hypothetical protein FLJ111264	0.38	2.04	downregulate stage
	444684	AW044070	Hs.147037	ESTs	0.36	2.25	downregulate stage
	444793	U52201	Hs.11550	oxidative 3 alpha hydroxysteroid dehydro	0.29	2.19	downregulate stage
	444938	AW047090	Hs.148144	ESTs	0.43	2.3	downregulate stage
10	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	0.13	2.64	downregulate stage
	445235	AB040222	Hs.132207	ESTs	0.13	2.4	downregulate stage
	445621	AF733918	Hs.145549	ESTs	0.25	1.91	downregulate stage
	445687	W50382	Hs.145927	ESTs	0.2	3.5	downregulate stage
	445650	AI282049	Hs.145560	ESTs	0.53	1.9	downregulate stage
15	446406	AB53691	Hs.25243	ESTs	0.07	3.25	downregulate stage
	446500	U79093	Hs.15154	anti-H-sepal-containing protein, X chrom	0.33	1.9	downregulate stage
	447695	AW379130	Hs.16563	phosphodiesterase 9A	0.28	1.85	downregulate stage
	447918	AI129320	Hs.16930	ESTs	0.29	2.46	downregulate stage
	448076	AF131123	Hs.20196	adenylyl cyclase 9	0.2	2.27	downregulate stage
20	448263	AB340462	Hs.162979	ribosomal protein L12	0.53	1.9	downregulate stage
	448303	BE602466	Hs.11524	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.39	1.84	downregulate stage
	448426	AB00389	Hs.233401	ESTs	0.16	1.97	downregulate stage
	448429	D17406	Hs.21223	calpain 1, basic, smooth muscle	0.12	5.43	downregulate stage
	448655	AB36997	Hs.159863	ESTs	0.32	2.86	downregulate stage
25	449301	AK001021	Hs.22805	hypothetical protein FLJ101619	0.17	2.86	downregulate stage
	449319	AF119274	Hs.22791	intermembrane protein with EGF-like and	0.24	1.86	downregulate stage
	449226	AB002365	Hs.23311	KIA0357 protein	0.1	4.96	downregulate stage
	449238	AA422229	Hs.55824	muscle-specific RING-finger protein homo	0.14	2.63	downregulate stage
	449422	AA001373	Hs.59521	ESTs	0.43	2.3	downregulate stage
30	449690	AA002140	Hs.33824	ESTs	0.5	2	downregulate stage
	449874	AA138866	Hs.10065	ESTs	0.53	2.7	downregulate stage
	449925	AB342493	Hs.24192	Homo sapiens cDNA: FLJ20767 fls, clone CO	0.11	5.57	downregulate stage
	450300	AL041440	Hs.58210	ESTs	0.41	2.13	downregulate stage
	450578	AF971773	Hs.232258	ESTs	0.44	2.25	downregulate stage
35	450810	BE207355	Hs.2551	transforming growth factor: beta 1 induce	0.51	1.86	downregulate stage
	450831	R37974	Hs.25255	ESTs	0.23	1.96	downregulate stage
	451331	AK002039	Hs.25243	Homo sapiens cDNA: FLJ11177 fls, clone PL	0.37	2.16	downregulate stage
	451533	NM_004657	Hs.26830	serum deprivation response (phosphatidyl)	0.1	9.36	downregulate stage
	451712	AF233565	Hs.27016	fls	0.35	2.43	downregulate stage
40	451948	AW045473	Hs.211126	ESTs	0.43	1.88	downregulate stage
	452422	AA521418	Hs.22701	ESTs	0.41	1.85	downregulate stage
	452463	R38452	Hs.300817	ESTs	0.09	4.05	downregulate stage
	452776	AK194540	Hs.13522	ESTs	0.36	2.16	downregulate stage
	452814	AB922790	Hs.55019	hypothetical protein FLJ21535	0.06	4.7	downregulate stage
45	453064	RA0334	Hs.301395	Homo sapiens cDNA: FLJ21204 fls, clone C	0.07	4.47	downregulate stage
	453351	AB257271	Hs.61814	Homo sapiens cDNA: FLJ2750 fls, clone K	0.33	3.05	downregulate stage
	453365	AW295374	Hs.31412	Homo sapiens cDNA: FLJ11422 fls, clone HE	0.03	7.14	downregulate stage
	453389	AA447617	Hs.24272	ESTs, Weakly similar to acetic carboxy	0.4	1.92	downregulate stage
	453454	AB594111	Hs.32959	receptor (calcitonin) activity modifying	0.24	3.29	downregulate stage
50	453500	AA76427	Hs.43125	ESTs	0.02	11.41	downregulate stage
	453652	AW564339	Hs.33476	hypothetical protein FLJ11937	0.39	2.04	downregulate stage
	453856	AA241020	Hs.50511	ESTs, Weakly similar to tyfua1 (Mmus)	0.43	1.85	downregulate stage
	453866	AW015661	Hs.135229	ESTs, Moderately similar to AF107203.1 a	0.26	2.42	downregulate stage
	453896	AA037615	Hs.42746	ESTs	0.2	1.88	downregulate stage
55	453702	AA037637	Hs.42126	ESTs	0.32	2.42	downregulate stage
	453725	W26543		gtx-405 Human retina cDNA randomly prime	0.2	2.06	downregulate stage
	453860	AA158996	Hs.211565	calcaynase transduction initiation factor	0.07	7.86	downregulate stage
	454076	AA01516	Hs.22209	secreted modular calcium-binding protein	0.16	2.49	downregulate stage
	454471	AW902125		gtx:QV0-NH1022-120500-220-b12 NH1022 Homo	0.41	2.45	downregulate stage
60	454537	AW611613		gtx:QV0-S10157-300999-017408 S10157 Homo	0.16	2.2	downregulate stage
	454750	AW982616		gtx:QV0-S10024-090406-167-a01 S10024 Homo	0.49	2.05	downregulate stage
	455073	AW854629		gtx:QV2-CT0261-301099-011401 CT0261 Homo	0.27	2.09	downregulate stage
	455455	AA102267	Hs.26756	Homo sapiens cDNA: FLJ20896 fls, clone A	0.32	2.07	downregulate stage
	455611	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	0.15	2.67	downregulate stage
65	456100	AB363961	Hs.109114	ESTs	0.2	2.5	downregulate stage
	456411	AA075083	Hs.157345	calcifolius receptor-related 1 (hnpocvir	0.35	1.9	downregulate stage
	457064	AA776743	Hs.191559	ESTs	0.17	2.34	downregulate stage
	457103	N74724	Hs.108473	ESTs	0.46	2.1	downregulate stage
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	0.29	2.59	downregulate stage
70	457625	T10071		gtx:QV2193-b4E3MA ColB-HAP-F1 Homo sapi	0.29	3.45	downregulate stage
	458482	AW648858	Hs.29485	ESTs	0.26	2.17	downregulate stage
	459622	AA372412	Hs.13755	Fbox and WD-40 domain protein 2	0.51	1.95	downregulate stage
	459841	W27965		gtx:54310 Human retina cDNA randomly prim	0.32	3.1	downregulate stage
	459937	AW439497	Hs.290958	EST	0.43	2.35	downregulate stage
75	460062				0.71	0.1	early stage
	460937				1.2	0.26	early stage
	460977				0.63	0.48	early stage
	461024				0.8	0.3	early stage
	461048				1.9	0.22	early stage
	461537				1.3	0.2	early stage
	461619				3.5	0.19	early stage

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5	402089			0.39	0.55	early stage
	402179			0.36	0.91	early stage
	402407			0	0.15	early stage
	402435			0.28	1.25	early stage
	402456			2.15	0.21	early stage
10	402622			1.8	0.14	early stage
	402646			0.17	1.55	early stage
	402654			0.41	0.86	early stage
	402716			0.14	0.85	early stage
	402846			0.61	0.52	early stage
15	402922			0.14	0.83	early stage
	403667			0.44	0.49	early stage
	403950			1	0.34	early stage
	404338			0.49	0.44	early stage
	404345	AAT30407	Hs.159156	0.38	0.4	early stage
20	404801	AW247252	Hs.75514	0.32	0.8	early stage
	404944			0.37	0.91	early stage
	404874			1.87	0.29	early stage
	404881			0.36	0.5	early stage
	404896	NM_000429	Hs.106845	1	0.36	early stage
25	404939	UB5198	Hs.256281	0.18	1.06	early stage
	405371			0.19	0.77	early stage
	405308			0.4	0.55	early stage
	405483			0.41	1	early stage
	405580			1.89	0.19	early stage
30	405606			0.22	0.63	early stage
	405720			0.37	0.61	early stage
	405863			0.53	0.26	early stage
	405867			0.24	1.1	early stage
	405920			0.38	1.15	early stage
35	406236			2.16	0.17	early stage
	406243			0.32	1.23	early stage
	406367			0.38	0.76	early stage
	406834	A031880		0.4	0.67	early stage
	406881	C18154		0.44	1.55	early stage
40	407411	AF060170		0.39	0.69	early stage
	407639	AW205599	Hs.252636	0.61	0.34	early stage
	408112	AW451082	Hs.248613	0.2	0.54	early stage
	408732	AL117490	Hs.47225	1	0.32	early stage
	409103	AF291237	Hs.112230	0.33	1.03	early stage
45	409400	AW502122		0.56	0.28	early stage
	410128	AW904589		1.26	0.37	early stage
	411474	AW814827		1	0.14	early stage
	412664	X55753	Hs.74019	0.36	0.44	early stage
	413266	BE300352		1.46	0.25	early stage
50	413341	H78472	Hs.191325	0.41	0.48	early stage
	414055	AW818687	Hs.5306	0.33	0.67	early stage
	414170	AA336596	Hs.3743	1.15	0.21	early stage
	414220	BE588194		0.16	0.52	early stage
	414276	BE287882		1.75	0.2	early stage
55	414327	BE408145	Hs.185254	0.1	0.99	early stage
	414389	BE549143		1	0.31	early stage
	414378	BE338558	Hs.66915	0.18	0.98	early stage
	414555	N98595	Hs.76422	0.48	0.67	early stage
	415199	AA181125	Hs.57893	0.76	0.72	early stage
60	417304	P15535		0.6	0.58	early stage
	417371	N74813	Hs.289149	0.3	0.58	early stage
	418133	RA3504	Hs.6161	1.29	0.29	early stage
	419273	BE271180	Hs.253490	0.54	0.28	early stage
	419716	AA553770		0.45	0.66	early stage
65	420380	AA330047	Hs.151167	1.45	0.12	early stage
	421745	AF259940	Hs.107740	0.33	0.71	early stage
	421813	BE048255		0.52	0.67	early stage
	422689	H12402	Hs.119122	1	0.26	early stage
	422743	BE304578	Hs.119598	0.2	0.57	early stage
70	422760	BE403561		0.41	0.94	early stage
	422880	AF229704	Hs.121524	3.75	0.1	early stage
	423457	F08208	Hs.155006	0.55	0.54	early stage
	426349	AA426234	Hs.70886	1	0.21	early stage
	426390	BE47704		0.28	0.85	early stage
75	426359	BE336638		0.31	0.59	early stage
	426521	AF161445	Hs.170219	0.11	0.69	early stage
	426670	AA363047	Hs.150718	1	0.55	early stage
	426899	AA363337	Hs.127269	0.33	0.71	early stage
	427827	AA416877	Hs.180105	1.16	0.41	early stage
	428651	AF156478	Hs.189401	1.85	0.24	early stage
	430727	X75917	Hs.2554	0.78	0.65	early stage

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5	430750	AI650360	He.102056	ESTs	2.15	0.17	early stage
	430755	AW571398		gb:EST363487 MAGE "ressequens, MAGL Homo	1.96	0.21	early stage
	431900	AW572048	He.192634	ESTs	0.38	0.73	early stage
10	432726	NM_008795	He.278721	H4 class II region expressed gene KE4	1.8	0.17	early stage
	432751	NM_014654	He.278840	swi1tmSUMO-specific protease	2.6	0.15	early stage
	433404	T32982	He.102720	ESTs	2.2	0.13	early stage
15	433782	AF090945	He.257475	gb:Homo sapiens clone HQ0670	3.3	0.15	early stage
	433877	BE146567	He.257475	nutrin (nuclear envelope membrane protein	0.65	0.7	early stage
	434463	AA223648	He.125180	growth hormone receptor	0.38	0.49	early stage
20	435752	AF210801	He.21590	Homo sapiens HSPC304 mRNA, partial cds	0.52	0.4	early stage
	436178	BE152396	He.146274	ESTs	1.66	0.14	early stage
	436351	AJ227892	He.160871	ESTs	1.35	0.16	early stage
25	435602	AT95222	He.160871	ESTs	0.17	1.46	early stage
	436777	AA731199	He.263130	ESTs	1	0.2	early stage
	436813	AW575714	He.129004	ESTs	0.19	1.45	early stage
30	436869	NM_014867	He.257661	Homo sapiens YAC clone 377A1 unknown mRNA	0.96	0.2	early stage
	437169	AA309512	He.116797	ubiquitin-conjugating enzyme E2D 3 (homo	0.07	1.8	early stage
	438649	AA813136	He.143014	ESTs	1.92	0.19	early stage
35	438681	AW084816	He.145208	KQA1556 protein	0.25	0.54	early stage
	438802	AA825978	He.136954	ESTs	1.8	0.14	early stage
	438867	R68867	He.264495	ESTs	1.05	0.32	early stage
40	440108	AA626223	He.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	1	0.19	early stage
	440357	AA864448	He.157235	ESTs	0.59	0.38	early stage
	440509	BE410132	He.134202	ESTs, Weakly similar to B41182 collagen	0.26	0.9	early stage
45	440605	Z40054	He.186659	ESTs	0.51	0.43	early stage
	442236	AW153574	He.270845	ESTs	1	0.18	early stage
	442266	AF155001	He.8308	naflate transporter 1	0.85	0.40	early stage
50	446739	AW136354	He.148203	ESTs	0.88	0.4	early stage
	447306	AI373163	He.170333	ESTs	0.16	0.6	early stage
	447346	AI525135	He.210507	ESTs	1.35	0.27	early stage
55	448255	NA5272	He.26912	ESTs	0.47	0.28	early stage
	448876	AI850778	He.199854	ESTs	0.19	0.88	early stage
	448778	AF074913		gb:Homo sapiens transcription factor Pax	0.57	0.53	early stage
60	448871	BE118709	He.195645	gb:U01279537F1 NH1_MGC_39 Homo sapiens c	0.28	0.94	early stage
	445180	AI653556		ESTs	0.48	0.45	early stage
	445213	BE116861		gb:U01279568F1 NH1_MGC_39 Homo sapiens c	0.73	0.58	early stage
65	449231	BE410360		gb:U01302340F1 NH1_MGC_21 Homo sapiens c	0.27	0.76	early stage
	449480	AL036852	He.256950	ESTs, Moderately similar to ALUT_HUMAN A	1	0.26	early stage
	449815	AI571000	He.159739	ESTs	1.2	0.15	early stage
70	450372	AW997908	He.154517	ESTs	0.29	0.83	early stage
	451236	AI757408	He.207026	ESTs, Weakly similar to 555205 transcript	0.35	0.77	early stage
	451283	H83979		gb:Y53411.1 Soares retina N265HR Homo	1	0.23	early stage
75	451375	AT952095	He.263902	Homo sapiens BAG clone RP11-48 U131 from	1.10	1.37	early stage
	452530	AI555118		gb:CC-RT021-2-10155-008 BT071 Homo sapien	1.35	0.21	early stage
	452550	AA026735		gc:950405.1 Soares fetal_liver_JNH1191V	0.44	0.55	early stage
80	454121	AW090624	He.244967	ESTs	2.85	0.17	early stage
	454554	AW847505		gb:R02-CT0210-289595-021-c10 CT0210 Homo	0.38	0.5	early stage
	454597	AW813726	He.15036	ESTs, Highly similar to J1-181353-1 HEP2C	0.43	0.6	early stage
85	454651	AW851827		gb:CC-LT0011-100100-012-c07 LT0011 Homo	0.77	0.32	early stage
	455040	AW852286		gb:QV0-CT0225-100400-187-c08 CT0225 Homo	0.26	0.52	early stage
	455225	AW956689		gb:CV3-BND046-150400-151-g03 BND046 Homo	1.7	0.18	early stage
90	455970	AT133687	He.714483	ESTs	0.95	0.45	early stage
	456335	AA020331		gb:Y53412.1 Soares fetal_liver_spleen_	0.64	0.43	early stage
	456450	AJ000038	He.84210	eyes absent (Drosophila) homolog 1	0.38	0.76	early stage
95	456526	AA782222	He.192008	ESTs	0.63	0.43	early stage
	456585	AF035528	He.153863	MAD (mothers against decapentaplegic, Dr	0.49	0.46	early stage
	456983	AI081687	He.170226	thyropoietin	0.27	0.75	early stage
100	457089	AA410566	He.98254	ESTs	0.34	0.48	early stage
	458198	A0286100	He.152739	ESTs	0.47	0.48	early stage
	458425	A0804057	He.301148	ESTs	0.4	0.37	early stage
105	458500	AI299739	He.91601	Homo sapiens cDNA FLJ12563 fs, clone NT	0.79	0.88	early stage
	458703	AW749121	He.262501	ESTs	1	0.23	early stage
	458757	T97083	He.148355	ESTs	1	0.17	early stage
110	459399	BE407712		gb:U0129745F1 NH1_MGC_21 Homo sapiens c	0.89	0.56	early stage
	460380				49	0.08	late stage
	460510	AB032963	He.43577	ATPase, Class I, type B3, member 2	0.68	0.94	late stage
115	460558	AW015759	He.235709	ESTs	1.26	0.45	late stage
	410077	AF097845	He.58570	deleted in cancer 1; RNA helicase HDEWD	6.2	0.12	late stage
	410295	AA741357	He.62041	idogen (enzyme)	0.77	0.86	late stage
120	410310	J02551	He.170226	exonuclease factor III (thromboplastin,	1.45	0.77	late stage
	410614	A091195	He.65029	growth arrest-specific 1	0.4	1.12	late stage
	410857	X63556	He.750	thrinin 1 (Marfan syndrome)	0.71	1.07	late stage
125	411573	AB029000	He.70823	KAA1077 protein	3.64	0.19	late stage
	412116	AW002168	He.784	Epstein-Barr virus induced gamma 2 (gamm	5.16	0.13	late stage
	412178	AW886246		gb:CC-NN0072-JN0566-011-E05 NN0072 Homo	7.65	0.09	late stage
130	412429	AW50262	He.75755	GRO2 oncogene	3.37	0.15	late stage
	412852	A0801777	He.6774	ESTs	0.46	1.24	late stage

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1	412828	AL133395	Hs.74521	p10n protein (p27-30) (Creutzfeldt-Jakob	3.6	0.11	late stage
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.62	0.14	late stage
	414183	AW967446	Hs.301711	ESTs	3.18	0.16	late stage
	414359	U52184	Hs.76920	caldesin 11, type 2, OB-caldesin (caldesin	5.81	0.73	late stage
5	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	0.37	0.59	late stage
	414504	AW069181	Hs.253523	ESTs, Weakly similar to Transformon-r	0.97	0.65	late stage
	414812	X72755	Hs.77387	monokine induced by gamma interferon	3.84	0.1	late stage
	415116	AA100363	Hs.269566	ESTs	7.45	0.07	late stage
10	415714	NM_002290	Hs.78672	tenascin, alpha 4	0.49	1.39	late stage
	415822	D59243		gbltHUN52E07B Clontech human placenta po	8.15	0.09	late stage
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	0.46	1.46	late stage
	417059	AL037872	Hs.81071	extracellular matrix protein 1	1.52	0.44	late stage
	417259	AW920338	Hs.81800	chondralin sulfate proteoglycan 2 (vers	2	0.39	late stage
	417333	AL049678	Hs.82503	syntrophin	0.2	2.67	late stage
15	417771	AA804686	Hs.82547	retinoic acid receptor responder (lizaro	4.56	0.12	late stage
	417849	AW291587	Hs.82733	nitrogen 2	1.81	0.38	late stage
	418005	A186520	Hs.83154	collagen, type XV, alpha 1	0.97	0.74	late stage
	418203	S7985	Hs.83842	calpogen K (tyrosinolytic)	1.21	0.56	late stage
	418875	W19971	Hs.233459	ESTs	2.63	0.33	late stage
20	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	7.65	0.07	late stage
	419925	AA159850	Hs.93765	Ipoma H1/G1C fusion partner	0.91	0.82	late stage
	420411	A191085	Hs.94078	ESTs	7.3	0.1	late stage
	420943	A178102	Hs.105341	ESTs	7.05	0.07	late stage
	421116	T19132	Hs.101850	retino-binding protein 1, cellular	0.99	0.42	late stage
25	421884	BE281591	Hs.106768	hypothetical protein FLJ10511	8.1	0.08	late stage
	421785	A156863	Hs.21351	ESTs	8.15	0.08	late stage
	422914	AW672237	Hs.13701	ESTs	1.05	0.69	late stage
	422550	BE297825	Hs.296049	microfilament-associated protein 4	0.28	1.53	late stage
30	422790	AA809875	Hs.25933	ESTs	2.59	0.28	late stage
	423057	AW951657	Hs.306818	ESTs	7.55	0.08	late stage
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fls, clone C	1.24	0.61	late stage
	423905	AW579930	Hs.135150	lung type 1 cell membrane-associated gly	2.12	0.24	late stage
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	0.29	2.45	late stage
35	423951	D13558	Hs.136348	osteoblast specific factor 2 (pascidin	4.47	0.17	late stage
	424247	X14406	Hs.234734	tyrosine (renal amyloidosis)	2.44	0.25	late stage
	424839	AA740832	Hs.120850	ESTs	2.74	0.23	late stage
	425780	BE242284	Hs.172199	adenylate cyclase 7	8.55	0.09	late stage
40	425974	A3002258	Hs.173035	KIAA0300 protein	1.59	0.35	late stage
	427055	A301740	Hs.173381	thymosin-like factor 2 (pascidin	0.72	1	late stage
	427882	AA340587	Hs.193797	ESTs	2.25	0.29	late stage
	428065	A630405	Hs.157313	ESTs	6.19	0.1	late stage
	428147	AW829935	Hs.234983	ESTs	8.42	0.08	late stage
	428685	A3007853	Hs.185140	KIAA0403 protein	6.85	0.08	late stage
45	428825	A084335	Hs.128703	ESTs	0.9	0.8	late stage
	429490	A1971131	Hs.250384	ESTs, Weakly similar to alternatively sp	1.59	0.39	late stage
	429500	X78555	Hs.289114	hexabrachion (tenascin C, cytostatin)	0.77	0.49	late stage
	431100	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.92	0.3	late stage
	431518	AW733360	Hs.262475	glycylglycyl-s1 HCL CGAP, IgG5 Homo sapi	1.93	0.44	late stage
50	431583	AL042513	Hs.262475	S-adenosylmethionine decarboxylase 1	4.69	0.17	late stage
	432314	AA533447	Hs.285173	ESTs	1.75	0.31	late stage
	432331	X97862	Hs.274358	Homo sapiens mRNA: cDNA DHPZ5081524 (f	0.35	1.58	late stage
	432559	AW452948	Hs.257531	ESTs	1.37	0.49	late stage
	433470	AW660584	Hs.3337	transmembrane 4 superfamily member 1	2.88	0.24	late stage
55	433588	T85301		glycyl78506:s1 Soares fetal liver speren	5.06	0.11	late stage
	436428	AW246900	Hs.283712	hypothetical protein	8.25	0.09	late stage
	437879	BE321867	Hs.3337	Transmembrane 4 superfamily member 1	1.6	0.26	late stage
	438873	A302471	Hs.124292	Homo sapiens cDNA: FLJ21323 fls, clone L	8.15	0.08	late stage
	439584	AA838114	Hs.122512	ESTs	8.6	0.09	late stage
	439653	AW021103	Hs.8631	hypothetical protein FLJ20073	2.21	0.27	late stage
60	440524	R71254	Hs.157938	ESTs	3.44	0.21	late stage
	440524	AF017987	Hs.7005	secreted frizzled-related protein 1	0.42	0.63	late stage
	441978	AA028403	Hs.09131	ESTs	6.5	0.09	late stage
	442739	NW_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydrol	7.95	0.06	late stage
	443862	AB79966	Hs.150603	ESTs	6.94	0.12	late stage
65	443895	A186242	Hs.211937	Homo sapiens cDNA FLJ13527 fls, clone PL	7.95	0.08	late stage
	444212	AW539676	Hs.10619	basement membrane-induced gene	2.91	0.28	late stage
	444331	AW193032	Hs.21414	ESTs	0.32	1.54	late stage
	445142	AW978484	Hs.93842	Homo sapiens cDNA: FLJ22554 fls, clone H	2.52	0.24	late stage
70	445701	AF055581	Hs.13131	lymphocyte adhesion protein	1.43	0.47	late stage
	445854	U31415	Hs.154532	down-regulated in ovarian cancer 1	0.54	1.39	late stage
	447523	AL048783	Hs.3430	small inducible cytokine A2 (monocyte ch	1.43	0.43	late stage
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgria	1.35	0.26	late stage
	447818	W79642	Hs.21905	ESTs	6.63	0.13	late stage
	449587	A196799	Hs.188514	ESTs	4.7	0.13	late stage
75	450455	AL117424	Hs.22005	chicken intracellular channel 4	0.84	1.31	late stage
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor I	0.59	1.18	late stage
	452698	NW_001295	Hs.301921	ESTs	2.31	0.26	late stage

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	453212	H15416	Hs.21855	ESTs	2.51	0.26	late stage
	455510	AA422029	Hs.143540	ESTs, Weakly similar to hyperpolarized catalytic translation elongation factor	8.6	0.06	late stage
	450775	R98224	Hs.2189		1	1	T2-T4 grade 3 papilloma marker
	450158				1	1	T2-T4 grade 3 papilloma marker
5	450392				1	1	T2-T4 grade 3 papilloma marker
	450422				1	1	T2-T4 grade 3 papilloma marker
	450720	U46873		gbcHuman Tigger1 transposable element, c	1	1	T2-T4 grade 3 papilloma marker
	450745	A053366	Hs.186955	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	T2-T4 grade 3 papilloma marker
	450740	AF084352		gbcHomo sapiens lipocalin-protein lipocalin B	1	1	T2-T4 grade 3 papilloma marker
10	450737	AW131324	Hs.246759	ESTs, Weakly similar to KIAA1074 protein	1	1	T2-T4 grade 3 papilloma marker
	450766	AF071107	Hs.27501	MAO [methyltransferase, decarboxylase, O-	1	1	T2-T4 grade 3 papilloma marker
	450716	L05224	Hs.303	ATPase, H+-transporting, lysosomal (yeast	1	1	T2-T4 grade 3 papilloma marker
	450738	AW118147	Hs.270935	ESTs	1	1	T2-T4 grade 3 papilloma marker
	450815	AW168847	Hs.260156	ESTs	1	1	T2-T4 grade 3 papilloma marker
15	450950	AA707814	Hs.7369	ESTs	1	1	T2-T4 grade 3 papilloma marker
	450938	T97490	Hs.50002	small inducible cytosine subfamily A (Cy	1.2	0.12	T2-T4 grade 3 papilloma marker
	450945	AA555092	Hs.50004	Homo sapiens mRNAC: cDNA DKFZP454O0515 (f	1	1	T2-T4 grade 3 papilloma marker
	4509195	NM_001874	Hs.169765	carboxypeptidase M	1	1	T2-T4 grade 3 papilloma marker
	4509281	AA069998		gbcHs27039.1 Stralagene neuroepithelium	1	1	T2-T4 grade 3 papilloma marker
20	451010	AW572853	Hs.257683	ESTs, Weakly similar to ALU3_HUMAN ALU S	1	0.5	T2-T4 grade 3 papilloma marker
	451017	AW592277	Hs.255056	ESTs	1	0.69	T2-T4 grade 3 papilloma marker
	451112	AW818158		gbcCM1-ST0277-161295-070-g07 ST0277 Homo	1	1	T2-T4 grade 3 papilloma marker
	451336	AW537675		gbcCV2-LT0035-260300-107-504 LT0035 Homo	1	1	T2-T4 grade 3 papilloma marker
25	451251	T15872	Hs.288713	ESTs, Weakly similar to hypothetical pro	1	1	T2-T4 grade 3 papilloma marker
	451465	HS2622		gbcST7g11.11 Scars' fetal liver splic	1	1	T2-T4 grade 3 papilloma marker
	451374	DE45159	Hs.122969	Homo sapiens cDNA FLJ14267, fl, clone PL	1	1	T2-T4 grade 3 papilloma marker
	451382	BF548104		gbc901078242F1 NHL_MGC_12 Homo sapiens c	1	1	T2-T4 grade 3 papilloma marker
	451479	HS4922	Hs.193358	ESTs, Moderately similar to diabetes mel	1	1	T2-T4 grade 3 papilloma marker
	451593	R49462	Hs.105541	ESTs	1	1	T2-T4 grade 3 papilloma marker
30	451442	P12923	Hs.7045	GL004 protein	1	1	T2-T4 grade 3 papilloma marker
	451625	T87587	Hs.272082	ESTs	1	1	T2-T4 grade 3 papilloma marker
	4517047	AA192840	Hs.1526	ATPase, Ca++ transporting, cardiac muscl	1	1	T2-T4 grade 3 papilloma marker
	451781	L10123	Hs.10715	surfactant protein A binding protein	1	1	T2-T4 grade 3 papilloma marker
	451787	N78771	Hs.17191	ESTs	1	1	T2-T4 grade 3 papilloma marker
35	451721	NM_001050	Hs.288550	aquaporin 4	1	1	T2-T4 grade 3 papilloma marker
	452094	AA802659	Hs.190716	ESTs	1	0.65	T2-T4 grade 3 papilloma marker
	452389	AA329082	Hs.205989	ESTs, Weakly similar to thrombospondin t	1	1	T2-T4 grade 3 papilloma marker
	452449	AB73205	Hs.183114	Homo sapiens cDNA FLJ14235, fl, clone NT	1	1	T2-T4 grade 3 papilloma marker
	452458	H83317		ESTs	1	1	T2-T4 grade 3 papilloma marker
40	452475	AL134728		gbcDKFZp547A1890_1 547 (pymycin: mtrf)	1	1	T2-T4 grade 3 papilloma marker
	452453	AA453195	Hs.124222	ESTs	1	1	T2-T4 grade 3 papilloma marker
	4531200	AP045623	Hs.260752	hook1 protein	1	1	T2-T4 grade 3 papilloma marker
	453138	AA538471	Hs.115242	developmentally regulated GTP-binding pr	1	1	T2-T4 grade 3 papilloma marker
45	453144	AL360891	Hs.143819	ESTs	1	1	T2-T4 grade 3 papilloma marker
	4531921	AA504470	Hs.88753	ESTs	1	1	T2-T4 grade 3 papilloma marker
	4532205	A190693	Hs.125251	ESTs	1	0.31	T2-T4 grade 3 papilloma marker
	453227	AW573628	Hs.102754	ESTs	1	1	T2-T4 grade 3 papilloma marker
	4534069	AF116561	Hs.263338	hypothetical protein PRO0800	1	0.41	T2-T4 grade 3 papilloma marker
	453278	AW596242	Hs.173495	ESTs	1	1	T2-T4 grade 3 papilloma marker
50	453985	A03438	Hs.132650	ESTs	1	0.36	T2-T4 grade 3 papilloma marker
	453927	AA708937	Hs.123002	ESTs, Moderately similar to A26641 NwK	1	1	T2-T4 grade 3 papilloma marker
	453935	AW104226	Hs.272063	ESTs, Weakly similar to STX2_HUMAN SERP	1	0.74	T2-T4 grade 3 papilloma marker
	453840	AA724411	Hs.156055	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453884	BE048957		gbcHm1.2x62.1 NCL_CGAP_RDF2 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
55	453751	AW576032		gbcST285191 MAGE sequences, MAGN Homo	1	1	T2-T4 grade 3 papilloma marker
	453748	AA748149	Hs.183114	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453759	AA767553	Hs.122895	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453771	AA811071	Hs.123349	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453747	AA509888	Hs.265367	ESTs	1	1	T2-T4 grade 3 papilloma marker
60	4539171	AA531133	Hs.294128	ESTs	1	0.35	T2-T4 grade 3 papilloma marker
	453914	AA540386	Hs.143534	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453939	A1215527	Hs.125589	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453972	BE044538	Hs.278159	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454004	AA573553	Hs.126317	ESTs	1	1	T2-T4 grade 3 papilloma marker
65	454270	BE68699	Hs.52005	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454313	A1056457	Hs.221642	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454327	AW018726	Hs.134850	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454542	N03037	Hs.42846	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454511	AAW18927	Hs.146345	ESTs	1	0.49	T2-T4 grade 3 papilloma marker
70	454588	AF070364	Hs.13415	Homo sapiens, clone 24571 mRNVA sequence	1	1	T2-T4 grade 3 papilloma marker
	454652	AAW40827	Hs.156241	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454739	A1815401	Hs.251967	Homo sapiens clone 765227 unknown mRNA	2.9	0.14	T2-T4 grade 3 papilloma marker
	454911	T85109	Hs.159180	ESTs	1	1	T2-T4 grade 3 papilloma marker
	454922	AW192780		ESTs	1	0.8	T2-T4 grade 3 papilloma marker
75	451373	A1792030		gbc035e11.y5 NCL_CGAP_Lus Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	452453	A1902519		gbcCV-BT069-101198-051 BT069 Homo sapien	1	1	T2-T4 grade 3 papilloma marker
	452534	AW083022	Hs.143425	Homo sapiens cDNA FLJ11980, fl, clone HE	1	0.67	T2-T4 grade 3 papilloma marker

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452536	BE063380		gbc:PMG-0T0275-291009-002-g10 BT0275 Homo	1.65	0.26	T2-T4 grade 3 papilloma marker
452640	AA027115	Ha.100205	ESTs, Weakly similar to AAAD_HUMAN ARYL A	1	1	T2-T4 grade 3 papilloma marker
452645	AB911325	Ha.212049	EST	1	1	T2-T4 grade 3 papilloma marker
453102	NM_007197	Ha.151684	Hist4 (Drosophila) homolog 10	1	1	T2-T4 grade 3 papilloma marker
453472	AL037926		gbc:DKFZp554M037_r1.584 (synonym: hlu2)	1	0.8	T2-T4 grade 3 papilloma marker
453609	AL045301	Ha.13427	ESTs	1	1	T2-T4 grade 3 papilloma marker
453677	AL079389		gbc:DKFZp34E2116_r1.434 (synonym: hlic3)	1	0.77	T2-T4 grade 3 papilloma marker
453704	R41808	Ha.100884	ESTs	1	1	T2-T4 grade 3 papilloma marker
453267	AW030681		gbc:Q44701033-070300-152-c12 DT0033 Homo	1	1	T2-T4 grade 3 papilloma marker
455880	DE153208		gbc:PMG-HIT033-050M00-007-F10 H10336 Homo	1	1	T2-T4 grade 3 papilloma marker
456520	AW834416	Ha.29417	HCF-binding transcription factor Zhangfs	1	1	T2-T4 grade 3 papilloma marker
456783	AJ271351	Ha.126180	B-cell translocation gene 4	1	0.71	T2-T4 grade 3 papilloma marker
456912	AA58843	Ha.150112	protein tyrosine phosphatase, receptor 1	1	1	T2-T4 grade 3 papilloma marker
457018	AA791620	Ha.350965	ESTs	1	1	T2-T4 grade 3 papilloma marker
457323	AW967813	Ha.201054	ESTs	1	1	T2-T4 grade 3 papilloma marker
457339	AW971949	Ha.291252	ESTs	1	1	T2-T4 grade 3 papilloma marker
457340	AA492071		gbc:me97604s1 NCL_G3AP_Xid1 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
457507	AW030048	Ha.161693	ESTs	1	1	T2-T4 grade 3 papilloma marker
458106	AF065581	Ha.37	acetyl-Coenzyme A acetyltransferase 1 (a)	1	1	T2-T4 grade 3 papilloma marker
458624	AJ362790	Ha.161801	ESTs	1	0.34	T2-T4 grade 3 papilloma marker
458936	AG07636	Ha.103069	ESTs	1	1	T2-T4 grade 3 papilloma marker
461002				1	1	T2-T4 grade 3 solid tumor marker
461866				1.35	0.14	T2-T4 grade 3 solid tumor marker
463615				1	1	T2-T4 grade 3 solid tumor marker
463776				1	1	T2-T4 grade 3 solid tumor marker
464113				1	0.43	T2-T4 grade 3 solid tumor marker
464488				1	0.17	T2-T4 grade 3 solid tumor marker
464653				1	1	T2-T4 grade 3 solid tumor marker
460676	AL391179	Ha.137011	Homo sapiens mRNA; cDNA DKFZp67P134 (fr	1	0.24	T2-T4 grade 3 solid tumor marker
460471				1	0.42	T2-T4 grade 3 solid tumor marker
460690	U29640	Ha.220529	cardioembryonic antigen-elaid cell ad	2.75	0.05	T2-T4 grade 3 solid tumor marker
467624	AW157431	Ha.246941	ESTs	3.06	0.16	T2-T4 grade 3 solid tumor marker
469153	W03754	Ha.508113	hypochelal protein FLJ20022	3.85	0.03	T2-T4 grade 3 solid tumor marker
469484	299115	Ha.54468	zinc finger protein 37a (KIX 21)	1.15	0.29	T2-T4 grade 3 solid tumor marker
469731	AA128966	Ha.56145	thymosin, beta, identified in neuroblast	1	0.34	T2-T4 grade 3 solid tumor marker
470025	BE220469	Ha.113592	ESTs	1	0.3	T2-T4 grade 3 solid tumor marker
470589	AW770768	Ha.266717	ESTs	1	0.28	T2-T4 grade 3 solid tumor marker
471840	AW665330		gbc:Q44-SN024-090K0-167-e01 SN0024 Homo	1	0.06	T2-T4 grade 3 solid tumor marker
472196	AA571111	Ha.89165	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
472305	AW635659		gbc:Q44-DT0021-301299-071-007 DT0021 Homo	1	0.53	T2-T4 grade 3 solid tumor marker
472753	AI060016	Ha.6390	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
473472	BE242870	Ha.75379	solute carrier family 1 (gal high salt)	1	0.69	T2-T4 grade 3 solid tumor marker
473530	AA130158	Ha.19977	ESTs, Moderately similar to ALUR_HUMAN A	1	0.29	T2-T4 grade 3 solid tumor marker
475027	D01010		gbc:UJAL1247 Human fetal lung Homo sapie	1	1	T2-T4 grade 3 solid tumor marker
478099	HI8826	Ha.22834	ESTs	1	0.74	T2-T4 grade 3 solid tumor marker
476655	AW698513	Ha.79428	DCL2adenovirus E15 19kD-interacting p	3.8	0.12	T2-T4 grade 3 solid tumor marker
476329	AW247430	Ha.84152	cystathionine-beta-synthase	2.85	0.08	T2-T4 grade 3 solid tumor marker
476347	AL033529	Ha.57124	Human DNA sequence from clone RP1-309H15	1	0.2	T2-T4 grade 3 solid tumor marker
472443	AW733003	Ha.102876	pancreatic lipase	1	0.38	T2-T4 grade 3 solid tumor marker
472660	AW297582	Ha.237062	ESTs	1	0.06	T2-T4 grade 3 solid tumor marker
472834	AA318334		gbc:ESTZ0402 Retinal II Homo sapiens cDNA	1	0.38	T2-T4 grade 3 solid tumor marker
472922	BB5519	Ha.145404	ESTs	1	0.61	T2-T4 grade 3 solid tumor marker
472104	AJ058273	Ha.123547	antigenic determinant of rock protein (p	2.95	0.12	T2-T4 grade 3 solid tumor marker
472634	AW699808	Ha.1690	heparin-binding growth factor binding pr	1	0.06	T2-T4 grade 3 solid tumor marker
474268	AA397653	Ha.144339	Human DNA sequence from clone 45C010 on	1	0.35	T2-T4 grade 3 solid tumor marker
475196	AL037915	Ha.155097	carbonic anhydrase II	2.75	0.06	T2-T4 grade 3 solid tumor marker
472099	AB029653	Ha.175560	cold Outbreak-homolog 2 (Drosophila, mous	1	0.09	T2-T4 grade 3 solid tumor marker
470300	U06085	Ha.238648	occasinin M receptor	1	0.25	T2-T4 grade 3 solid tumor marker
470198	AA501455	Ha.249230	ribonuclease L (2',5'-oligopoadenylate	1	0.28	T2-T4 grade 3 solid tumor marker
473277	AA501806	Ha.249965	ESTs	1	0.22	T2-T4 grade 3 solid tumor marker
473740	AA514596	Ha.263705	ESTs	1	1	T2-T4 grade 3 solid tumor marker
474270	AA011543	Ha.26363	ESTs	1	0.41	T2-T4 grade 3 solid tumor marker
475055	AF200492	Ha.211238	interleukin-1 homology 1	1.8	0.19	T2-T4 grade 3 solid tumor marker
476231	AA411194	Ha.120051	ESTs	2.06	0.14	T2-T4 grade 3 solid tumor marker
477010	AA741368	Ha.291454	ESTs	2.4	0.17	T2-T4 grade 3 solid tumor marker
478144	A035192	Ha.135474	ESTs, Weakly similar to DDIX_HUMAN ATP-D	1	0.13	T2-T4 grade 3 solid tumor marker
478361	AA805936	Ha.146217	Homo sapiens cDNA: FLJ23077, lte, clone L	1	0.3	T2-T4 grade 3 solid tumor marker
478376	BE541211	Ha.34804	Homo sapiens cDNA: FLJ11472, lte, clone HE	1	0.57	T2-T4 grade 3 solid tumor marker
479370	AW274399	Ha.155853	ESTs	1	0.17	T2-T4 grade 3 solid tumor marker
480221	AW02498	Ha.270942	ESTs, Weakly similar to ALUB_HUMAN ALU S	1	0.05	T2-T4 grade 3 solid tumor marker
480404	AC15881	Ha.125516	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
481523	AW514253	Ha.150872	ESTs, Weakly similar to ALUF_HUMAN III	1	1	T2-T4 grade 3 solid tumor marker
482277	AW448914	Ha.262291	ESTs	2.4	0.16	T2-T4 grade 3 solid tumor marker
482736	AW002370	Ha.131035	ESTs	1	0.29	T2-T4 grade 3 solid tumor marker
482907	AC105684	Ha.133029	ESTs	1	1	T2-T4 grade 3 solid tumor marker
484754	T83911	Ha.11881	transmembrane 4 superfamily member 4	1	0.61	T2-T4 grade 3 solid tumor marker
485550	AJ242754	Ha.137306	ESTs	1	0.5	T2-T4 grade 3 solid tumor marker

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	446149	BE242960	He.203181	ESTs	1	0.25	T2-T4 grade 3 solid tumor marker
	446153	AAQ26880	He.25252	Home sapiens cDNA FLJ13803 (a, clone PL	1	0.21	T2-T4 grade 3 solid tumor marker
	446434	AI823410	He.169149	carboxypeptidase alpha 1 (pancreas alpha 5)	1	1	T2-T4 grade 3 solid tumor marker
	446926	AB91463	He.245916	ESTs	1	0.31	T2-T4 grade 3 solid tumor marker
5	446951	AI540111	He.171261	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449121	AS15858	He.154980	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449539	W80363	He.58846	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	450461	AW591528	He.220272	ESTs	1	0.58	T2-T4 grade 3 solid tumor marker
	450469	AV55046	He.281306	ESTs	1	0.43	T2-T4 grade 3 solid tumor marker
10	450684	AA872605	He.25333	interleukin 1 receptor, type II	1	0.05	T2-T4 grade 3 solid tumor marker
	451099	RS7295	He.25864	interleukin 13 receptor, alpha 2	1.55	0.11	T2-T4 grade 3 solid tumor marker
	451106	BE327071	He.26590	E-myc avian myelocytomatosis viral nat	1	0.95	T2-T4 grade 3 solid tumor marker
	451130	AT32260	He.211347	ESTs	1	0.65	T2-T4 grade 3 solid tumor marker
	451412	AW136378	He.208000	ESTs	1	1	T2-T4 grade 3 solid tumor marker
15	451806	NM_003720	He.27076	RNA 3'-terminal phosphate cyclase	1.35	0.22	T2-T4 grade 3 solid tumor marker
	452114	NZ2597	He.8236	ESTs	1	0.10	T2-T4 grade 3 solid tumor marker
	452343	AW565092	He.51455	ESTs	1	0.44	T2-T4 grade 3 solid tumor marker
	454622	U70071			1	1	T2-T4 grade 3 solid tumor marker
20	455226	AW879551		dbcHSU70071 Human Home sapiens cDNA don	1	0.31	T2-T4 grade 3 solid tumor marker
	457592	AL104958	He.268677	gbc:CM1-PT0013-131269-057-059 PT0013 Homo	1	0.24	T2-T4 grade 3 solid tumor marker
	100147	D13666	He.136348	ESTs. Moderately similar to ALUT_HUMAN	20.591	0.036	upregulate stage
	101153	L20961	He.152213	osteoblast specific factor 2 (osteob)	1	0.525	upregulate stage
	101724	M68225	He.620	"Wegless-type MMTV" integrin alpha fam	20.67	0.037	upregulate stage
	101809	M68849	"He.323733	"gap junction protein, beta 2, 2B0 (don	20.78	0.019	upregulate stage
25	102144	U17793	He.75577	"tannin, beta 3 (nicotinic (128K), kalai	18.448	0.042	upregulate stage
	102211	U22070	He.157877	putative transmembrane protein	2.062	0.28	upregulate stage
	102523	JS6083	He.37110	"melanoma antigen, family A, 9"	1	0.306	upregulate stage
	102915	X07820	He.2258	matrix metalloproteinase 10 (stromelys	3.27	0.041	upregulate stage
30	103036	SA4525	"He.53165	matrix metalloproteinase 1 (interstitial	13.63	0.034	upregulate stage
	103119	X53528	He.2377	"cathelin 3, type 1, P-cadherin (abcat	7.236	0.054	upregulate stage
	103312	X53593	He.3185	"lymphocyte antigen 6 complex, locus D"	0.908	0.485	upregulate stage
	103478	Y07755	He.38991	S100 calcium-binding protein A2	2.928	0.219	upregulate stage
	103587	Z20303	He.82128	ST4 oncofetal trophoblast glycoprotein	3.166	0.15	upregulate stage
35	103632	AA650897	He.11890	GPI-anchored melastasin-associated prote	1.642	0.516	upregulate stage
	107151	AA821169	He.8697	ESTs	2.421	0.174	upregulate stage
	107901	AAQ20418	"He.111758	keratin 5A	1.259	0.343	upregulate stage
	107922	AAQ28028	He.81460	"Home sapiens Ig superfamily member LN	14.22	0.049	upregulate stage
	108195	AA175945	He.73625	"RAB6 interacting, kinesin-like (rablin	11.13	0.039	upregulate stage
	108424	AAQ27919	He.33552	hyaluronan synthase 3	1.737	0.518	upregulate stage
40	110005	N05684	He.17404	ESTs	20.33	0.021	upregulate stage
	112444	RS1309	He.70823	KJAA1077 protein	3.941	0.181	upregulate stage
	115030	AA253214	He.158249	"gap junction protein, beta 5 (connexin	1.932	0.502	upregulate stage
	115957	AA411502	He.83325	Transmembrane protease, serine 4"	7.394	0.101	upregulate stage
	115979	AA147822	He.59517	"Home sapiens, clone MGC35281, mRNA, com	1.667	0.445	upregulate stage
45	115935	AA456830	He.41590	desmocollin 3	4.899	0.154	upregulate stage
	118314	N83402	He.48882	ESTs	6.75	0.059	upregulate stage
	118336	N63604	He.47166	hTGT1	1.801	0.197	upregulate stage
	119845	W75520	He.53581	G protein-coupled receptor 87	1.95	0.123	upregulate stage
50	120488	AA253400	He.157599	tumor protein 63 kDa with strong homolo	4.191	0.211	upregulate stage
	121027	AA239840	He.05785	"Home sapiens cDNA: FLJ1245 (a, clone	14.25	0.058	upregulate stage
	124059	U13573	He.267133	"ESTs, Weakly similar to ORF YGL050w (S	4.99	0.158	upregulate stage
	126955	U31578	He.153877	"Home sapiens cDNA: FLJ23336 (a, clone H	2.433	0.305	upregulate stage
	128610	L38628	He.10247	acidified endosome cell adhesion molecu	4.34	0.14	upregulate stage
55	129041	H58973	"He.155992	"soluble carrier family 2 (facilitated gl	2.003	0.455	upregulate stage
	129466	L42583	"He.111758	keratin 6A	11.584	0.042	upregulate stage
	130627	Z23608	He.1695	matrix metalloproteinase 12 (macrophage	2.375	0.233	upregulate stage
	132349	Y02736	"He.191286	"serine protease inhibitor, Kazal type 1	5.4	0.132	upregulate stage
	132710	W53726	He.35279	"serine (or cysteine) proteinase inhibi	3.888	0.187	upregulate stage
	133391	U57579	He.727	"inhibin, beta A (activin A, activin AB	1.517	0.334	upregulate stage
60	134110	AA242758	"He.79195	"LIV-1 protein, estrogen regulator"	2.221	0.287	upregulate stage
	140288	X07620	He.2259	matrix metalloproteinase 10 (stromelys	4.85	0.03	upregulate stage
	140297	AI127076	He.238081	hypothetical protein DKF-zp564c12/8	3.54	0.13	upregulate stage
	140345	AS041269	He.272263	Home sapiens mRNA for keratin 10, parlo	8.95	0.07	upregulate stage
65	140419	AF084545	He.81800	chondroitin sulfate proteoglycan 2 (vers	10.7	0.06	upregulate stage
	140485				1	0.05	upregulate stage
	140559	MS7639	He.155585	receptor tyrosine kinase-like orphan rec	1.52	0.51	upregulate stage
	140528				3.47	0.23	upregulate stage
	140577				1	0.25	upregulate stage
70	140598				7.2	0.08	upregulate stage
	140644				1	1	upregulate stage
	140666				1.42	0.43	upregulate stage
	140750				8.7	0.1	upregulate stage
	140773				1.11	0.51	upregulate stage
	140844				5.65	0.04	upregulate stage
75	140845				2.3	0.28	upregulate stage
	140846				1.34	0.5	upregulate stage
	140880				9.4	0.06	upregulate stage

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				1	1	upregulate stage
				1	0.51	upregulate stage
				7	0.06	upregulate stage
				1	0.17	upregulate stage
5				5.18	0.14	upregulate stage
				1	1	upregulate stage
				1	1	upregulate stage
				9.1	0.06	upregulate stage
				1.42	0.5	upregulate stage
10				1	0.33	upregulate stage
				6.5	0.11	upregulate stage
				1	0.31	upregulate stage
				1	1	upregulate stage
				2.65	0.17	upregulate stage
15				12	0.05	upregulate stage
				9.15	0.08	upregulate stage
				8.75	0.09	upregulate stage
				1	1	upregulate stage
20				29.75	0.02	upregulate stage
				11.35	0.06	upregulate stage
				5.15	0.37	upregulate stage
				1	0.69	upregulate stage
				3.15	0.15	upregulate stage
				4.4	0.14	upregulate stage
25				8.75	0.06	upregulate stage
				1	0.36	upregulate stage
				5.15	0.1	upregulate stage
				9.05	0.08	upregulate stage
				1	1	upregulate stage
30				9.6	0.07	upregulate stage
				9.85	0.09	upregulate stage
				9.4	0.09	upregulate stage
				1.07	0.05	upregulate stage
				1	1	upregulate stage
35				9.6	0.06	upregulate stage
				1.5	0.21	upregulate stage
				5.15	0.12	upregulate stage
				1	1	upregulate stage
40				1.5	0.28	upregulate stage
				1	0.37	upregulate stage
				1	0.43	upregulate stage
				1.12	0.57	upregulate stage
				0.26	1.38	upregulate stage
45				7.7	0.09	upregulate stage
				1.13	0.62	upregulate stage
				6.05	0.1	upregulate stage
				4.5	0.11	upregulate stage
				3.2	0.13	upregulate stage
50				10.7	0.05	upregulate stage
				10.35	0.08	upregulate stage
				1	1	upregulate stage
				2.45	0.34	upregulate stage
				1	1	upregulate stage
				4.45	0.14	upregulate stage
55				1.35	0.58	upregulate stage
				1	1	upregulate stage
				9.15	0.08	upregulate stage
				1	1	upregulate stage
				1	1	upregulate stage
				1.3	0.2	upregulate stage
60				1	0.36	upregulate stage
				1	0.28	upregulate stage
				7.05	0.06	upregulate stage
				1	0.33	upregulate stage
65				1	1	upregulate stage
				1	1	upregulate stage
				0.89	0.9	upregulate stage
				2.74	0.26	upregulate stage
				9.35	0.08	upregulate stage
70				1	0.24	upregulate stage
				3.65	0.15	upregulate stage
				2.05	0.16	upregulate stage
				1	1	upregulate stage
				1	0.18	upregulate stage
75				1	0.56	upregulate stage
				1	0.22	upregulate stage
				9.65	0.08	upregulate stage

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	407910	AA650274	Ha.41206	fibronectin leucine rich transmembrane p	13.6	0.05	upregulate stage
	407911	AF104922	Ha.41565	growth differentiation factor 8	1	1	upregulate stage
	407912	AW104401	Ha.243489	ESTs, Weakly similar to AF151881.1 CGL-1	10.35	0.07	upregulate stage
	407935	U31995	Ha.41463	carilage paired-class homoprotein 1	4.26	0.12	upregulate stage
5	407939	W06506	Ha.41565	glucuronidyl transferase, fetal lung, NAH119W	8.75	0.09	upregulate stage
	407944	R34008	Ha.239727	deamnosin 2	9.2	0.05	upregulate stage
	407945	X69208	Ha.606	ATPase, Co++ transporting, alpha polypep	1.45	0.25	upregulate stage
	407946	AA229495	Ha.154292	ESTs	8.4	0.07	upregulate stage
	407949	W21614	Ha.247657	ESTs	3.32	0.2	upregulate stage
10	407974	AW68123	Ha.146401	small inducible cytokine subfamily C, me	3.55	0.14	upregulate stage
	407983	U40371	Ha.41718	phosphodiesterase 1C, calmodulin-depende	8.95	0.07	upregulate stage
	407984	AW135309	Ha.244331	ESTs	4.5	0.12	upregulate stage
	408000	L11590	Ha.620	bovine pemphigoid antigen 1 (230240K)	2.95	0.16	upregulate stage
	408014	AA72782	Ha.41746	protein kinase, cGMP-dependent, type II	1.31	0.53	upregulate stage
15	408031	AA081395	Ha.42173	Homo sapiens cDNA FLJ10366.fst, clone NT	3.6	0.17	upregulate stage
	408045	AW139121	Ha.183643	ESTs	1	0.36	upregulate stage
	408063	BC085948	Ha.42346	calcineurin-binding protein calcitriol-1	10.75	0.05	upregulate stage
	408062	NM_007057	Ha.42350	ZW10 Interactor	4.7	0.13	upregulate stage
	408101	AW68504	Ha.123073	CDG2-related protein kinase 7	4.5	0.14	upregulate stage
20	408141	U93205	Ha.45152	ESTs, Moderately similar to neurogenic b	4.4	0.13	upregulate stage
	408170	AW204515	Ha.31835	ESTs	5.85	0.13	upregulate stage
	408184	AW168741	Ha.22245	ESTs	1	1	upregulate stage
	408224	AW175597	Ha.22245	gb:O16-BT0078-19089-005-E02 BT0078 Homo	1	0.44	upregulate stage
25	408230	AA053401	Ha.27127	ESTs, Moderately similar to ALU1_HUMAN A	9.55	0.04	upregulate stage
	408241	AW176546	Ha.27127	gb:MRD-CT0065-20-085-001-a01 CT0065 Homo	2.8	0.17	upregulate stage
	408258	AL138247	Ha.42346	gb:CKF2g547D237_r1.547 (myocyte hsr1)	1	0.81	upregulate stage
	408277	AW177550	Ha.42346	gb:J3-H70090-300639-008-004 HT0090 Homo	1	1	upregulate stage
	408306	BE141591	Ha.42346	gb:PM2-H10134-220955-002-410 HT0134 Homo	1	1	upregulate stage
30	408352	AA053875	Ha.65310	ESTs	1	1	upregulate stage
	408360	AB060150	Ha.43444	hypothetical protein FLJ20534	5.15	0.08	upregulate stage
	408363	AW115318	Ha.23165	ESTs	5.35	0.07	upregulate stage
	408366	AA330406	Ha.40840	ESTs	1	0.61	upregulate stage
	408442	R59508	Ha.21435	ESTs	1	1	upregulate stage
35	408514	AW205555	Ha.255503	ESTs	1	0.34	upregulate stage
	408572	AA255511	Ha.255508	ESTs, Moderately similar to ALU4_HUMAN A	1	0.33	upregulate stage
	408617	R61736	Ha.124128	ESTs	2.75	0.14	upregulate stage
	408633	AW563372	Ha.46677	PRO2000 protein	3.14	0.25	upregulate stage
	408706	AW438303	Ha.255935	ESTs	8.45	0.09	upregulate stage
40	408713	NM_001248	Ha.47042	extracellular de triphosphate diphosphoty	2.81	0.21	upregulate stage
	408725	AA151335	Ha.15565	ESTs	5.1	0.08	upregulate stage
	408728	AL137379	Ha.47125	hypothetical protein FLJ13612	3.1	0.11	upregulate stage
	408738	NM_014785	Ha.47313	KIA0268 gene product	4.4	0.13	upregulate stage
	408739	W01535	Ha.42387	ESTs	5.55	0.11	upregulate stage
	408754	N31255	Ha.151123	ESTs	1	1	upregulate stage
	408765	AA057268	Ha.146013	ESTs	8.75	0.09	upregulate stage
	408805	H69512	Ha.48265	vaccinia related kinase 1	4.55	0.12	upregulate stage
	408813	A1580000	Ha.48205	RNA helicase family	3.65	0.17	upregulate stage
	408817	AA524523	Ha.279854	PRO1596 protein	6.15	0.12	upregulate stage
50	408845	BE215451	Ha.254515	ESTs	1	0.32	upregulate stage
	408902	AW014869	Ha.55510	ESTs	3.3	0.15	upregulate stage
	408908	BE262227	Ha.48615	serine/threonine kinase 15	5.65	0.1	upregulate stage
	408916	AA725323	Ha.22853	ESTs	10	0.08	upregulate stage
	408933	AA589795	Ha.152133	ESTs, Highly similar to ADP-ribosylation	0.9	0.51	upregulate stage
55	408943	NM_007070	Ha.49105	FKBP-associated protein	3.45	0.16	upregulate stage
	408950	BE158386	Ha.300576	ESTs	8.3	0.1	upregulate stage
	409032	AW201807	Ha.50720	ESTs	8.4	0.08	upregulate stage
	409093	BE243554	Ha.50441	CGI-04 protein	1.71	0.45	upregulate stage
	409099	AK000725	Ha.50575	hypothetical protein FLJ20718	10.1	0.07	upregulate stage
	409142	AL136877	Ha.50758	chromosome-associated polypeptide C	11.85	0.05	upregulate stage
60	409203	AA780473	Ha.687	cytochrome P450, subfamily IVB, polypept	2.83	0.24	upregulate stage
	409231	AA446544	Ha.692	tumor-associated calcium signal transduc	5.34	0.08	upregulate stage
	409262	AK000331	Ha.52296	hypothetical protein FLJ20624	6.7	0.09	upregulate stage
	409357	MT3628	Ha.54415	casein, kappa	1.6	0.2	upregulate stage
	409402	AF208254	Ha.695	crystallin B (alpha II)	1.57	0.56	upregulate stage
65	409405	AA071869	Ha.126400	ESTs, Highly similar to RL30_HUMAN (SIS R	2.6	0.12	upregulate stage
	409408	AW367357	Ha.126400	gb:RAR-STD116-30129-021-R38 STD116 Homo	4.3	0.15	upregulate stage
	409420	Z15608	Ha.54451	aminin, gamma 2 (picon (100kD), kalin	8.28	0.06	upregulate stage
	409509	AL036523	Ha.127008	ESTs	10.2	0.06	upregulate stage
70	409566	AA071889	Ha.127008	gb:zms94601.1.1 Strategic clone HD27 (937	1	0.56	upregulate stage
	409575	AAW119225	Ha.256247	ESTs	5.25	0.14	upregulate stage
	409582	R27430	Ha.271565	ESTs	7.3	0.07	upregulate stage
	409632	W74001	Ha.55279	serine (or cysteine) proteinase inhibito	3.78	0.19	upregulate stage
	409642	AW460808	Ha.257347	ESTs	9.55	0.07	upregulate stage
	409674	A935146	Ha.278611	UDP-N-acetyl-alpha-D-galactosaminopolyp	1	0.29	upregulate stage
75	409691	789383	Ha.246042	ESTs	1	1	upregulate stage
	409703	NM_006187	Ha.56009	Z-5-olipoadomate synthetase 3	2.22	0.36	upregulate stage
	409727	N63786	Ha.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.57	upregulate stage

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49760	AA302840		gltEST10534 Adipose tissue, white 1 Homo	9.95	0.06	upregulated stage
49789	BE256027	Hs.180946	ribosomal protein L5	1	0.83	upregulated stage
49794	AW885691		gbrCA-C10701-240300-013-b04 OT0071 Homo	1	1	upregulated stage
49997	AW805510	Hs.87056	hypothetical protein FLJ21634	3.65	0.07	upregulated stage
49986	AW91944	Hs.121320	ESTs	4.35	0.14	upregulated stage
49989	R37868	Hs.13333	ESTs	1	0.21	upregulated stage
49995	AW900597	Hs.30164	ESTs	5.06	0.12	upregulated stage
410013	AF071713	Hs.57904	mep-aes1 (Drosophila) homolog, profile	3.06	0.25	upregulated stage
410044	BE566749	Hs.55169	highly expressed in cancer, rich in leuc	3.15	0.09	upregulated stage
410071	AW52558		gbrFC1-217079-009100-011-h04 ST0276 Homo	2.5	0.18	upregulated stage
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 f6, clone HE	8	0.05	upregulated stage
410114	AW590540	Hs.271280	ESTs	5.1	0.14	upregulated stage
410117	AW301596	Hs.59550	hypothetical protein FLJ10724	1	1	upregulated stage
410153	BC311026	Hs.15390	Homo sapiens cDNA FLJ12591 f6, clone NT	4.7	0.11	upregulated stage
410181	AI468210	Hs.251265	proliferative regulator 1 (PRPL 1, Arabidops	1	0.23	upregulated stage
410196	AI336442	Hs.59338	hypothetical protein FLJ10808	6.06	0.09	upregulated stage
410252	AW521102	Hs.61418	microfilament-associated protein 1	5.55	0.12	upregulated stage
410255	AW000337	Hs.51465	hypothetical protein	10.1	0.07	upregulated stage
410275	AI654545	Hs.68301	ESTs	2.98	0.25	upregulated stage
410278	AW514395	Hs.282230	ESTs	1	0.28	upregulated stage
410325	AG023154	Hs.62264	RAW0937 protein	6.85	0.13	upregulated stage
410358	BE244680	Hs.62643	dual specific phosphotyrosine and 3-ph	1	1	upregulated stage
410388	AA531480	Hs.22030	hepatocyte nuclear factor 3, alpha	1	0.33	upregulated stage
410399	BE068889	Hs.63236	zyneclin, gamma (broad cancer-specific	1.07	0.78	upregulated stage
410420	AA224053	Hs.172405	ESTs, Moderate similar to 152835 H-NUC	1	0.14	upregulated stage
410429	AA310900	Hs.53657	proteoglycan Corecetin A, cartilage, beta p	11.25	0.07	upregulated stage
410442	X73424	Hs.53788	gbrCVO-CT0247-089100-006-e10 CT0247 Homo	5.8	0.08	upregulated stage
410475	AW749327		gbrCVO-CT0237-231295-049-03 ST0537 Homo	9.8	0.00	upregulated stage
410465	NS5428		gbrb305.0151 Soares senescent_fibroblas	11.3	0.06	upregulated stage
410501	AI675898	Hs.63289	ESTs	4.75	0.1	upregulated stage
410503	AW975748	Hs.158662	Homo sapiens cDNA: FLJ23421 f6, clone H	6.6	0.1	upregulated stage
410520	AW752710		gbrL3-CT0219-281099-024-03 CT0219 Homo	1	1	upregulated stage
410534	AW905138		gbrCVO-NH1071-260406-207-g07 NH1071 Homo	3.1	0.16	upregulated stage
410537	AW753108		hypothetical protein FLJ11006	10.35	0.08	upregulated stage
410553	AW016524	Hs.58764	ESTs	1.67	0.41	upregulated stage
410560	NS2920		gbrv43605.1 Soares mal'anancyia 2N6bNM	9	0.07	upregulated stage
410581	BE540255	Hs.6594	Homo sapiens cDNA: FLJ22044 f6, clone H	6.2	0.11	upregulated stage
410582	AW858528		gbrCM3-CT0341-150300-119-h11 CT0341 Homo	1	1	upregulated stage
410579	AW301628	Hs.84831	RAJ0403 protein	11.1	0.06	upregulated stage
410594	AW818553	Hs.260456	ESTs	1	1	upregulated stage
410594	NM_005033	Hs.66370	lipase, endothelial	3.55	0.1	upregulated stage
410688	BE379794	Hs.65403	hypothetical protein	1.82	0.41	upregulated stage
410730	AW368880	Hs.293560	ESTs	5.25	0.07	upregulated stage
410751	AJ357918		gbrEST06726 Fetal lung III Homo sapiens	1	1	upregulated stage
410754	TS3840		gbrv16.10.61 Stratagene lung (537210) H	3.1	0.14	upregulated stage
410782	AF226053	Hs.66170	HSKM-6 protein	5.55	0.1	upregulated stage
410784	AW578159	Hs.750164	ESTs, Weakly similar to coded for by C.	1	0.2	upregulated stage
410782	AW554660	Hs.208838	Homo sapiens cDNA FLJ12673 f6, clone NT	1.75	0.25	upregulated stage
410794	AF240010	Hs.154686	ESTs	1	0.67	upregulated stage
410834	U48420	Hs.56521	Machado-Joseph disease (sphingomyelinar	3.2	0.17	upregulated stage
410844	AW807073		gbrRAR-ST0052-031199-018-d05 ST0062 Homo	1	0.8	upregulated stage
410855	X97795	Hs.56718	RAD54 (Saccharomyces)	6.5	0.12	upregulated stage
410910	AW10204		gbrRAR-ST0155-021199-017-d08 ST0125 Homo	9.35	0.08	upregulated stage
410973	AW812278		gbrRCB-ST0174-211059-011-h12 ST0174 Homo	1	1	upregulated stage
410976	R36207	Hs.25092	ESTs	8.35	0.1	upregulated stage
410997	AW812877		gbrRC3-ST0186-300100-017-e04 ST0186 Homo	1	1	upregulated stage
410998	W28247	Hs.82067	CA4004 protein	2.45	0.18	upregulated stage
411036	AA857218	Hs.297007	ESTs	4.05	0.14	upregulated stage
411110	H93006		gbrvY7D1.1 Soares fetal liver spleen	1	0.36	upregulated stage
411132	AW819131		gbrCM1-ST0283-071299-061-d06 ST0283 Homo	1	1	upregulated stage
411137	AW819465		gbrRC5-ST0283-071299-031-d04 ST0283 Homo	3.65	0.18	upregulated stage
411167	AW118067		gbrCVO-ST0294-100400-151-g01 ST0294 Homo	3.2	0.2	upregulated stage
411169	AW820178		gbrCVO-ST0294-100400-185-g07 ST0294 Homo	1	0.27	upregulated stage
411170	AW820603		gbrCVO-ST0298-140200-042-b05 ST0298 Homo	1	1	upregulated stage
411193	AW821404		gbrL2-ST0311-211299-028-F12 ST0311 Homo	1	0.24	upregulated stage
411242	BE146808		gbrCIV4-HT0225-191059-013-g01 HT0222 Homo	2.55	0.25	upregulated stage
411245	AW833441		gbrCIV4-TT0008-271099-020-g01 TT0008 Homo	5.62	0.09	upregulated stage
411263	BE257802	Hs.69360	kristin like 6 (maltic centromere assoc	2.4	0.32	upregulated stage
411282	AW958011		gbrCVO-EN0040-170000-161-d07 EN0040 Homo	1	1	upregulated stage
411284	N26515	Hs.135591	ESTs, Weakly similar to unnamed protein	3.28	0.12	upregulated stage
411294	AW859725	Hs.42686	ESTs	1	1	upregulated stage
411327	AW836922		gbrCIV1-1T0036-150200-074-b06 LT0036 Homo	1	0.37	upregulated stage
411338	AW731782	Hs.116122	ESTs, Weakly similar to unnamed protein	5	0.13	upregulated stage
411339	BE146588		gbrRC3-HT0470-126200-163-b10 HT0470 Homo	1	0.25	upregulated stage
411383	AA301394	Hs.60749	CA4007 gene product	3.6	0.18	upregulated stage
411387	AW842339	Hs.130815	hypothetical protein FLJ21870	8.75	0.09	upregulated stage
411400	AA311919	Hs.68951	GART protein	12.1	0.07	upregulated stage

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411426	AW846012		gbcRC2-CT0163-230555-003-E01 CT0163 Homo	1	0.74	upregulate stage
411461	AW847937		gbcAL3-CT0213-210203-042-002 CT0213 Homo	1	1	upregulate stage
411526	AW850327		gbcAL3-CT0215-221195-028-008 CT0215 Homo	1	1	upregulate stage
411580	AW851188		gbcAL3-CT0220-160200-071-HS CT0220 Homo	2.8	0.17	upregulate stage
411588	BE144593		gbcMFR4-H10167-141199-002-004 H10167 Homo	1	1	upregulate stage
411571	AA122353	Hi.70811	hypothetical protein FLJ20618	3.55	0.14	upregulate stage
411605	AW068831	Hi.20479	ESTs	9.6	0.08	upregulate stage
411626	AW753453	Hi.71103	KNA1225 protein	1	1	upregulate stage
411630	U42345	Hi.71115	Pu1-like protein cancer tumor suppressor	4.1	0.11	upregulate stage
411643	AI924619	Hi.192570	Homo sapiens cDNA: FLJ22028 fs, clone H	1	0.28	upregulate stage
411653	AF070578	Hi.71158	Homo sapiens clone 24874 mRNA sequence	6.9	0.08	upregulate stage
411727	AW684443		gbcCMC-CT0341-260100-160410 CT0341 Homo	1	1	upregulate stage
411771	AW93247		gbcRC2-BN0033-160200-014-K29 BN0033 Homo	2.8	0.14	upregulate stage
411787	AW963558		gbcMFR3-SN0010-240300-102-010 SN0010 Homo	1	1	upregulate stage
411788	AW877793		gbcFMD1-NN0063-230400-233-007 NN0063 Homo	3.7	0.15	upregulate stage
411826	AW547946		gbcFMD-AT0011-240300-001-a09 MT0011 Homo	3.25	0.13	upregulate stage
411835	U25343	Hi.72550	lysoalbumin-modified molluscy lipocalin [R]	1	1	upregulate stage
411860	T66120		gbcg56804Ls1 Soares fetal liver spleen	1	0.22	upregulate stage
411874	AA08108	Hi.20403	ESTs	6.76	0.11	upregulate stage
411917	AW676360	Hi.3592	Homo sapiens cDNA: FLJ22555 fs, clone H	1	0.33	upregulate stage
411928	AA888624	Hi.19121	adaptor-related protein complex 2, alpha	4.76	0.12	upregulate stage
411932	AW673549		gbcRC2-PT0205-160100-012-M02 PT0205 Homo	1	0.38	upregulate stage
411943	BE523436	Hi.7962	ESTs, Weakly similar to putative [C]oleg	3.82	0.23	upregulate stage
411945	AL033527	Hi.92137	v-myc arisan myelocytomatosis viral onco	4.65	0.15	upregulate stage
411991	X58822	Hi.73010	Interferon, omega 1	2.45	0.14	upregulate stage
412040	D65519	Hi.73008	nerve-specific Y receptor Y8 [pseudogene]	4.8	0.14	upregulate stage
412088	AW64496	Hi.106532	ESTs	2.82	0.18	upregulate stage
412134	AW655660		gbcQV4-NN0036-270400-187-g08 NN0036 Homo	8.74	0.01	upregulate stage
412140	AA215651	Hi.73625	RAB6 interacting, Kinesin-like [milkins]	10.05	0.04	upregulate stage
412221	AW528491	Hi.285908	heat shock 70kD protein 1, alpha	1	0.91	upregulate stage
412296	AW538233		gbcQV4-CT0023-080200-107-a05 DT0020 Homo	1	1	upregulate stage
412327	AW537356		gbcQV5-DT0043-121299-041-a05 DT0043 Homo	1	1	upregulate stage
412357	AW528537		gbcQV1-DT0072-110200-066-K5 DT0072 Homo	1	0.24	upregulate stage
412359	AW637985		gbcQV3-LT0048-140200-053-a05 LT0048 Homo	1	0.41	upregulate stage
412367	AW54864		gbcQV5-ET0001-025300-228-a05 ET0001 Homo	1	0.22	upregulate stage
412369	BZ271224	Hi.268273	Homo sapiens cDNA FLJ13346 fs, clone QV	4.46	0.14	upregulate stage
412530	AA786269	Hi.266273	Homo sapiens cDNA FLJ13346 fs, clone QV	9.3	0.08	upregulate stage
412537	AL031778	Hi.797	nuclear transcription factor Y, alpha	4.25	0.14	upregulate stage
412547	W27151		gbc23412 Human retina cDNA randomly prim	1	1	upregulate stage
412589	T51714		gbcEST33147 Human Embryo Homo sapiens cD	1	0.28	upregulate stage
412636	NM_004415	Hi.74316	desmoplakin (DPI, DPL)	12.05	0.05	upregulate stage
412648	AA116211	Hi.89569	EST	1	0.28	upregulate stage
412668	AA687195	Hi.110056	ESTs	10.75	0.07	upregulate stage
412671	AW977234		gbcEST39993 MAGE resequences, MAGE Homo	2.85	0.3	upregulate stage
412873	AL042957	Hi.31845	ESTs	4.8	0.11	upregulate stage
412723	AA848459	Hi.179512	ESTs	2.55	0.11	upregulate stage
412739	AA118018	Hi.271809	Homo sapiens cDNA: FLJ22406 fs, clone H	1.6	0.24	upregulate stage
412744	ND1101		gbcg52603L1 Soares melanocyte ZbH/M/Ho	2	0.23	upregulate stage
412778	AA120882	Hi.155244	ESTs	1	1	upregulate stage
412811	H05382	Hi.21400	ESTs	1	0.49	upregulate stage
412838	D01870		gbcHUM218F119 Clontech human aorta polyA	1	0.34	upregulate stage
412851	BE004149	Hi.31161	ESTs	1	1	upregulate stage
413075	D69829	Hi.70953	ESTs	1	0.77	upregulate stage
413109	AW389445	Hi.110855	ESTs	3.53	0.1	upregulate stage
413117	BE068107	Hi.138464	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.22	upregulate stage
413119	BE065941		gbcRC2-BT0319-120100-312-412 BT0319 Homo	1	0.87	upregulate stage
413141	B2180323		gbcQV4-H10405-170100-066-412 H10405 Homo	5.45	0.12	upregulate stage
413159	AA878200		Homo sapiens cDNA FLJ13362 fs, clone PL	2.54	0.19	upregulate stage
413228	AA127518	Hi.195870	ESTs	1	1	upregulate stage
413373	U75679	Hi.75257	Hairpin binding protein, histone	3.05	0.11	upregulate stage
413378	BE563085	Hi.833	interferon-stimulated protein, 15 kDa	1.46	0.5	upregulate stage
413394	BE144434		gbcMRC-HT0165-131100-004-002 HT0165 Homo	1	1	upregulate stage
413324	V00571	Hi.75294	corlicortrophin releasing hormone	6.95	0.03	upregulate stage
413342	AA128535		gbc24240L1 Soares_pregnant uterus_NNH	1	1	upregulate stage
413430	FZ2979	Hi.24560	Homo sapiens cDNA FLJ13047 fs, clone HT	3	0.18	upregulate stage
413707	BE16879		gbcCM4-H10385-240100-165-04 H10385 Homo	1	0.28	upregulate stage
413743	BE161004		gbcFMC-H10425-170100-002-003 H10425 Homo	1	1	upregulate stage
413765	U17780	Hi.301103	Human DNA sequence from clone ZFL2.16 on	22.7	0.03	upregulate stage
413782	KW613780	Hi.13500	ESTs	5.95	0.07	upregulate stage
413792	BE168794		gbcCM4-H10501-240300-019-a01 H10501 Homo	1	1	upregulate stage
413804	T64682		gbcg46802L1 Stratagene liver (837224)	0.99	0.75	upregulate stage
413833	Z15005	Hi.75573	centromere protein E [21kDa]	2.55	0.17	upregulate stage
413851	BE174303	Hi.44561	heat shock protein hsp70-related protein	1.25	0.24	upregulate stage
413818	AW018606	Hi.71245	ESTs	4	0.11	upregulate stage
413869	AW925374	Hi.84395	ESTs	10.85	0.07	upregulate stage
414091	T83742		gbcg567g02.s1 Soares fetal liver spleen	8.9	0.1	upregulate stage
414099	U13133	Hi.75760	steatocort carrier protein 2	10.3	0.06	upregulate stage

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5	141416	AA587370	Ha.71584	ESTs	1	1	upregulate stage
	141427	AA431883	Ha.135270	ESTs	2.85	0.13	upregulate stage
	141488	AA138189	Ha.145335	ESTs	8.96	0.05	upregulate stage
	141476	AW972564	Ha.389	Charg-Layton crystal protein	7.06	0.05	upregulate stage
10	141504	AK621278	Ha.185989	DKF-ZP64M2423 protein	1	0.24	upregulate stage
	141538	N80751	Ha.301471	ESTs	10.3	0.08	upregulate stage
	144447	AA147545	Ha.109509	ESTs	3.4	0.16	upregulate stage
	144454	AA788491	Ha.6783	Homo sapiens cDNA: FLJ22724 ts, clone H	3.4	0.15	upregulate stage
15	144500	AA148808	Ha.204045	ESTs	0.17	0.21	upregulate stage
	144569	AF105293	Ha.113253	prostate cancer associated protein 1	3.1	0.18	upregulate stage
	144575	H11257	Ha.259233	ESTs	3.1	0.15	upregulate stage
	144587	H87472	Ha.34274	ESTs	4.6	0.11	upregulate stage
20	145643	I45177	Ha.115316	ESTs	1	0.28	upregulate stage
	145658	S58528	Ha.76781	ATP-binding cassette, sub-family D (ALD)	7.75	0.08	upregulate stage
	144681	T57401	Ha.21529	ESTs	1	0.26	upregulate stage
	144693	S78296	Ha.76938	niemann neuronal intermediate filament	2.72	0.25	upregulate stage
25	144735	BE458018	Ha.261504	ESTs	1	0.38	upregulate stage
	144737	AI160386	Ha.125957	ESTs	5.5	0.1	upregulate stage
	144747	U30872	Ha.77204	centromere protein F (360/400KD, mitotin	3.19	0.24	upregulate stage
	144774	X02419	Ha.77274	plasminogen activator, urokinase	1.45	0.49	upregulate stage
30	144783	AW959569	Ha.76539	zinc finger protein 8 (C/MPX1)	4.65	0.13	upregulate stage
	144795	A752416	Ha.77326	insulin-like growth factor binding prote	1.7	0.46	upregulate stage
	144833	T07114		gbtEST05003 Fetal brain, Striatum (col	4.5	0.13	upregulate stage
	144893	AA020505	Ha.77560	CDC28 protein kinase 1	3.36	0.22	upregulate stage
35	144885	AA157631	Ha.269276	ESTs	2.7	0.21	upregulate stage
	144918	A212887	Ha.72222	Homo sapiens cDNA FLJ13459 fs, clone PL	0.37	0.69	upregulate stage
	144886	CI7372		gbtCI7372 Clontech human scrla polyA+ mR	1	0.42	upregulate stage
	145025	AW207091	Ha.72307	ESTs	5.3	0.06	upregulate stage
40	145033	D31476	Ha.301448	Homo sapiens cDNA FLJ12152 fs, clone MA	1	1	upregulate stage
	145060	AD223810	Ha.43213	ESTs, Weakly similar to IEFS_1/HUMAN TRANS	6.05	0.1	upregulate stage
	145069	T15448	Ha.131837	ESTs, Weakly similar to ORF_U1276 (S.c	4.5	0.13	upregulate stage
	145095	D59592	Ha.34745	ESTs	1	0.44	upregulate stage
45	145095	AA021770	Ha.77917	ubiquitin carboxyl-terminal esterase L3	2.27	0.23	upregulate stage
	145104	D60076		gbtHU0846104 Clontech human fetal brain	3.95	0.13	upregulate stage
	145114	D60489		gbtHU1114058 Clontech human fetal brain	2.65	0.2	upregulate stage
	145138	C18356	Ha.75045	tissue factor pathway inhibitor 2	5.8	0.05	upregulate stage
50	145139	AW975942	Ha.46524	ESTs	1.15	0.21	upregulate stage
	145148	Z38153	Ha.48627	ESTs	2.5	0.2	upregulate stage
	145153	C83508	Ha.7000	ESTs	0.55	0.09	upregulate stage
	145178	D39503		gbtHU0804025 Human fetal brain (Tfujwa	1	0.15	upregulate stage
55	145217	H23983	Ha.26922	ESTs	1	0.31	upregulate stage
	145227	AW821113	Ha.72402	ESTs	6.3	0.11	upregulate stage
	145238	R37780	Ha.21422	ESTs	1	1	upregulate stage
	145241	F02208	Ha.27214	ESTs	1	1	upregulate stage
60	145295	R41450	Ha.6546	ESTs	1	0.53	upregulate stage
	145295	F05085		gbtSC01A011 normalized infant brain cDN	5.65	0.1	upregulate stage
	145327	H22789	Ha.1061	membrane protein, palmitoylated 1 (55KD)	8.15	0.09	upregulate stage
	145330	Z44893	Ha.21422	ESTs	3	0.2	upregulate stage
65	145335	T77654	Ha.78362	Human clone 23839 mRNA sequence	1	0.57	upregulate stage
	145337	Z44881	Ha.6012	ESTs	8.9	0.07	upregulate stage
	145352	F05565		gbtHSC1C0051 normalized infant brain cDN	1	1	upregulate stage
	145364	F06771		gbtHSC1K0031 normalized infant brain cDN	1	1	upregulate stage
70	145371	R15220		gbtR9322.1 Scars infant brain 1/18 H	4.1	0.13	upregulate stage
	145412	F08048	Ha.62132	ESTs	4.25	0.16	upregulate stage
	145451	H19415	Ha.269720	ESTs, Moderately similar to ALU1_HUMAN A	4.1	0.15	upregulate stage
	145462	R52022	Ha.72693	ESTs	4.65	0.11	upregulate stage
75	145466	R37637	Ha.12286	ESTs	5.4	0.13	upregulate stage
	145509	R40000	Ha.51968	ESTs	1	0.44	upregulate stage
	145511	A1732617	Ha.182362	ESTs	5.3	0.03	upregulate stage
	145542	R13474	Ha.290203	ESTs	5.7	0.08	upregulate stage
80	145559	Z43930		gbtHSC1OH121 normalized infant brain cDN	1	0.74	upregulate stage
	145600	F12654		gbtHSC3C0021 normalized infant brain cDN	1	0.43	upregulate stage
	145616	F12545	Ha.12294	ESTs	1	1	upregulate stage
	145625	Z43847		gbtHSC1MC051 normalized infant brain cDN	1	1	upregulate stage
85	145635	F13168		gbtHSC3JF101 normalized infant brain cDN	1	0.26	upregulate stage
	145750	AA157712		gbtZ1H56.1 Striatum INT neuron (EST	1	0.63	upregulate stage
	145786	AW415156	Ha.257924	Homo sapiens cDNA FLJ13782 ts, clone PL	9	0.08	upregulate stage
	145793	AW528585	Ha.78851	KIA00217 protein	5.2	0.11	upregulate stage
90	145793	R23574	Ha.23545	ESTs	1	1	upregulate stage
	145799	AA653718	Ha.226491	DKF-ZP43404513 protein	4.25	0.12	upregulate stage
	145837	H06279	Ha.21708	ESTs	1	0.57	upregulate stage
	145857	AA861115	Ha.301646	Homo sapiens cDNA FLJ11381 fs, clone HE	8.05	0.07	upregulate stage
95	145905	A751367	Ha.238741	Homo sapiens cDNA FLJ22586 ts, clone H	12.2	0.06	upregulate stage
	145947	U04045	Ha.79934	muls (E, cdy) homolog 2 (ovine cancer,	12.2	0.06	upregulate stage
	145948	AA282226		gbt-zd-006.41 NC1_C35P_GCE1 Homo sapiens	1	1	upregulate stage
	145979	H16427	Ha.271501	ESTs	4.85	0.13	upregulate stage
100	145989	A1267700	Ha.111128	ESTs	4.45	0.08	upregulate stage

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5	416018	AW138239	He.78977	proprotein convertase subtilisin/kexin 1	1	1	upregulated stage
	416062	R12816	He.21184	ESTs	1.46	0.24	upregulated stage
	416053	R16359	He.130648	ESTs	4.35	0.14	upregulated stage
	416061	R45816	He.28119	ESTs	1	1	upregulated stage
	416065	BE267931	He.18684	proliferating cell nuclear antigen	4.72	0.17	upregulated stage
10	416097	BE387371	He.301304	Homo sapiens cDNA; FLJ21017 fls, clone C	5.76	0.11	upregulated stage
	416111	AA033813	He.79018	chromatin assembly factor 1, subunit A (8.4	0.09	upregulated stage
	416135	AW138568	He.45119	ESTs	2.29	0.2	upregulated stage
	416155	A807264	He.205442	ESTs, Weakly similar to AF117610.1 inner	5.1	0.13	upregulated stage
	416173	RS2782		gbqy9908r.1 Soares infant brain 1MB H	3.7	0.12	upregulated stage
15	416195	AW131940	He.104030	ESTs	1.1	0.16	upregulated stage
	416196	W51566	He.73372	ESTs	3.25	0.14	upregulated stage
	416203	H27794	He.26555	ESTs	1	0.32	upregulated stage
	416209	AA236776	He.19078	MAO2 (mitotic arrest deficient, yeast, h	4.15	0.12	upregulated stage
	416226	N55342	He.34372	ESTs	2.36	0.21	upregulated stage
20	416239	ALJ38450	He.48948	ESTs	4.06	0.14	upregulated stage
	416241	N52639	He.32663	ESTs	5	0.09	upregulated stage
	416264	H51703	He.13640	ESTs	1	0.65	upregulated stage
	416269	AA177138	He.161671	ESTs	4.07	0.2	upregulated stage
	416276	U41050	He.79136	LNA-1 protein, estrogen regulated	1.84	0.45	upregulated stage
25	416280	H44180	He.181759	ESTs	1	1	upregulated stage
	416309	R84594	He.79194	GMP-responsive element binding protein	8.36	0.08	upregulated stage
	416324	H07983	He.1870	phenylalanine hydroxylase	5.15	0.13	upregulated stage
	416332	H91284	He.244461	ESTs	1	1	upregulated stage
	416343	H45213		gbly1560r.1 Soares fetal liver spleen	1	1	upregulated stage
30	416353	W71727	He.191297	ESTs, Moderately similar to ALU5_HUMAN	1.48	0.59	upregulated stage
	416386	R94675		gbly73e10r.1 Soares fetal liver spleen	9.2	0.09	upregulated stage
	416437	N48990	He.37204	ESTs	4.16	0.12	upregulated stage
	416476	H58137	He.286639	ESTs	1	0.22	upregulated stage
	416537	T99086	He.144504	nuclear receptor co-repressor 1	5.45	0.12	upregulated stage
35	416539	Y07329	He.78384	sphingolipid membrane protein 1	3.45	0.09	upregulated stage
	416575	W02414	He.38383	ESTs	4.96	0.1	upregulated stage
	416624	H89044		gblyr7f05r.1 Soares fetal liver spleen	1	0.22	upregulated stage
	416644	H07071	He.269135	ESTs	5.66	0.12	upregulated stage
	416656	U33272	He.79432	Birb12 (congenital contractural ara	3.65	0.05	upregulated stage
40	416682	R99700	He.36152	ESTs	1	0.26	upregulated stage
	416690	H84078	He.108551	ESTs	5.36	0.13	upregulated stage
	416709	R99369	He.253108	hemoglobin, gamma G	5.4	0.13	upregulated stage
	416712	N85576	He.16122	ESTs	1	0.25	upregulated stage
	416715	H79460	He.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.32	upregulated stage
45	416731	T58116	He.10306	ESTs	1	0.4	upregulated stage
	416734	H81213	He.14625	ESTs	3.8	0.16	upregulated stage
	416736	R11275	He.194485	ESTs	11.5	0.06	upregulated stage
	416738	N25216	He.42250	ESTs	1	0.42	upregulated stage
	416858	N27833	He.290128	ESTs	2.6	0.22	upregulated stage
50	416883	AW140128	He.184902	ESTs	11.3	0.07	upregulated stage
	416923	N34498	He.42829	ESTs	1	0.61	upregulated stage
	416936	N21362	He.42887	ESTs, Weakly similar to ORF2 [Mycovirus	1	1	upregulated stage
	417018	H46638	He.86867	yes-1 Yamaguchi sarcoma viral related	11.3	0.05	upregulated stage
	417079	U65590	He.81134	Interleukin 1 receptor antagonist	5.04	0.15	upregulated stage
55	417134	N15120	He.269058	ESTs	1	0.24	upregulated stage
	417165	NW_002484	He.81469	nucleotide binding protein 1 (E.coli hfr	1.98	0.32	upregulated stage
	417216	AA025247	He.285754	mel proto-oncogene (hepatocyte growth fa	2.96	0.21	upregulated stage
	417286	AL121369	He.281117	ESTs	1	0.3	upregulated stage
	417283	N62840	He.48648	ESTs	1.06	0.27	upregulated stage
60	417308	H69720	He.81892	GAAD101 gene product	9.2	0.09	upregulated stage
	417320	AA195687	He.287324	ESTs	2.6	0.16	upregulated stage
	417336	T98387		gblyr6f02r.1 Soares fetal liver spleen	1	1	upregulated stage
	417404	NW_007360	He.82101	pleckstrin homology-like domain, family	2.75	0.09	upregulated stage
	417409	BE272506	He.82109	synexin 1	1.92	0.44	upregulated stage
65	417448	AA203135	He.130185	ESTs	5.45	0.1	upregulated stage
	417453	H71913	He.128685	ESTs, Moderately similar to unnamed prol	4.65	0.13	upregulated stage
	417516	L24203	He.82237	stenin-3/angiotensin group D-associated	1.59	0.49	upregulated stage
	417540	AA203600	He.152250	ESTs	1	1	upregulated stage
	417576	AA339449	He.82285	phosphoribosylglycylamide formyltransfer	5.65	0.1	upregulated stage
70	417581	R26668	He.21104	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.15	0.09	upregulated stage
	417596	R07343	He.226823	ESTs	4.35	0.14	upregulated stage
	417599	AA204688	He.136201	ESTs, Weakly similar to ALU7_HUMAN ALU S	0.94	0.9	upregulated stage
	417620	R02530	He.191198	ESTs	9.1	0.07	upregulated stage
	417636	R14190	He.188179	ESTs	1	0.32	upregulated stage
75	417650	T05670	He.100540	ESTs	1	0.22	upregulated stage
	417715	AA956587	He.86366	ESTs	6.31	0.09	upregulated stage
	417720	AA205625	He.209057	ESTs	4.65	0.11	upregulated stage
	417742	R64719		gbt5522h.1 WATM1 Homo sapiens cDNA cbs	4.15	0.13	upregulated stage
	417750	AA267220	He.280523	neuroblastoma RAS viral (v-ras) oncogene	5.9	0.08	upregulated stage
	417780	Z13482	He.82272	collagen, type XI, alpha 1	2.3	0.14	upregulated stage
	417789	R50978	He.287054	ESTs	1.05	0.19	upregulated stage

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	417791	AW065336	Hs.111471	ESTs	5.35	0.1	upregulate stage
	417850	AA215724	Hs.82741	pinnae, polypeptide 1 (49kD)	1	1	upregulate stage
	417898	AA604199	Hs.291651	ESTs	2.15	0.21	upregulate stage
	417975	AA641638	Hs.30265	Homo sapiens cDNA: FLJ23185 fls, clone L	3.7	0.13	upregulate stage
5	418004	U37615	Hs.87539	adenylyl dehydrogenase B	1.57	0.5	upregulate stage
	418007	M13505	Hs.83169	matrix metalloproteinase 1 (interstitial)	17.9	0.02	upregulate stage
	418027	AB037807	Hs.83293	hypothetical protein	8.6	0.09	upregulate stage
	418030	BC207573	Hs.63321	neurofilin B	12.2	0.04	upregulate stage
	418064	AW071156	Hs.293902	ESTs, Weakly similar to gphyl-4-hydroxy	4.26	0.14	upregulate stage
10	418113	AL272141	Hs.63484	SRV (tax determining region V)-box 4	5.21	0.15	upregulate stage
	418134	AA397769	Hs.86617	ESTs	1	0.3	upregulate stage
	418153	R13696	Hs.112630	ESTs	1	0.3	upregulate stage
	418180	GS516026	Hs.63724	Human clone 23773 mRNA sequence	8.79	0.09	upregulate stage
	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fls, clone C	3.75	0.13	upregulate stage
15	418203	XS4942	Hs.83758	CDG28 protein kinase 2	13.85	0.04	upregulate stage
	418216	AA662240	Hs.283099	AF15q14 protein	9.75	0.07	upregulate stage
	418236	AW594035	Hs.172572	hypothetical protein FLJ20063	10.75	0.05	upregulate stage
	418250	U32925	Hs.63816	adenosine monophosphate deaminase (bov)	5.25	0.12	upregulate stage
	418259	AA219404	Hs.137289	ESTs	11.5	0.07	upregulate stage
20	418288	AA810596	Hs.86643	ESTs	1	0.43	upregulate stage
	418298	CC1966	Hs.86571	ESTs	1	0.45	upregulate stage
	418372	AA311833	Hs.64318	replication protein A1 (70kD)	9.04	0.08	upregulate stage
	418375	AA216840	Hs.137516	ldgolin-like 1	3.25	0.15	upregulate stage
	418422	AW440088	Hs.59425	Homo sapiens cDNA: FLJ23323 fls, clone H	8.95	0.1	upregulate stage
	418454	AA315038	Hs.82741	gblg-EST16795: Colon carcinoma (HCC) cell	2.25	0.15	upregulate stage
	418462	BC501598	Hs.85266	histH1, beta 4	1.53	0.59	upregulate stage
	418465	U34073	Hs.85273	hypothetical (17-beta) dehydrogenase 1	1.21	0.71	upregulate stage
	418478	U36945	Hs.1174	cyclin-dependent kinase inhibitor 2A (mo	2.69	0.23	upregulate stage
30	418480	AA223925	Hs.86902	ESTs	1	1	upregulate stage
	418498	T76249	Hs.85701	gdyd7905.1 Soares fetal liver spleen	2.47	0.47	upregulate stage
	418515	NL_000218	Hs.85701	phosphoenolpyruvate-3-kinase, catalytic, al	5.4	0.14	upregulate stage
	418545	AA224827	Hs.85701	gblnc32904.1 NCLCGAP_P2: Homo sapiens	2.72	0.23	upregulate stage
	418573	AA225188	Hs.85701	gblnc21040.1 NCLCGAP_P1: Homo sapiens	9.35	0.07	upregulate stage
35	418577	AA225247	Hs.269300	ESTs, Weakly similar to B34087 hypothel	1	0.77	upregulate stage
	418578	U32455	Hs.86294	glutamate receptor, metabotropic 8	1	1	upregulate stage
	418580	AT732672	Hs.252307	ESTs	1	0.59	upregulate stage
	418592	X99225	Hs.284153	Fanconi anemia, complementation group A	4.75	0.13	upregulate stage
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	1	0.23	upregulate stage
40	418624	AT734060	Hs.104211	ESTs	7.35	0.09	upregulate stage
	418691	NL_001949	Hs.1186	Human mRNA for KIAA0075 gene, partial of	3	0.15	upregulate stage
	418693	AK001100	Hs.87013	Homo sapiens cDNA FLJ10238 fls, clone HE	17.2	0.04	upregulate stage
	418675	AW295723	Hs.87223	bone morphogenetic protein receptor, typ	1	1	upregulate stage
	418696	Z36930	Hs.87268	aminex A6	2.11	0.3	upregulate stage
	418697	FE1950	Hs.22581	ESTs	8.75	0.07	upregulate stage
45	418693	AT750878	Hs.87409	thrombospondin 1	4.5	0.06	upregulate stage
	418704	AA227235	Hs.83286	ESTs	1	0.33	upregulate stage
	418712	Z42183	Hs.86984	gbl-HS06F041 normalized infant brain cDN	1	0.81	upregulate stage
	418717	AB344300	Hs.86984	ESTs	4.7	0.12	upregulate stage
	418723	AA504428	Hs.10467	ESTs, Weakly similar to Weak similarity	5.95	0.1	upregulate stage
50	418738	AW388633	Hs.6682	ESTs	3.8	0.09	upregulate stage
	418752	AL133559	Hs.88144	hypothetical protein FLJ12476	1	1	upregulate stage
	418757	AB541193	Hs.168728	Homo sapiens cDNA FLJ15150 fls, clone NT	9.15	0.09	upregulate stage
	418844	BC5282	Hs.1202	archivione 12-lypoxygenase	9.25	0.06	upregulate stage
	418857	D31771	Hs.89404	men (Drosophila) homeo box homolog 2	1.83	0.43	upregulate stage
55	418875	AA740816	Hs.253674	ESTs	11.3	0.06	upregulate stage
	418903	AW989665	Hs.154848	ESTs	1	1	upregulate stage
	418915	AA747778	Hs.116077	ESTs	4.75	0.12	upregulate stage
	418939	AW530803	Hs.85497	lamin B1	2.6	0.13	upregulate stage
60	418945	BE246782	Hs.85499	archivione 5-lipoxygenase	1.45	0.53	upregulate stage
	418975	AA503082	Hs.126883	ESTs	1	0.23	upregulate stage
	419059	T8215	Hs.85499	gdyd7905.1 Soares fetal liver spleen	1	0.38	upregulate stage
	419078	MS1116	Hs.85684	insulinoma-associated 1	1.25	0.18	upregulate stage
	419121	AA374372	Hs.85626	parathyroid hormone-like hormone	1	1	upregulate stage
	419159	AW651980	Hs.252348	ESTs, Weakly similar to ORF2: function u	1.59	0.23	upregulate stage
65	419163	U30669	Hs.86983	cyclinHme P450, subfamily XXIV (vitamin	3.55	0.05	upregulate stage
	419219	AA248073	Hs.186723	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.27	upregulate stage
	419226	AL342451	Hs.87413	ESTs	1	0.37	upregulate stage
	419235	AW470411	Hs.288433	neurofmin	11.9	0.07	upregulate stage
	419285	AA238005	Hs.221303	ESTs	4.35	0.14	upregulate stage
	419327	AA521504	Hs.186719	ESTs	1	1	upregulate stage
	419335	AA426520	Hs.51061	progesterone binding protein	10.8	0.06	upregulate stage
	419356	AL43202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.84	0.47	upregulate stage
	419413	AA337040	Hs.87589	ESTs	1	1	upregulate stage
	419436	AA591939	Hs.15093	ESTs, Highly similar to AF161358.1 HSPC0	6.6	0.1	upregulate stage
75	419452	U33635	Hs.30572	PTK7 protein tyrosine kinase 7	1.81	0.64	upregulate stage
	419472	AW578338	Hs.87846	gbl-EST330147 MAGC resequences, MAGC Homo	1	1	upregulate stage
	419475	AA243420	Hs.87846	ESTs	1.1	0.24	upregulate stage

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	149477	AA828279	Hs.272128	gbz00307.s1 NCL_CGAP_GCB1 Homo sapiens	1	0.56	upregulated stage
	149484	AA243474	Hs.42389	Homo sapiens cDNA FLJ13901 fs, clone TH1	1	0.22	upregulated stage
	149506	NQ0912	Hs.42389	ESTs	1	1	upregulated stage
	149554	A732138	Hs.42418	ESTs	1	0.5	upregulated stage
5	149569	A371651	Hs.91143	Jagged 1 (Alagille syndrome)	1	0.91	upregulated stage
	149594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.1	0.08	upregulated stage
	149595	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide exchan	1	1	upregulated stage
	149598	NM_014810	Hs.92200	NA-0480 gene product	5.2	0.12	upregulated stage
	149737	I24185	Hs.92914	hypothetical protein	11.7	0.07	upregulated stage
	149743	AA040872	Hs.127478	ESTs	6.1	0.09	upregulated stage
	149752	AA249573	Hs.152618	ESTs	1.8	0.17	upregulated stage
	149789	H27374	Hs.103483	ESTs	1	0.36	upregulated stage
	149805	AW369405	gb:EST370019 MAGE resequences, MAGU Homo	1	0.34	upregulated stage	
	149807	R77402	gb:Y7591.1.s1 Soares placenta NCo2HP Homo	1	0.67	upregulated stage	
	149831	AW448930	Hs.5415	ESTs	7.05	0.1	upregulated stage
	149833	AA251131	Hs.220897	ESTs	1.25	0.53	upregulated stage
	149834	AA251139	Hs.220897	gbz00307.12.s1 NCL_CGAP_GCB1 Homo sapiens	1	1	upregulated stage
	149923	AW081455	Hs.120219	ESTs	5.89	0.13	upregulated stage
	149945	AW250975	Hs.189923	ESTs	1	0.24	upregulated stage
	149962	AA630111	Hs.291917	ESTs	1	1	upregulated stage
	149970	AW612022	Hs.263271	ESTs	9.15	0.09	upregulated stage
	149986	AJ345455	Hs.78915	CA-binding protein transcription factor	3.05	0.17	upregulated stage
	149998	AA252891	Hs.88025	gbz002609.r1 NCL_CGAP_GCB1 Homo sapiens	1	0.47	upregulated stage
	150016	AW016908	Hs.88025	ESTs	1	0.8	upregulated stage
	150047	AA478658	Hs.94531	breaklin A-inhibited guanine nucleotide	4.8	0.11	upregulated stage
	150076	AA627860	Hs.293717	ESTs	5.35	0.12	upregulated stage
	150111	AA255992	Hs.293717	gbz002111.r1 NCL_CGAP_GCB1 Homo sapiens	5.3	0.11	upregulated stage
	150145	AA659880	Hs.295284	ESTs	1	1	upregulated stage
	150159	AS572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fs, clone C	14.8	0.04	upregulated stage
	150181	AA63069	Hs.175319	ESTs	4.7	0.11	upregulated stage
	150184	A118408	Hs.95565	hypothetical protein	4.35	0.15	upregulated stage
	150226	AA773709	Hs.152818	ubiquitin specific protease 8	3.1	0.18	upregulated stage
	150230	AL034344	Hs.288020	Homo sapiens cDNA FLJ11796 fs, clone HE	10.35	0.06	upregulated stage
	150236	AA255763	Hs.291111	ESTs	14.45	0.14	upregulated stage
	150270	AA257590	Hs.293717	gbz00307.r1 NCL_CGAP_GCB1 Homo sapiens	10.05	0.08	upregulated stage
	150297	AJ828272	Hs.88323	ESTs	9.45	0.09	upregulated stage
	150344	BE483721	Hs.97101	putative G protein-coupled receptor	11.7	0.05	upregulated stage
	150392	AJ242930	Hs.97363	KIAA0328 protein	1.7	0.22	upregulated stage
	150413	AW971824	Hs.102605	ESTs	1	1	upregulated stage
	150445	AJ262213	Hs.193014	ESTs	1	1	upregulated stage
	150471	AA262452	Hs.192268	ESTs	3.95	0.13	upregulated stage
	150479	AW183895	Hs.188572	ESTs	4.95	0.12	upregulated stage
	150493	AJ635113	Hs.270386	Homo sapiens mRNA; cDNA DKFZps54H0616 (I	4.4	0.15	upregulated stage
	150552	AJ020492	Hs.98006	hypothetical protein	11.55	0.05	upregulated stage
	150572	AL035593	Hs.99015	Human DNA sequence from clone 310J6 on c	1.35	0.22	upregulated stage
	150643	W87731	Hs.44581	gbz00559.10.r1 Soares_fetal_liver_spee_n	1.25	0.25	upregulated stage
	150650	AA455706	Hs.44581	heat shock protein hsp70-related protein	7.3	0.09	upregulated stage
	150654	AJ279091	Hs.104420	ESTs	1	0.27	upregulated stage
	150655	RA4405	Hs.300868	ESTs	1	1	upregulated stage
	150717	AA284447	Hs.271887	ESTs	9	0.09	upregulated stage
	150734	AW972872	Hs.293736	ESTs	5.2	0.13	upregulated stage
	150756	AA411800	Hs.169900	ESTs	1	1	upregulated stage
	150789	AJ70057	Hs.159892	ESTs	8.85	0.06	upregulated stage
	150802	U22376	Hs.1334	v-myc avian myeloblastosis viral oncogen	4.8	0.12	upregulated stage
	150851	AA281062	Hs.250734	ESTs	8.35	0.08	upregulated stage
	150880	AJ039221	Hs.105520	ESTs	1	1	upregulated stage
	150923	AF057021	Hs.273321	differentially expressed in hematopoiesi	10.4	0.03	upregulated stage
	150928	AA281809	Hs.95410	gbz010601.r1 NCL_CGAP_GCB1 Homo sapiens	1	1	upregulated stage
	150936	AA458112	Hs.47198	ESTs	8.71	0.07	upregulated stage
	150947	AA491044	Hs.47198	ESTs	1	0.38	upregulated stage
	151017	AW979181	Hs.263221	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	upregulated stage
	151064	AA245432	Hs.19327	tumor necrosis factor, alpha-induced pro	1.28	0.82	upregulated stage
	151070	AA263185	Hs.19327	ESTs	2.2	0.14	upregulated stage
	151100	AW351839	Hs.124680	Homo sapiens cDNA: FLJ21763 fs, clone C	1.59	0.28	upregulated stage
	151102	AJ070053	Hs.89217	ESTs	2.65	0.19	upregulated stage
	151103	AJ259315	Hs.27104	ESTs	5	0.1	upregulated stage
	151114	AW975051	Hs.250156	ESTs	4.7	0.12	upregulated stage
	151118	AA71925	Hs.89257	ESTs	1	0.39	upregulated stage
	151155	H87879	Hs.102267	lysyl oxidase	1.15	0.18	upregulated stage
	151159	AW978216	Hs.136249	ESTs	1	0.44	upregulated stage
	151187	NM_014721	Hs.102471	KIAA0890 gene product	5.7	0.11	upregulated stage
	151218	NM_000489	Hs.72912	cytochrome P450, subfamily 1 (aromatic c	0.07	2.55	upregulated stage
	151221	AW278914	Hs.300877	ESTs	8.75	0.07	upregulated stage
	151229	AJ065590	Hs.7088	Homo sapiens cDNA: FLJ23000 fs, clone L	1.94	0.29	upregulated stage
	151281	AA026563	Hs.88133	ESTs	19.9	0.07	upregulated stage
	151282	AA267448	Hs.9343	Homo sapiens cDNA FLJ14265 fs, clone PL	2.65	0.16	upregulated stage
	151278	A367919	Hs.99891	ESTs	1	0.58	upregulated stage

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421280	AA81180.4		gbb39a05.s1 NCL_OGAP_1GCB1 Homo sapiens	1	0.34	upregulate stage
421282	AA286514	Ha.183259	ESTs	9	0.08	upregulate stage
421306	AA806207	Ha.125809	ESTs	1	0.95	upregulate stage
421308	AA687522	Ha.152843	ESTs	2.85	0.15	upregulate stage
421373	AA608226	Ha.167771	ESTs	2.45	0.14	upregulate stage
421379	Y15221	Ha.103582	small inducible cytokine subfamily B (C)	1.6	0.26	upregulate stage
421381	AA361752		gblEST171314 T-cell lymphoma Homo sapiens	5.05	0.09	upregulate stage
421418	AA508639		gbb39a05.s1 NCL_OGAP_1GCB1 Homo sapiens	5.55	0.1	upregulate stage
421433	AB25102	Ha.134605	ESTs	9.9	0.07	upregulate stage
421461	AA329177	Ha.50031	ESTs	11.9	0.06	upregulate stage
421491	H99959	Ha.42736	ESTs	3	0.2	upregulate stage
421493	EE100341	Ha.104525	ectodermal-neural crest (with 3TB-like	2.51	0.32	upregulate stage
421558	NM_014720	Ha.105151	Slc20-related carrier/transporter kinase	5	0.29	upregulate stage
421577	BE646451	Ha.105526	single-minded (Drosophila) homolog 1	5.75	0.12	upregulate stage
421673	H54384	Ha.36892	ESTs	1	1	upregulate stage
421686	AF189723	Ha.106778	ATPase, Ca++ transporting, type 2C, memb	9.45	0.07	upregulate stage
421708	AW754341		gbcCMB-CT0341-101259-130-h12 CT0341 Homo	1	0.47	upregulate stage
421735	AL119871	Ha.1420	fibroblast growth factor receptor 3 (sch	1.97	0.33	upregulate stage
421838	AAW81089	Ha.108805	Homo sapiens mRNA; cDNA DKFZ5569M0047 (f	7.05	0.1	upregulate stage
421869	AB003592	Ha.109050	contafid 6	1	1	upregulate stage
421925	ESG310	Ha.109620	acidic epididymal glycoprotein-like 1	1	1	upregulate stage
421948	L42523	Ha.111159	vaselin 5A	61.9	0.01	upregulate stage
421968	AA367185	Ha.109518	ras homolog gene family, member H	10.17	0.07	upregulate stage
421991	NM_014918	Ha.104088	GAO59C protein	4.5	0.17	upregulate stage
422025	UB0736	Ha.110626	trinucleotide repeat containing 9	6.5	0.08	upregulate stage
422072	AB016255	Ha.111138	FLJ400712 gene product	3.2	0.08	upregulate stage
422084	AF126536	Ha.102027	F-box only protein 5	6.55	0.09	upregulate stage
422169	L10543	Ha.112341	protease inhibitor 3, skin-derived (SKAL	1.66	0.17	upregulate stage
422168	AA586894	Ha.112408	S100 calcium-binding protein AF (psorias	3.95	0.1	upregulate stage
422182	AA143892	Ha.106882	Homo sapiens cDNA: FLJ21536 fs, clone H	2.8	0.16	upregulate stage
422204	AA530015		gblEST142407 Fetal brain 1 Homo sapiens e	1	1	upregulate stage
422221	AA317595	Ha.119908	nuclear protein NCPANCP58	1	1	upregulate stage
422271	AB038995	Ha.114159	RAB-5b protein	5.04	0.16	upregulate stage
422278	AF072873	Ha.114218	ritized (Drosophila) homolog 6	3.48	0.24	upregulate stage
422282	AF019225	Ha.114309	apoptoprotein 1	4.54	0.14	upregulate stage
422322	AB022192	Ha.115240	pericentromeric biogenesis factor 13	1	0.53	upregulate stage
422330	D30783	Ha.115283	ephrinA1	4.45	0.06	upregulate stage
422342	AA309272		gblEST180209 Liver, hepatocellular carc	2.25	0.19	upregulate stage
422406	AF025441	Ha.116203	Cip-interacting protein 5	9.5	0.07	upregulate stage
422487	AJ011901	Ha.198287	metc-4, tracheobronchial	7.55	0.04	upregulate stage
422491	AA338548	Ha.117545	neurostatin	0.64	1.24	upregulate stage
422504	AA311407		gblEST182167 Jurkat T-cells V Homo sapie	3.6	0.11	upregulate stage
422505	AL120862	Ha.124185	ESTs	2.8	0.14	upregulate stage
422508	AJ003027	Ha.117852	ATP-binding cassette, sub-family D (ALD)	5.35	0.14	upregulate stage
422530	AW972300	Ha.118110	bone marrow stromal cell antigen 2	2.57	0.31	upregulate stage
422540	AW60751	Ha.122895	Homo sapiens cDNA: FLJ23548 fs, clone L	1	0.59	upregulate stage
422588	AA312730		gblEST116351 Monocytes, stimulated H ho	3	0.14	upregulate stage
422678	AA247778	Ha.119165	Homo sapiens mRNA; cDNA DKFZ546249 (fr	10.7	0.07	upregulate stage
422782	AL031320	Ha.119576	Human DNA sequence from clone RP1-20N2 o	5.1	0.13	upregulate stage
422809	AK061379	Ha.121028	hypothetical protein FLJ10649	5.94	0.1	upregulate stage
422823	D89974	Ha.121102	varin 2	10	0.07	upregulate stage
422852	AA386178	Ha.121563	hypothetical protein FLJ20641	1	0.27	upregulate stage
422938	NM_001009	Ha.1564	ectodermal protein A (TPD)	7.2	0.08	upregulate stage
422964	AW438478	Ha.126895	ESTs	11.75	0.07	upregulate stage
422981	AF026445	Ha.122752	TATA box binding protein (TBP)-associated	3.06	0.14	upregulate stage
423001	AA320214	Ha.20863	ESTs	5.1	0.09	upregulate stage
423030	BC187629	Ha.173536	melanoma antigen, family E, 1, carcino	1	0.49	upregulate stage
423100	AA323114		gblEST25873 Cerebellum II Homo sapiens c	1	1	upregulate stage
423121	AW864848		gblPM2-SN0018-29030-003-c05 SN0018 Homo	2.8	0.19	upregulate stage
423165	AA131493	Ha.124752	ribosomal protein factor 126	1	0.27	upregulate stage
423196	M01553	Ha.1634	cell division cycle 25A	8.95	0.17	upregulate stage
423217	NM_000054	Ha.172635	collagen, type VII, alpha 1 (epidermome)	1.2	0.57	upregulate stage
423262	NM_005479	Ha.126057	frequently rearranged in advanced T-cell	9.75	0.07	upregulate stage
423296	AW557193	Ha.3327	Homo sapiens cDNA: FLJ22215 fs, clone H	4.95	0.12	upregulate stage
423309	BE060775	Ha.126782	anti-viral protein	1.58	0.34	upregulate stage
423347	AB654112	Ha.234557	ESTs	1	0.45	upregulate stage
423359	NM_014170	Ha.127495	HSPC135 protein	1	0.69	upregulate stage
423368	AA364195		gblEST75015 Pituitary gland II Homo sapiens	1	0.95	upregulate stage
423389	AA171608	Ha.54347	ESTs	3.95	0.14	upregulate stage
423430	AF112861	Ha.128511	RAD51A, S. cerevisiae, homolog of, B	1.52	0.43	upregulate stage
423441	BE8849	Ha.127657	absent in melanoma 1 like	6.25	0.1	upregulate stage
423453	AW450737	Ha.128791	CGI-05	8.45	0.09	upregulate stage
423500	AF020763	Ha.129705	clone 1500 unknown protein	1	0.8	upregulate stage
423578	AW364543	Ha.272830	ESTs	11.54	0.07	upregulate stage
423625	AW021173	Ha.18912	Homo sapiens cDNA: FLJ21909 fs, clone H	3.4	0.17	upregulate stage
423632	AA328924		gblEST32558 Embryo, 12 week I Homo sapie	1	0.71	upregulate stage
423642	AW452650	Ha.157148	Homo sapiens cDNA FLJ11883 fs, clone HE	8.35	0.1	upregulate stage

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5	425322	U83830	Ha.155637	protein kinase, DNA-activated, catalytic	14.7	0.05	upregulate stage
	425382	AA355936		gb:EST64410 Jervik T-cells VI Homo sapi	1	1	upregulate stage
	425397	J04088	Ha.156348	lipotelectinase (DNA) II alpha (17090)	8.24	0.09	upregulate stage
	425403	AL023753	Ha.156408	Human DNA sequences from clone 1189H on	1	0.22	upregulate stage
	425415	M13903	Ha.157091	ESTs, Weakly similar to AF156135 1 novel	1.19	0.55	upregulate stage
10	425420	BES36511	Ha.224645	ESTs, Weakly similar to AF156135 1 novel	2.86	0.13	upregulate stage
	425483	AK000740	Ha.157988	hypothetical protein FLJ20793	9	0.07	upregulate stage
	425485	118994	Ha.157984	protein kinase C, δ iso	3.6	0.07	upregulate stage
	425487	R18484	Ha.190075	ESTs	1	0.63	upregulate stage
	425492	AL021918	Ha.159174	zinc finger protein 164 (Kruppel-like)	3.2	0.15	upregulate stage
15	425607	U09860	Ha.158333	protease, serine, 7 (serine/threonine)	1	1	upregulate stage
	425608	AA300486	Ha.162448	ESTs	4.7	0.14	upregulate stage
	425614	A034963	Ha.156256	twelchin	2.65	0.14	upregulate stage
	425641	D79758	Ha.143355	Homo sapiens cDNA FLJ13207 f1a, clone NT	4.88	0.1	upregulate stage
	425660	AA521184	Ha.105604	ESTs	1	0.31	upregulate stage
20	425665	AK001050	Ha.159056	hypothetical protein FLJ10108	1.25	0.19	upregulate stage
	425672	AA361463		gb:EST70790 T-cell lymphoma -homo sapiens	1	1	upregulate stage
	425707	AF115402	Ha.11713	ET4-like factor 5 (ole domain transcript)	3.96	0.13	upregulate stage
	425726	AF085808	Ha.159330	uroporphlin	0.92	0.79	upregulate stage
	425742	AJ001454	Ha.159425	lesican 3	1	1	upregulate stage
25	425786	T2017	Ha.159528	Homo sapiens clone 2460 mRNA sequence	1	0.39	upregulate stage
	425811	AL009104	Ha.159557	carboxypeptidase alpha 2 (RAG cohort 1, impor	1.89	0.44	upregulate stage
	425843	BE313280	Ha.159827	death associated protein 3	3.1	0.15	upregulate stage
	425852	AK001504	Ha.159651	death receptor 6	1.72	0.47	upregulate stage
	425883	AL137708	Ha.151031	Homo sapiens mRNA: cDNA DKFZP434K0322 (f	0.95	0.88	upregulate stage
30	426010	AA135653	Ha.15975	Homo sapiens cDNA: FLJ21007 f1a, clone C	0.74	0.34	upregulate stage
	426028	NM_001110	Ha.172028	a disintegrin and metalloproteinase domain	14.3	0.04	upregulate stage
	426101	AL049887	Ha.159361	Homo sapiens mRNA: cDNA DKFZP664F112 (f	11.75	0.05	upregulate stage
	426108	AA522037	Ha.158458	programmed cell death 5	3.23	0.18	upregulate stage
	426115	H08895	Ha.155733	leucyl(tyr)-l-aminopeptidase	0.22	0.22	upregulate stage
35	426188	NM_001152	Ha.157503	signal transducer and activator of trans	1.97	0.4	upregulate stage
	426192	AL137201	Ha.158625	KIAA00175 protein	1	0.29	upregulate stage
	426281	AW242243	Ha.158670	peroxisomal fatty-acylated protein	2.8	0.15	upregulate stage
	426283	NM_003937	Ha.159139	lysine aminotransferase (L-lysine: NAD(P)+	14.75	0.04	upregulate stage
	426451	A058165	Ha.158946	GATA-binding protein 3	3.05	0.28	upregulate stage
40	426482	U59111	Ha.158995	dermatan sulphate proteoglycan 3	1	0.36	upregulate stage
	426490	NM_001521	Ha.170087	aryl hydrocarbon receptor	14.17	0.05	upregulate stage
	426514	BE316633	Ha.301122	bone morphogenetic protein 7 (osteogenic	1.15	0.47	upregulate stage
	426581	AA361437		gb:EST94514 Activated T-cells 1 Homo sap	5.65	0.11	upregulate stage
	426711	AA383411	Ha.180669	conserved gene amplified in osteosarcoma	11.05	0.05	upregulate stage
45	426731	AW300411	Ha.130332	ESTs	2.4	0.21	upregulate stage
	426759	A050401	Ha.21213	ESTs	9.5	0.06	upregulate stage
	426786	AA319798	Ha.172247	eukaryotic translation elongation factor	5.25	0.09	upregulate stage
	426788	U08616	Ha.172290	SV40SWT related, matrix associated, acti	6.65	0.14	upregulate stage
	426818	AA554827	Ha.124841	ESTs, Weakly similar to ALJUS_HUMAN ALJUS	9	0.08	upregulate stage
50	426824	D87717	Ha.172652	KIAA0013 gene product	1	0.87	upregulate stage
	426827	AW067805	Ha.172665	methyltetrahydrofolate dehydrogenase	8.55	0.09	upregulate stage
	426921	A0537145	Ha.172865	cleavage stimulation factor, 2' pre-RNA,	1	0.15	upregulate stage
	426935	NM_000088	Ha.172526	collagen, type I, alpha 1	1.15	0.72	upregulate stage
	426997	BES20738	Ha.173125	peptidylprolyl isomerase F (cyclophilin	11.06	0.06	upregulate stage
55	427071	AA397958	Ha.159219	ESTs	5.75	0.08	upregulate stage
	427126	AA620813	Ha.159127	ESTs	2.55	0.18	upregulate stage
	427134	AA384096	Ha.173861	EST	3.4	0.13	upregulate stage
	427142	AA396510	Ha.133148	ESTs	1	0.25	upregulate stage
	427259	AA400096		gb:z1907.611 Soares_leslie_NHT Homo sap	1	0.22	upregulate stage
60	427338	D26867	Ha.174905	KIAA0033 protein	5.9	0.1	upregulate stage
	427315	AA178949	Ha.175693	Homo sapiens mRNA: cDNA DKFZP564N0763 (f	6.12	0.11	upregulate stage
	427356	AAW023482	Ha.97849	ESTs	2.7	0.13	upregulate stage
	427370	A243815	Ha.97740	ESTs	3.6	0.14	upregulate stage
	427376	AA401533	Ha.19440	ESTs	2.1	0.16	upregulate stage
65	427378	BE314866	Ha.173584	5-oxopropyl CoA transferase	0.8	0.39	upregulate stage
	427470	AW090924	Ha.178357	Homo sapiens cDNA FLJ13567 f1a, clone PL	3.4	0.16	upregulate stage
	427519	AW086233	Ha.180696	ESTs	8.23	0.1	upregulate stage
	427521	AW973362	Ha.299056	ESTs	7.75	0.1	upregulate stage
	427528	AJ077143	Ha.179565	mitochondriome maintenance deficient (S,	5.7	0.15	upregulate stage
70	427566	A0745815		gb:U72869-z2 Soares_NFL_T-CEB, S1 Homo s	1	1	upregulate stage
	427581	NM_014788	Ha.179703	KIAA0129 gene product	11.45	0.06	upregulate stage
	427585	D31152	Ha.179729	collagen, type X, alpha 1 (Schmid metaph	3.25	0.16	upregulate stage
	427603	A090038	Ha.98006	ESTs	1	1	upregulate stage
	427646	A078042	Ha.271545	ESTs	5.7	0.11	upregulate stage
75	427657	A073025	Ha.43674	ESTs	1	0.34	upregulate stage
	427742	AA411880	Ha.190888	ESTs	2.4	0.16	upregulate stage
	427814	W26363	Ha.180900	Williams-Beuren syndrome chromosome reg	9.13	0.08	upregulate stage
	427839	AA508823	Ha.186244	ESTs	1.9	0.19	upregulate stage
	427878	C97768	Ha.161622	GCH-47 protein	4.1	0.14	upregulate stage
	427922	AK001534	Ha.161112	HSPC126 protein	2.6	0.19	upregulate stage
	427933	AW074643	Ha.190571	ESTs	4.55	0.14	upregulate stage

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	427934	AA810541	Hs.291866	ESTs	1	1	upregulate stage
	427944	AA417878	Hs.48401	ESTs, Weakly similar to ALUR, HUMAN ALU S	6.15	0.11	upregulate stage
	427961	AW293155	Hs.143134	ESTs	4.85	0.11	upregulate stage
	427966	NA5214	Hs.262367	Homo sapiens cDNA: FLJ121837 fls, clone H	3.55	0.13	upregulate stage
5	428003	AL110200	Hs.181384	Homo sapiens mRNA; cDNA DKFZp968I0622 (f	1.45	0.36	upregulate stage
	428004	AA449563	Hs.300220	ESTs	3.55	0.12	upregulate stage
	428010	AA806554	Hs.183375	ESTs	1	0.38	upregulate stage
	428057	AS343641	Hs.185708	ESTs	10.1	0.06	upregulate stage
	428068	AB211626	Hs.191602	ESTs	1	0.5	upregulate stage
10	428071	AF1212848	Hs.182339	etc homologous factor	6.4	0.09	upregulate stage
	428182	B5386042	Hs.230317	ESTs, Weakly similar to JM27 (H.sapiens)	1	0.23	upregulate stage
	428192	AA424051		gbczw06003.1 Soares, total_kidney, Rb27H98,	2.45	0.16	upregulate stage
	428227	AA321549	Hs.2248	small inducible cytokine subfamily B (Cyt	9.25	0.04	upregulate stage
	428403	AI353048	Hs.235954	luciferase (luc) repeat (in FLJ) intradon	9.45	0.06	upregulate stage
15	428436	BE080180		gbcRC4BT0626-120200-011-410 BT0629 Homo	1	1	upregulate stage
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.43	0.16	upregulate stage
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.2	0.07	upregulate stage
	428529	AW252022	Hs.185577	Homo sapiens cDNA: FLJ126335 fls, clone NT	1	1	upregulate stage
	428576	AW009330	Hs.167621	ESTs	1	0.3	upregulate stage
20	428605	A8037862	Hs.187596	KIAA1441 protein	3.25	0.05	upregulate stage
	428664	AK001666	Hs.186995	similar to SALL1 (rat) (Drosophila)-like	3.8	0.08	upregulate stage
	428685	AF131353	Hs.185527	Homo sapiens clone 25016 mRNA sequence	1	1	upregulate stage
	428716	AL122118	Hs.190614	Homo sapiens mRNA; cDNA DKFZp434O1221 (f	1	0.65	upregulate stage
	428763	AW070204	Hs.178176	ESTs	1.6	0.23	upregulate stage
25	428768	AF062283	Hs.193515	B-cell CLL/lymphoma 10	9.6	0.08	upregulate stage
	428829	R14069	Hs.194251	Homo sapiens mRNA; cDNA DKFZp968I213 (fr	5.45	0.11	upregulate stage
	428839	AI757756	Hs.82302	ESTs	10	0.06	upregulate stage
	428881	AI281368	Hs.98516	ESTs	1.4	0.18	upregulate stage
30	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein	1	1	upregulate stage
	428988	AA442900	Hs.27047	ESTs	3.06	0.13	upregulate stage
	429042	AW015405	Hs.236520	ESTs	1	0.56	upregulate stage
	429057	AF155557	Hs.194819	stannin-like protein 1	0.95	0.53	upregulate stage
	429066	AA868555	Hs.176222	ESTs	6	0.11	upregulate stage
35	429072	AI376228	Hs.106043	Friend leukemia virus integration 1	1	1	upregulate stage
	429083	Y06387	Hs.227817	812.2-related protein A1	11.2	0.03	upregulate stage
	429091	AA935658	Hs.187539	ESTs	63	0.08	upregulate stage
	429115	AA446728	Hs.285020	Homo sapiens cDNA: FLJ14058 fls, clone MA	4.1	0.17	upregulate stage
	429127	AA748382	Hs.107233	ESTs	1	0.23	upregulate stage
	429135	AA446566	Hs.99560	ESTs, Moderately similar to similar to K	1	1	upregulate stage
40	429170	NM_001354	Hs.5265	dual specificity phosphatase 4	8.6	0.08	upregulate stage
	429174	BE559598	Hs.197803	KIAA0160 protein	8.4	0.06	upregulate stage
	429236	AA448407		gbczw68d1.1.s1 Soares, testis_NHT Homo sap	1	0.36	upregulate stage
	429268	AA205396	Hs.198481	RAR-related orphan receptor B	25	0.16	upregulate stage
	429300	AB011108	Hs.198951	serine/threonine-protein kinase PRP4 hom	4.25	0.15	upregulate stage
45	429334	CB3078	Hs.185180	Homo sapiens cDNA: FLJ23036 fls, clone S	2.95	0.11	upregulate stage
	429344	R64038	Hs.195538	Inhibin, beta C	2.51	0.28	upregulate stage
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.19	0.68	upregulate stage
	429376	AB877889	Hs.43227	ESTs	1	1	upregulate stage
50	429412	NM_009235	Hs.2407	PCU domain, class 2, associating factor	8.15	0.07	upregulate stage
	429460	AA824451	Hs.94292	Homo sapiens cDNA: FLJ23311 fls, clone H	3.3	0.17	upregulate stage
	429482	AW452421	Hs.16652	ESTs	1	1	upregulate stage
	429492	AF076974	Hs.203952	transformation/transcription domain-asso	1.52	0.59	upregulate stage
	429496	AF156227	Hs.203963	lymphoid protein FLJ10339	2.9	0.15	upregulate stage
	429572	AW295375	Hs.38474	ESTs	1	0.95	upregulate stage
55	429584	AB187785	Hs.183037	protein kinase, cAMP-dependent, regulato	6.55	0.1	upregulate stage
	429602	AD218490	Hs.44445	ESTs, Weakly similar to Ketch motif cont	1	1	upregulate stage
	429597	NM_003816	Hs.2445	a diacylglycerol and neutral sphingolipase doma	5.6	0.14	upregulate stage
	429601	AI804293	Hs.115406	ESTs, Weakly similar to AF143548 1 trans	1.38	0.58	upregulate stage
	429602	AA521463	Hs.183424	ESTs	1	0.34	upregulate stage
60	429617	X85994	Hs.211563	R-cell CLL/lymphoma 7A	10.8	0.07	upregulate stage
	429623	BE501732	Hs.30622	Homo sapiens cDNA FLJ13016 fls, clone NT	3.4	0.12	upregulate stage
	429631	AA459612	Hs.132740	EST	3.19	0.22	upregulate stage
	429644	AA655892	Hs.156379	ESTs	3.4	0.15	upregulate stage
	429653	NM_009365	Hs.211581	neural-regulatory transcription factor 1	1.45	0.17	upregulate stage
65	429664	L20433	Hs.211588	PCU domain, class 4, transcription facto	1.47	0.74	upregulate stage
	429673	AA498407	Hs.211636	protein tyrosine phosphatase, non-recept	3.19	0.22	upregulate stage
	429695	AI383469	Hs.159300	ESTs	4.4	0.1	upregulate stage
	429782	NM_005754	Hs.220959	Rac-GTPase-activating protein SH3-domain	4.25	0.13	upregulate stage
70	429813	AW1139578	Hs.180291	ESTs	1	0.95	upregulate stage
	429826	AB011944	Hs.222267	IKB3 protein	4.2	0.14	upregulate stage
	429836	AW904027	Hs.102541	ESTs, Weakly similar to The KIAA0191 gene	3.25	0.14	upregulate stage
	429859	NM_007060	Hs.229952	protein tyrosine phosphatase, receptor t	1	0.36	upregulate stage
	429913	AA480698	Hs.99552	gbcyw6cd2.1 Soares fetal liver spleen	1.25	0.2	upregulate stage
75	429917	H80572	Hs.102766	ESTs	4.8	0.13	upregulate stage
	429921	AA526811	Hs.105053	ESTs	1	0.63	upregulate stage
	429950	AW081908	Hs.105053	ESTs	3.7	0.13	upregulate stage
	429971	AF079550	Hs.227038	glial cells missing (Drosophila) homolog	1	0.83	upregulate stage

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	429979	AA463338	Ha	gbcx37a10.1 Soares, Nhr-MPu, S1 Homo sapi	1	0.32	upregulate stage
	429982	AW449534	Ha	99607 Homo sapiens cDNA FLJ13941 f1, clone TH	6.45	0.08	upregulate stage
	429986	AF022047	Ha	22777 site scd3l homolog (Drosophila) homoio	0.78	0.58	upregulate stage
	430020	AJ536029	Ha	99607 Homo sapiens cDNA FLJ13941 f1, clone TH	1	0.36	upregulate stage
5	430021	AA463913	Ha	221160 ESTs	1	0.56	upregulate stage
	430049	AW277085	Ha	99615 ESTs	3.55	0.17	upregulate stage
	430060	NM_002941	Ha	301198 roundabout (axon guidance receptor, Dros	1	0.53	upregulate stage
	430076	AA461115	Ha	221160 gbcx30r11.1 MCL CMAP, CG81 Homo sapiens	5.4	0.12	upregulate stage
10	430134	BE380149	Ha	105223 ESTs, Weakly similar to conalins receptor	3.6	0.13	upregulate stage
	430184	AB013802	Ha	234750 contactin 5	1	1	upregulate stage
	430195	AW969308	Ha	189594 ESTs	9.15	0.1	upregulate stage
	430279	R85974	Ha	16275 ESTs	1.2	0.52	upregulate stage
	430287	AW182459	Ha	125759 ESTs, Weakly similar to tumor suppressor	4.05	0.15	upregulate stage
	430291	AV680345	Ha	238126 CG4.45 protein	7.2	0.08	upregulate stage
15	430299	W28673	Ha	106747 serine carboxypeptidase 1 precursor prot	11.9	0.06	upregulate stage
	430350	BC169639	Ha	240770 gbcx31M1H0627-29500-005-a05 H10627 Homo	7.1	0.09	upregulate stage
	430387	AV072884	Ha	240770 nuclear cap binding protein subunit 2, 2	5.9	0.11	upregulate stage
	430486	3C062109	Ha	241551 chloride channel, calcium activated, fam	2.56	0.2	upregulate stage
	430488	D15959	Ha	4220 ESTs, Moderately similar to tetraacycline	10.5	0.08	upregulate stage
20	430612	AF182294	Ha	241578 U6 snRNA-associated Sm-like protein LSM6	11.2	0.06	upregulate stage
	430519	AF123634	Ha	43210 F-box only protein 4	5.35	0.11	upregulate stage
	430550	AK000052	Ha	243756 hypothetical protein FLJ20055	1	1	upregulate stage
	430561	BE065227	Ha	178391 gbcx31-310314.310300-015-006 310314 Homo	1	1	upregulate stage
	430563	AA461269	Ha	178391 ESTs	1	0.45	upregulate stage
	430598	AK001954	Ha	247112 hypothetical protein FLJ10902	4.75	0.14	upregulate stage
	430630	AW269920	Ha	2621 cystatin A (rat) Aa	2.52	0.25	upregulate stage
	430634	AB066651	Ha	26685 ESTs	1.24	0.61	upregulate stage
	430637	BE160081	Ha	252290 S100 calcium-binding protein A11 (calcig	1.79	0.47	upregulate stage
	430640	AA462538	Ha	252290 gbcx29066.1 Soares ovary tumor NhrHOT H	5.15	0.08	upregulate stage
30	430645	3C350122	Ha	157367 ESTs	6.4	0.09	upregulate stage
	430726	AL031224	Ha	247850 Human DNA sequences from clone 336H on c	1	0.27	upregulate stage
	430733	AW975920	Ha	263361 ESTs	3.5	0.13	upregulate stage
	430781	AW088127	Ha	276358 ESTs	1	1	upregulate stage
	430791	AA462253	Ha	272068 ESTs, Moderately similar to alternative	1.61	0.42	upregulate stage
35	430817	AA487242	Ha	165105 ESTs	1	1	upregulate stage
	430888	3C155293	Ha	76064 ribosomal protein L27a	3.05	0.17	upregulate stage
	430918	NM_000643	Ha	248131 glutamate receptor, metabotropic 6	9.05	0.09	upregulate stage
	430926	LC0557	Ha	248138 5-hydroxytryptamine (serotonin) receptor	0.51	0.51	upregulate stage
40	430954	AA400346	Ha	46330 ESTs	1.03	0.89	upregulate stage
	431009	BE149782	Ha	248213 gap junction protein, beta 6 (connexin 3	2.64	0.03	upregulate stage
	431023	A1263133	Ha	176925 ESTs	2.55	0.15	upregulate stage
	431030	AA830525	Ha	251068 ESTs	1	0.47	upregulate stage
	431041	AA409687	Ha	105278 ESTs	1	0.36	upregulate stage
	431070	AA409164	Ha	249184 transcription factor 19 (SCT1	1.65	0.45	upregulate stage
45	431082	AA491600	Ha	161942 ESTs	9.85	0.06	upregulate stage
	431089	BE041395	Ha	263878 ESTs, Weakly similar to unknown protein	43.15	0.01	upregulate stage
	431146	Z33836	Ha	250495 Human DNA sequence from PAC 82J11 and co	1	0.4	upregulate stage
	431173	AW971198	Ha	224068 ESTs	6.3	0.12	upregulate stage
50	431246	AA498933	Ha	151887 ESTs	1	1	upregulate stage
	431263	R04628	Ha	226351 ESTs	1	0.8	upregulate stage
	431267	AW969661	Ha	124047 ESTs	1	0.31	upregulate stage
	431287	BE044098	Ha	274901 ESTs	1	1	upregulate stage
	431322	AW970822	Ha	117108 gbEST382704 MAGE resequences, MAGK/Homo	10.8	0.06	upregulate stage
	431332	AA503297	Ha	117108 ESTs	6.55	0.1	upregulate stage
55	431343	AW970603	Ha	300541 Homo sapiens cDNA FLJ11881 f1, clone HE	5.85	0.09	upregulate stage
	431348	AA371059	Ha	251636 ubiquitin specific protease 3	1.58	0.52	upregulate stage
	431347	A133461	Ha	251664 insulin-like growth factor 2 (somatomedin)	1.12	0.47	upregulate stage
	431381	AA577114	Ha	105727 ESTs	1	0.36	upregulate stage
60	431448	A137517	Ha	286381 hypothetical protein DKF2P664O1278	2.72	0.13	upregulate stage
	431494	AA591355	Ha	128608 ESTs	3.75	0.13	upregulate stage
	431510	AA590082	Ha	112264 ESTs	3.75	0.13	upregulate stage
	431560	BE244135	Ha	260238 hypothetical protein FLJ10842	9.1	0.08	upregulate stage
	431571	AW900466	Ha	180610 splicing factor protein/histamine rich (7.5	0.11	upregulate stage
	431596	T34708	Ha	275227 Sec23 (S. cerevisiae) homolog A	8.2	0.06	upregulate stage
65	431610	AW006972	Ha	254963 hypothetical protein FLJ10110	6.4	0.1	upregulate stage
	431613	AA076915	Ha	264482 Aqp12 (aquaporin 12, S. cerevisiae)-like	5.8	0.11	upregulate stage
	431630	NM_002204	Ha	265929 integrin, alpha 3 (embryon CD45C, alpha	1.3	0.50	upregulate stage
	431663	NM_015659	Ha	267182 TRX3-like protein	1.6	0.52	upregulate stage
	431670	AW971287	Ha	305333 gbEST382704 MAGE resequences, MAGL/Homo	1	1	upregulate stage
70	431680	AA305686	Ha	267695 IICP-Gal-betaGalNAc beta 1,3-galactosyltr	0.1	0.06	upregulate stage
	431691	A208511	Ha	292510 ESTs	4.15	0.12	upregulate stage
	431692	AL021331	Ha	267749 unc53 (Caenorhabditis) homolog A	4.2	0.13	upregulate stage
	431694	AW970112	Ha	252637 ESTs	1	0.83	upregulate stage
	431726	NM_015361	Ha	263653 KAPAZ029 protein	10.1	0.07	upregulate stage
75	431736	A912234	Ha	151245 ESTs	9.9	0.08	upregulate stage
	431753	X70029	Ha	2841 neuronectin U	1	0.23	upregulate stage
	431781	AA515474	Ha	99908 nuclear receptor coactivator 4	1	0.36	upregulate stage

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431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	1	0.65	upregulated stage
431814	BE26242	Hs.270847	dela-lubulin	3.35	0.18	upregulated stage
431817	X66233	Hs.271079	zinc finger protein 80 (p117)	1	1	upregulated stage
431828	AA57294	Hs.167496	gpm3312a1 NCL_CGAP_Lip2	4	0.12	upregulated stage
431840	AD70238	Hs.167496	ESTs	1	1	upregulated stage
431850	X17033	Hs.271896	integrin, alpha 2 (CD49, alpha 2 subunit	2.89	0.27	upregulated stage
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	1	0.18	upregulated stage
431951	AD06355	Hs.136470	ESTs	6.4	0.11	upregulated stage
431958	X63429	Hs.272177	cadherin 3, type 1, P-cadherin (placenta	9.09	0.07	upregulated stage
431989	AW572870	Hs.291069	ESTs	1	0.23	upregulated stage
431992	NM_002742	Hs.2891	protein kinase C, mu	3.9	0.15	upregulated stage
432015	AL167504	Hs.159115	ESTs	6.05	0.09	upregulated stage
432023	AW373128	Hs.214168	ESTs	0.59	0.86	upregulated stage
432028	A_272209	Hs.272354	Interleukin 1 receptor accessory protein	1	0.48	upregulated stage
432039	AF220217	Hs.272374	Homo sapiens rsec15-like protein mRNA, p	1	0.24	upregulated stage
432065	AA401039	Hs.2593	protein phosphatase 4 (formerly X), cata	1.38	0.64	upregulated stage
432069	AW975568	Hs.254100	ESTs	4.25	0.15	upregulated stage
432072	N62537	Hs.265109	ESTs	5.9	0.09	upregulated stage
432083	I28303	Hs.272630	glycylserine 1 (Soybean breast 3N08Bst Homo	7.9	0.08	upregulated stage
432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	1	0.28	upregulated stage
432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.5	0.25	upregulated stage
432169	Y00571	Hs.2510	phosphotriester pyrophosphatase synthetase	6.1	0.11	upregulated stage
432215	AW076609	Hs.2934	ribonucleotide reductase H1 polypeptide	2.44	0.29	upregulated stage
432222	A204955	Hs.272630	gpm3303x3.1 Stratiogene schizoz brain S1	15	0.02	upregulated stage
432225	AA531129	Hs.190297	ESTs	9.57	0.06	upregulated stage
432237	AK001526	Hs.274132	hypothetical protein FLJ11064	1	0.44	upregulated stage
432239	X61334	Hs.2538	matrix metalloproteinase 13 (collagenase	4.3	0.01	upregulated stage
432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.95	0.15	upregulated stage
432308	AA534197	Hs.272630	ESTs	1	1	upregulated stage
432374	W6801	Hs.301065	Homo sapiens cDNA FLJ11346 fs, clone PL	1.97	0.4	upregulated stage
432375	BE53068	Hs.2592	S100 calcium-binding protein P	1.16	0.28	upregulated stage
432407	AA221036	Hs.285026	HERV-H LTR-associated 1	3.75	0.18	upregulated stage
432410	X66561	Hs.2592	Sp4 transcription factor	1	1	upregulated stage
432415	Y16971	Hs.28914	ESTs	7.3	0.07	upregulated stage
432432	AA541323	Hs.115831	ESTs	6.35	0.13	upregulated stage
432435	BE218846	Hs.262070	ESTs	5.35	0.1	upregulated stage
432441	AW252425	Hs.163484	ESTs	15.4	0.04	upregulated stage
432518	AW575836	Hs.54319	ESTs	1	0.59	upregulated stage
432530	X62018	Hs.3053	zinc finger protein with interaction dom	8.15	0.06	upregulated stage
432536	NM_002104	Hs.3058	granzyme A (serine protease, granzyme 3;	10.15	0.05	upregulated stage
432614	AA557153	Hs.195853	ESTs	1	0.33	upregulated stage
432642	BE297635	Hs.3069	heat shock 70kD protein 98 (hsc70-2)	10.5	0.07	upregulated stage
432661	AW973623	Hs.283528	ESTs	1	1	upregulated stage
432666	AW20409	Hs.122510	ESTs, Weakly similar to unnamed protein	1	0.16	upregulated stage
432689	ALD43482	Hs.267115	ESTs	4.15	0.12	upregulated stage
432673	AB028859	Hs.278805	ER-associated DNAJ: ER-associated Hsp40	10.24	0.06	upregulated stage
432678	AA524244	Hs.135567	ESTs	1	0.89	upregulated stage
432690	AF161490	Hs.278627	peroxylglyoxylase lyase	4.55	0.12	upregulated stage
432724	X66569	Hs.278627	gpm3303x3.1 Homo sapiens mRNA for ligase-like protein	1	1	upregulated stage
432758	NM_014091	Hs.278920	PRO1510 protein	1	1	upregulated stage
432773	NM_014124	Hs.278935	PRO255 protein	1	1	upregulated stage
432789	D63561	Hs.104	KIAA0442 gene product	3.46	0.22	upregulated stage
432829	W60377	Hs.5772	ESTs	1.33	0.43	upregulated stage
432840	AK001403	Hs.275621	hypothetical protein FLJ20530	4.5	0.14	upregulated stage
432900	BE178025	Hs.7542	hypothetical protein FLJ20080	1	0.3	upregulated stage
432917	NM_014125	Hs.275612	PRO3027 protein	6.33	0.12	upregulated stage
432935	AW210230	Hs.121709	ESTs	0.85	0.11	upregulated stage
432953	AA572869	Hs.225791	ESTs	1	0.19	upregulated stage
433001	AF217513	Hs.275905	clone HQ0310 PRO3310p1	29.9	0.03	upregulated stage
433005	AW359074	Hs.275905	gpm3303x3.1 Homo sapiens cDNA FLJ20099 fs, clone CO	1	0.59	upregulated stage
433129	AA577814	Hs.159115	ESTs	4.75	0.12	upregulated stage
433135	AB036698	Hs.159115	ESTs	6	0.1	upregulated stage
433201	AB040896	Hs.21104	KIAA1463 protein	9.2	0.09	upregulated stage
433211	H11650	Hs.12808	MARK	1.8	0.45	upregulated stage
433218	AB040372	Hs.278854	KIAA1462 protein	5.45	0.44	upregulated stage
433222	AW514472	Hs.239416	ESTs, Moderately similar to ALUR_HUMAN	5.45	0.12	upregulated stage
433230	AW136134	Hs.220277	ESTs	7.3	0.09	upregulated stage
433237	AB040530	Hs.297021	Homo sapiens cDNA FLJ13211 fs, clone NT	1	1	upregulated stage
433365	AF026944	Hs.293797	ESTs	4.95	0.08	upregulated stage
433371	T26451	Hs.30318	gpm3303x3.1 Homo sapiens cDNA FLJ20099 fs, clone CO	1	0.12	upregulated stage
433354	AB017753	Hs.93810	central nervous system malformations 1	4.5	0.11	upregulated stage
433424	B68262	Hs.163566	ESTs	1	1	upregulated stage
433440	AF062127	Hs.142869	gpm3303x3.1 Homo sapiens cDNA FLJ20099 fs, clone CO	1	1	upregulated stage
433452	AW269506	Hs.142869	ESTs	9.82	0.08	upregulated stage
433456	AA534447	Hs.124296	ESTs	9.45	0.08	upregulated stage
433467	AA420457	Hs.65955	ESTs	1.11	0.74	upregulated stage
433479	AW511459	Hs.249672	ESTs	3.35	0.13	upregulated stage

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5	433484	BE264397	Ha.148674	ESTs	1	0.27	upregulate stage
	433515	AA595800	Ha.190246	ESTs	3.05	0.14	upregulate stage
	433602	AU79949	Ha.24966	ESTs	1	1	upregulate stage
	433613	AA336126	Ha.5669	ESTs	2.8	0.12	upregulate stage
	433625	AW955674	Ha.161762	ESTs	1	0.53	upregulate stage
10	433658	L03678	Ha.156110	Immunoglobulin kappa constant	9.65	0.05	upregulate stage
	433672	BE281165	Ha.288038	TLS associated serine-arginine protein 1	7.9	0.08	upregulate stage
	433730	AK002135	Ha.3542	hypothetical protein FLJ11273	6.7	0.11	upregulate stage
	433735	AA69895	Ha.108663	ESTs	8.35	0.08	upregulate stage
	433895	AI287912	Ha.3628	mitogen-activated protein kinase kinase	4.43	0.16	upregulate stage
15	433904	AI399956	Ha.208956	ESTs	5.5	0.12	upregulate stage
	433929	AJ375499	Ha.21379	ESTs	7	0.09	upregulate stage
	433966	AF113017	Ha.294301	PRO1388 protein	7.95	0.06	upregulate stage
	433967	AF113018	Ha.294302	PRO1621 protein	2.65	0.1	upregulate stage
	434006	AF113688		ghHomo sapiens clone FL54530	7.85	0.08	upregulate stage
20	434037	AF116601	Ha.283048	hypothetical protein PRO0128	8.81	0.09	upregulate stage
	434064	AA68045	Ha.160735	hypothetical protein PRO0062	6.35	0.09	upregulate stage
	434065	AF116673	Ha.255029	hypothetical protein PRO1025	1	1	upregulate stage
	434092	AA625155		gbaf7006.s1 Soares_NHMPA_S1 Homo sapi	1	1	upregulate stage
	434094	AA305599	Ha.238205	hypothetical protein PRO2013	11.5	0.06	upregulate stage
25	434138	AA625804		gzaa080401.s1 Soares_Jessie_NHT Homo sap	3.55	0.11	upregulate stage
	434162	AW687314	Ha.34371	ESTs	1.65	0.22	upregulate stage
	434194	AF119847	Ha.283940	Homo sapiens PRO1550 mRNA, partial cds	7.85	0.09	upregulate stage
	434217	AW014795	Ha.23349	ESTs	3.8	0.13	upregulate stage
	434228	Z42647	Ha.283978	Homo sapiens PRO2751 mRNA, complete cds	5.55	0.11	upregulate stage
30	434271	AA697778	Ha.291677	ESTs	1	0.36	upregulate stage
	434280	BE005398		gcCM1-EN0116-152400-163-h22 BN0116 Homo	5.45	0.07	upregulate stage
	434322	AI125686	Ha.152727	ESTs	2.65	0.18	upregulate stage
	434351	AW674991	Ha.191852	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.61	upregulate stage
	434354	AW674512	Ha.292783	ESTs	1	1	upregulate stage
35	434358	AA121038	Ha.3838	neum-inducible kinase	10.7	0.08	upregulate stage
	434484	BE063921	Ha.295971	ESTs	10.15	0.07	upregulate stage
	434486	AB037829	Ha.3862	regulator of nonsense transcripts 2; DKF	7.6	0.09	upregulate stage
	434484	W73939	Ha.104338	hypothetical protein	5.1	0.15	upregulate stage
	434513	AF143888	Ha.18213	Homo sapiens clone IMAGE:121736 mRNA seq	1	1	upregulate stage
40	434534	H90477	Ha.41407	ESTs	1	0.18	upregulate stage
	434540	NM_016045	Ha.5184	TH1 drosophila homolog	12.4	0.06	upregulate stage
	434599	AJ311205	Ha.58609	ESTs	1.75	0.38	upregulate stage
	434575	AI133446	Ha.269864	ESTs	9.7	0.06	upregulate stage
	434627	AJ221894	Ha.33511	ESTs	1.65	0.17	upregulate stage
45	434629	AA789081	Ha.4029	glioma-amplified sequence-41	9	0.07	upregulate stage
	434683	AA641972	Ha.130658	ESTs	4.55	0.15	upregulate stage
	434731	AA648849	Ha.121518	ESTs	6.5	0.1	upregulate stage
	434785	AA831115	Ha.150473	ESTs	1	0.71	upregulate stage
	434773	AA648962	Ha.152847	ESTs	10.55	0.08	upregulate stage
50	434792	AA642053	Ha.134568	ESTs	5.45	0.11	upregulate stage
	434828	D90070	Ha.38	phorbol-12-myristate-13-acetate-induced	1	0.34	upregulate stage
	434876	AF160477	Ha.245781	Homo sapiens ty1 superfamily receptor LNI	1.4	0.57	upregulate stage
	434909	AJ479212	Ha.17283	hypothetical protein FLJ10850	1	0.91	upregulate stage
	434928	BE543289	Ha.50252	Homo sapiens HSPC283 mRNA, partial cds	4.9	0.13	upregulate stage
55	434939	AF161422	Ha.21590	Homo sapiens HSPC304 mRNA, partial cds	1	1	upregulate stage
	434963	AW574957	Ha.238719	Homo sapiens cDNA FLJ12142 fs, clone MA	10.75	0.07	upregulate stage
	434970	AW222292	Ha.250468	ESTs	9.05	0.08	upregulate stage
	434980	AW770553	Ha.203640	ESTs	4.95	0.14	upregulate stage
	434997	AW575155	Ha.202163	ESTs	1	0.36	upregulate stage
60	435013	H91923	Ha.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.16	0.71	upregulate stage
	435030	AJ203316	Ha.184655	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.95	0.14	upregulate stage
	435047	AA454585	Ha.54573	cathepsin-like protein VR20	3.31	0.2	upregulate stage
	435081	AI851474	Ha.183044	ESTs	1.4	0.2	upregulate stage
	435080	AI831760	Ha.155111	ESTs	9.05	0.08	upregulate stage
65	435087	AW675241	Ha.23587	ESTs	1	1	upregulate stage
	435108	AW675018	Ha.287440	Homo sapiens cDNA FLJ11682 fs, clone HE	1	0.2	upregulate stage
	435136	R27299	Ha.10172	ESTs	8.9	0.07	upregulate stage
	435159	AA688879	Ha.116649	ESTs	1.35	0.25	upregulate stage
	435182	AJ911044	Ha.213863	ESTs	1	1	upregulate stage
70	435166	AJ891470	Ha.158616	ESTs	5.5	0.12	upregulate stage
	435212	AW300100	Ha.194185	ESTs	1	1	upregulate stage
	435237	AJ026836	Ha.114689	ESTs	8.75	0.1	upregulate stage
	435256	W87434	Ha.106915	ESTs, Moderately similar to ALU1_HUMAN A	3.4	0.14	upregulate stage
	435266	AF557016	Ha.13072	cytochrome-like protein C17	3.2	0.14	upregulate stage
75	435257	AA677026	Ha.191217	ESTs	4.5	0.12	upregulate stage
	435298	AA677696	Ha.189196	ESTs	1	1	upregulate stage
	435307	V93610	Ha.192003	ESTs	1	0.67	upregulate stage
	435347	AW014873	Ha.116963	ESTs	2.45	0.14	upregulate stage
	435382	NS4493		gbyv40005.s1 Soares fetal liver spleen	1	0.56	upregulate stage
	435408	W07897	Ha.4302	ESTs	0.84	0.97	upregulate stage
	435491	T98543	Ha.191900	ESTs	1	0.3	upregulate stage

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5	435525	AI831297	Ha.123310	ESTs	3.25	0.15	upregulate stage
	435597	AW205188	Ha.163027	ESTs	1	0.57	upregulate stage
	435637	AF220061	Ha.110853	uncharacterized hematopoietic stem/prog	8.76	0.09	upregulate stage
	435647	A655240	Ha.458623	ESTs	1.19	0.25	upregulate stage
	435736	AA686633	Ha.286543	ESTs	2.9	0.16	upregulate stage
10	435762	AW043836	Ha.212460	ESTs	1	1	upregulate stage
	435809	H00213	Ha.191330	ESTs	1.25	0.23	upregulate stage
	435826	A1544089	Ha.117860	ESTs	6.55	0.08	upregulate stage
	435854	AL278120	Ha.4068	DRFZP564D166 protein	3.76	0.29	upregulate stage
	435979	W003698	Ha.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.25	upregulate stage
15	435981	H74319	Ha.188620	ESTs	6.35	0.11	upregulate stage
	435990	A015862	Ha.131763	ESTs	4.25	0.08	upregulate stage
	435999	AA703771	Ha.269903	ESTs, Moderately similar to ALU1_HUMAN A	1	1	upregulate stage
	436016	AA806465	Ha.121536	ESTs	1.45	0.23	upregulate stage
	436023	T81819		gcyd5905.1 Scores fetal liver spleen	9.15	0.07	upregulate stage
20	436092	A021963	Ha.271432	ESTs	1	0.23	upregulate stage
	437115	AW512033	Ha.102094	ESTs	1.9	0.21	upregulate stage
	437116	A2271173	Ha.142890	ESTs	1	1	upregulate stage
	437120	A1248193	Ha.119860	ESTs	0.81	0.08	upregulate stage
	437149	AT54308	Ha.159452	ESTs	2.4	0.19	upregulate stage
25	437158	AA705466	Ha.115900	ESTs	1	0.25	upregulate stage
	437170	AW450381	Ha.14529	ESTs	1	0.01	upregulate stage
	437202	AA706315	Ha.192057	ESTs	1	1	upregulate stage
	437246	AW450583	Ha.119991	ESTs	3.85	0.11	upregulate stage
	437274	AA732755	Ha.120299	ESTs	2.85	0.13	upregulate stage
30	437282	FB1919	Ha.727104	ESTs	3.95	0.11	upregulate stage
	437299	AW020787	Ha.8111	hypothetical protein FLJ20720	6	0.09	upregulate stage
	437300	AA831601	Ha.275736	ESTs	1	1	upregulate stage
	437328	BE085236	Ha.181244	major histocompatibility complex, class	2.49	0.28	upregulate stage
	437360	AA682796	Ha.136754	ESTs	2.4	0.17	upregulate stage
35	437363	A4843806	Ha.124434	ESTs	3.35	0.1	upregulate stage
	437383	BE085178		chrRC1-B'0314-020200-012-H01 BT034 Homo sapiens cDNA FLJ11441 fs, clone HE	1	0.67	upregulate stage
	437396	AA683487	Ha.259112	Homo sapiens cDNA FLJ11441 fs, clone HE	4	0.15	upregulate stage
	437408	AW274577	Ha.252954	ESTs	9.1	0.09	upregulate stage
	437422	AA716141	Ha.147027	ESTs	1	0.26	upregulate stage
40	437425	AA357003	Ha.17546	hypothetical protein FLJ23499	1	1	upregulate stage
	437463	H06502	Ha.6655	ESTs	5.45	0.12	upregulate stage
	437476	AA326108	Ha.53631	ESTs, Weakly similar to enhancer-of-split	7.75	0.07	upregulate stage
	437507	AA721209	Ha.201630	ESTs	2.45	0.18	upregulate stage
	437516	AA776843	Ha.122864	ESTs	3.15	0.21	upregulate stage
45	437522	AA721381	Ha.129876	ESTs	4.75	0.1	upregulate stage
	437578	AA091435	Ha.134859	ESTs	3.4	0.12	upregulate stage
	437670	AB950021	Ha.201536	ESTs	6.85	0.11	upregulate stage
	437740	AW075133		gLEST387230 WAGE resequences, MAGN Homo	7.4	0.09	upregulate stage
	437764	AW076004	Ha.291731	ESTs	1	1	upregulate stage
50	437785	AA745597	Ha.291400	ESTs	1	1	upregulate stage
	437823	AA749885	Ha.293845	ESTs	4.8	0.12	upregulate stage
	438311	AA820113	Ha.291918	ESTs	1.6	0.27	upregulate stage
	438320	AA767346	Ha.291814	ESTs	1	1	upregulate stage
	438844	AA768458	Ha.122812	ESTs	1.5	0.28	upregulate stage
55	438853	BE328074	Ha.148661	ESTs	5.05	0.14	upregulate stage
	438860	H112751	Ha.5327	PRO1914 protein	8.95	0.08	upregulate stage
	438825	AA742327	Ha.250887	ESTs	1	1	upregulate stage
	437044	ALC35884	Ha.69517	ESTs, Highly similar to differentially e	1.01	0.5	upregulate stage
	437067	AA745563		gtxm60E4.1 NCL_OGAP_Pr18 Homo sapiens	1	1	upregulate stage
60	437144	ALD49488	Ha.7859	ESTs	1	1	upregulate stage
	437170	H03202	Ha.181694	ESTs	8.7	0.08	upregulate stage
	437181	AA306615	Ha.125343	ESTs, Weakly similar to KIAA0758 protein	4.4	0.06	upregulate stage
	437207	T27603	Ha.15929	Homo sapiens cDNA FLJ12910 fs, clone NT	1.4	0.22	upregulate stage
	437214	BE023238		gIL2-B'070734-240400-072-A12 BT0734 Homo	5.65	0.09	upregulate stage
65	437240	AA747537		gtrm5605.1 NCL_OGAP_OCB1 Homo sapiens	1	0.45	upregulate stage
	437257	A0290865	Ha.290931	ESTs, Weakly similar to unknown [S. cere	3.8	0.14	upregulate stage
	437258	ALD41243	Ha.174104	ESTs	9.72	0.08	upregulate stage
	437267	AW511443	Ha.258110	ESTs	4.25	0.12	upregulate stage
	437274	AA747985		gtxm75.10.s1 NCL_OGAP_Ew1 Homo sapiens	1	0.19	upregulate stage
70	437289	AA746182	Ha.160377	ESTs	1	0.61	upregulate stage
	437311	AA370041	Ha.5456	SW/SNF related, matrix associated, acti	3.1	0.17	upregulate stage
	437324	AL162077		gblHomo sapiens mRNA; cDNA DKFp761A1210	1	0.25	upregulate stage
	437330	AL353944	Ha.50115	Homo sapiens mRNA; cDNA DKFp761J1112 (I	7.95	0.07	upregulate stage
	437338	BE322386		Homo sapiens mRNA; cDNA DKFp761J21615 (I	1	1	upregulate stage
75	437438	AL329620	Ha.142127	hypothetical protein DKFp761P2111	9.15	0.09	upregulate stage
	437471	AL390169		gblHomo sapiens mRNA; cDNA DKFp547D064	1	1	upregulate stage
	437553	AE269535	Ha.130467	ESTs, Weakly similar to MAT18_HUMAN CHLOR	1	0.55	upregulate stage
	437567	AW627590	Ha.268554	Homo sapiens cDNA: FLJ21405 fs, clone C	1	1	upregulate stage
	437575	AW564585	Ha.38529	ESTs	10.25	0.06	upregulate stage
	437717	AA804765	Ha.132853	ESTs	1	0.77	upregulate stage
	437722	AW292947	Ha.122872	ESTs	9.75	0.05	upregulate stage

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5	437752	AA767375	Hs.201631	ESTs	6.7	0.08	upregulate stage
	437770	AA767891	Hs.122897	ESTs	2.57	0.24	upregulate stage
	437798	AA811167	gbcRC2-ST0165-300999-011-g02 ST0165 Homo	1	1	upregulate stage	
	437799	RS103	Hs.90787	ESTs	1	1	upregulate stage
	437852	BE0001836	Hs.256897	ESTs, Weakly similar to dJ3850.12.1 [Hsa	1.77	0.3	upregulate stage
10	437886	BE256411	Hs.31314	retinoblastoma-binding protein 7	8.8	0.08	upregulate stage
	437897	AA811524	Hs.25203	Homo sapiens cDNA FLJ11896 ts, clone HE	3.8	0.17	upregulate stage
	437898	AA833024	Hs.24357	ESTs	1	0.69	upregulate stage
	437937	AB17222	Hs.121655	ESTs	1	0.38	upregulate stage
	437938	AB50087	gbcw05d02.x1 NCI_GCAP_Kdr12 Homo sapien	1.37	0.52	upregulate stage	
15	437983	AI303023	Hs.30211	hypocellul protein FLJ22313	8.82	0.08	upregulate stage
	438011	BE466173	Hs.145698	splicing factor (CCT3)	9	0.08	upregulate stage
	438032	BCD45424	Hs.152952	ESTs	6.65	0.13	upregulate stage
	438060	NR0101	Hs.33790	ESTs	3.25	0.13	upregulate stage
	438077	AA777330	Hs.50429	ESTs	1	1	upregulate stage
20	438081	HA9546	Hs.259954	ESTs	3.75	0.11	upregulate stage
	438102	AA777793	Hs.137850	xylokinase (H. influenzae) homolog	1	0.33	upregulate stage
	438112	W65726	Hs.140793	ESTs	1	0.55	upregulate stage
	438113	AI467908	Hs.8882	ESTs	1.21	0.55	upregulate stage
	438119	AW932217	Hs.203951	ESTs, Moderately similar to AF116721 B9	11.75	0.07	upregulate stage
25	438144	AA778894	Hs.113364	ESTs	1	1	upregulate stage
	438153	AI258532	Hs.140150	ESTs	1	1	upregulate stage
	438171	AW976507	Hs.293515	ESTs	2.82	0.24	upregulate stage
	438271	L21934	Hs.14553	sterol O-acetyltransferase (acyl-Coenzyme	1	1	upregulate stage
	438280	AA843719	Hs.122341	ESTs	3.5	0.13	upregulate stage
30	438321	AA570535	Hs.5153	CG-49 protein	0.4	0.08	upregulate stage
	438326	AA804268	Hs.123229	ESTs	4.85	0.11	upregulate stage
	438334	AA800922	Hs.261985	ESTs	1	1	upregulate stage
	438366	AA805790	glms4301.s1 NC_GCAP_GCB1 Homo sapiens	1	0.34	upregulate stage	
	438370	AA843242	Hs.45523	ESTs	4	0.14	upregulate stage
35	438374	AA321690	Hs.8193	Homo sapiens mRNA; cDNA DKF2p434C1717 f	1	0.84	upregulate stage
	438377	AA808070	Hs.291716	ESTs	1	0.24	upregulate stage
	438378	AW970629	Hs.86434	Homo sapiens cDNA: FLJ21816 ts, clone H	6.85	0.11	upregulate stage
	438401	AI443321	Hs.107494	ESTs	1	1	upregulate stage
	438403	AA808067	Hs.252226	ESTs	2.75	0.14	upregulate stage
40	438412	AA808076	Hs.130814	ESTs	1	1	upregulate stage
	438448	AA807344	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	1	0.34	upregulate stage
	438451	AI081872	Hs.220281	ESTs	5.7	0.03	upregulate stage
	438473	HO7085	Hs.135501	ESTs	1	1	upregulate stage
	438487	AB84733	Hs.88620	HDQC2BP protein	1	0.21	upregulate stage
45	438529	AW007287	Hs.26538	Homo sapiens cDNA: FLJ21086 fs, clone C	1	0.36	upregulate stage
	438534	AW204052	Hs.123644	ESTs	1	0.37	upregulate stage
	438593	AA814330	Hs.242605	ESTs	3.55	0.15	upregulate stage
	438609	AW297035	Hs.128115	ESTs	3.12	0.22	upregulate stage
	438728	AA815202	Hs.25657	ESTs	1	0.67	upregulate stage
50	438746	AB85815	Hs.184727	ESTs	1.5	0.35	upregulate stage
	438805	AA828043	Hs.117387	ESTs	0.35	0.07	upregulate stage
	438812	AA828199	Hs.41287	ESTs	1	0.57	upregulate stage
	438817	AI023755	Hs.153242	ESTs	4.2	0.08	upregulate stage
	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF140422.2 unino	4.05	0.12	upregulate stage
55	438913	AI330429	Hs.172445	ESTs	5.4	0.11	upregulate stage
	438950	123780	Hs.144530	ESTs	1	1	upregulate stage
	438961	HA2135	Hs.101948	ESTs	7.85	0.08	upregulate stage
	438990	AF058590	gblHomo sapiens full length insert cDNA	1	0.83	upregulate stage	
	439026	RO8078	Hs.117767	ESTs	1	0.27	upregulate stage
60	439052	AF055917	Hs.37521	ESTs	1	0.22	upregulate stage
	439057	H59221	Hs.271461	ESTs	1	0.22	upregulate stage
	439176	AI445444	Hs.100394	ESTs	5.8	0.12	upregulate stage
	439179	AA831250	Hs.229593	ESTs	1	1	upregulate stage
	439183	AW970000	gbcEST385591 MAGE resequences, MAGK Homo	4.5	0.13	upregulate stage	
65	439208	AKC00209	Hs.190962	dyschord p52 subunit	11.9	0.06	upregulate stage
	439212	AF087039	Hs.134877	ESTs	11.4	0.07	upregulate stage
	439223	AW238299	Hs.23945	ESTs	2.70	0.26	upregulate stage
	439312	AA833032	Hs.270745	ESTs	8.9	0.08	upregulate stage
	439330	AF088147	gblHomo sapiens full length insert cDNA	1	0.16	upregulate stage	
70	439351	W37898	Hs.65158	ESTs, Weakly similar to weak similarity	1	0.31	upregulate stage
	439430	AF124250	Hs.6594	breast cancer cell estrogen resistance 3	3.9	0.15	upregulate stage
	439444	AI277682	Hs.54578	ESTs	11	0.07	upregulate stage
	439453	BE236474	Hs.6595	thyroid hormone receptor interactor 13	12.21	0.05	upregulate stage
	439476	AA835340	Hs.155430	ESTs	1	0.65	upregulate stage
75	439492	AF086310	Hs.103150	ESTs	5.43	0.1	upregulate stage
	439527	AW288119	Hs.202539	ESTs	5.25	0.1	upregulate stage
	439550	H10438	gblEST385591 Sources infant brain 1N15 H	3.2	0.18	upregulate stage	
	439560	BE558647	Hs.47899	hypocellul protein FLJ12520	1.81	0.32	upregulate stage
	439565	AF060385	Hs.145699	ESTs	8.96	0.07	upregulate stage
	439592	AF060413	Hs.63399	ESTs	1	1	upregulate stage
	439605	AF060431	Hs.134835	ESTs	9.15	0.09	upregulate stage

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5	439606	W79123	Hs.58561	ESTs, Weakly similar to K01_HUMAN PROBA	8.45	0.06	upregulate stage
	439750	AL359053	Hs.57664	Human sapiens mRNA full length insert cDN	5.43	0.14	upregulate stage
	439760	AL109688	Hs.6793	gbrHomo sapiens mRNA full length insert	5	0.09	upregulate stage
	439861	A1149320	Hs.144463	ESTs	2.75	0.21	upregulate stage
	439862	AB17647	Hs.146170	hypothetical protein FLJ22969	0.3	0.11	upregulate stage
10	439926	AW014875	Hs.137007	ESTs	33.5	0.02	upregulate stage
	439942	AW937391	Hs.6481	ESTs	9.9	0.08	upregulate stage
	439953	AW217529	Hs.6793	platelet-activating factor acetylhydrola	5.59	0.15	upregulate stage
	439979	AW60291	Hs.9882	hypothetical protein FLJ10430	6.95	0.07	upregulate stage
	439987	AA86116	Hs.223232	ESTs	2.45	0.17	upregulate stage
15	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.75	0.07	upregulate stage
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.68	0.41	upregulate stage
	440012	AA81072	gbrHs.26551	Scorpaenidae, WHIT Homo sap	1	1	upregulate stage
	440126	AA875145	Hs.66194	ESTs	1	1	upregulate stage
	440164	RA3809	Hs.22688	ESTs	1	1	upregulate stage
20	440228	AF126392	Hs.7089	insulin induced protein 2	1	1	upregulate stage
	440249	A1246590	Hs.125325	ESTs	1.74	0.44	upregulate stage
	440284	A5912032	Hs.181059	ESTs	1	1	upregulate stage
	440334	SE276112	Hs.7185	zinc finger protein 259	9.45	0.09	upregulate stage
	440348	AW015802	Hs.47023	ESTs	1	0.33	upregulate stage
25	440351	AF603033	Hs.7179	RAD1 (S. pombe) homolog	3.75	0.16	upregulate stage
	440366	F08229	Hs.125723	ESTs	3.5	0.12	upregulate stage
	440462	T71629	Hs.100554	ESTs	1.54	0.52	upregulate stage
	440527	AV657117	Hs.184164	ESTs	3.75	0.14	upregulate stage
	440613	A1733034	Hs.137079	ESTs	3.95	0.11	upregulate stage
30	440705	AA904244	Hs.153235	ESTs	3.9	0.14	upregulate stage
	440856	AW933377	Hs.136939	ESTs	8.35	0.09	upregulate stage
	440899	AW449445	Hs.172690	diacylglycerol kinase, alpha (80kD)	2.55	0.2	upregulate stage
	440917	AA309651	Hs.160025	ESTs	1	0.17	upregulate stage
	440980	AL424005	Hs.1117	trypsinolytic peptidase II	8.9	0.09	upregulate stage
35	440994	A1150011	Hs.193341	ESTs	1.29	0.58	upregulate stage
	441092	T99269	Hs.126556	EST	4.9	0.11	upregulate stage
	441107	AA317075	Hs.190620	ESTs	5.9	0.09	upregulate stage
	441131	A1733222	Hs.126632	ESTs	9.55	0.09	upregulate stage
	441143	AB627894	Hs.159550	ESTs	3.8	0.13	upregulate stage
40	441205	AW137827	Hs.176904	ESTs	4.75	0.12	upregulate stage
	441206	SE552314	Hs.131823	ESTs, Weakly similar to TERA_HUMAN H1sa	1	1	upregulate stage
	441284	AA927170	Hs.23290	ESTs	4.3	0.14	upregulate stage
	441316	A076234	Hs.175130	ESTs	1.74	0.45	upregulate stage
	441334	A1700025	Hs.117564	ESTs	1	1	upregulate stage
45	441346	AA931077	Hs.188889	Human sapiens cDNA, FLJ12021 fls, clone HE	1	1	upregulate stage
	441378	AA331828	Hs.128848	ESTs	4.5	0.1	upregulate stage
	441383	AW294408	Hs.222068	ESTs	1	1	upregulate stage
	441421	AA359792	Hs.201768	ESTs	1	0.24	upregulate stage
	441470	SE503874	Hs.301988	ESTs	0.53	0.93	upregulate stage
50	441474	AW274946	Hs.144476	ESTs	1	1	upregulate stage
	441484	AA335481	Hs.58972	ESTs	1	0.33	upregulate stage
	441485	A1792586	Hs.189130	ESTs	4.25	0.1	upregulate stage
	441508	AW015203	Hs.232732	ESTs	1	1	upregulate stage
	441562	AW578981	Hs.52184	hypothetical protein FLJ20618	4.05	0.12	upregulate stage
55	441599	AW473362	Hs.127221	ESTs	1	0.29	upregulate stage
	441612	AB02629	Hs.113560	Human sapiens cDNA, FLJ11631 fls, clone HE	8.75	0.08	upregulate stage
	441616	SE569122	Hs.74111	PNA-binding protein (autoantigenic)	1.14	0.71	upregulate stage
	441843	A1740504	Hs.205728	ESTs	1	0.33	upregulate stage
	441877	AW271702	Hs.59739	ESTs	1	0.28	upregulate stage
60	441893	AA384673	Hs.7943	RPB5-mediated protein	1	0.43	upregulate stage
	441703	AW392054	Hs.182943	ESTs	3.85	0.08	upregulate stage
	441732	AW298818	Hs.127341	ESTs	4.65	0.14	upregulate stage
	441759	C16126	Hs.161377	ESTs	4.55	0.13	upregulate stage
	441762	AW592203	Hs.144789	ESTs	1	0.23	upregulate stage
65	441790	AW294609	Hs.132208	ESTs	9	0.08	upregulate stage
	441794	AW137794	Hs.253338	ESTs	4.5	0.12	upregulate stage
	441799	AW292776	Hs.127872	ESTs	1	0.22	upregulate stage
	441801	AW247399	Hs.211874	ESTs	8	0.05	upregulate stage
	441804	AB33206	Hs.128104	ESTs	2	0.19	upregulate stage
70	441855	AA792327	Hs.145903	ESTs	0.87	0.96	upregulate stage
	441869	AA306207	Hs.286241	Human sapiens cDNA, FLJ22898 fls, clone H	0.17	0.07	upregulate stage
	441990	T66139	Hs.113631	ESTs	3.55	0.12	upregulate stage
	442029	AW956598	Hs.14456	neural precursor cell expressed, develop	4.65	0.14	upregulate stage
	442030	WB1767	Hs.108060	ESTs	1	0.35	upregulate stage
75	442054	AA422867	Hs.88594	ESTs	8.8	0.08	upregulate stage
	442071	BE048433	Hs.276043	ESTs	9.15	0.09	upregulate stage
	442083	AA976040	Hs.128464	ESTs	1	1	upregulate stage
	442134	AA984369	Hs.205088	ESTs	1	0.63	upregulate stage
	442202	EE272862	Hs.106534	Human sapiens cDNA, FLJ22825 fls, clone H	9.9	0.08	upregulate stage
	442203	A921423	Hs.250146	ESTs	1	1	upregulate stage
	442214	A0881733	Hs.129003	ESTs	2.2	0.25	upregulate stage

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	442216	A0733468	Ha.125006	ESTs	1	1	upregulated stage	
	442295	A0827248	Ha.224398	Human sapless cDNA FLJ11469 fs, clone HE	1.49	0.31	upregulated stage	
	442319	BE048144	Ha.177877	CG-102 protein	1	0.29	upregulated stage	
5	442432	SE033989	Ha.281718	Human sapless cDNA: FLJ23468 fs, clone H	22.35	0.03	upregulated stage	
	442510	AF150179	Ha.246690	ESTs	1	0.63	upregulated stage	
	442516	AF150226		gla:AF150226 Human mRNA from cd34+ stem c	1	1	upregulated stage	
	442539	AL119506	Ha.58220	Human sapless cDNA: FLJ23055 fs, clone L	1	0.23	upregulated stage	
	442552	R02626	Ha.835372	son of savantless (Drosophila) homolog 1	9	0.08	upregulated stage	
	442592	SE193594	Ha.347398	ESTs	6.55	0.1	upregulated stage	
	442594	A059007	Ha.188378	ESTs	1	1	upregulated stage	
	442577	AA292998	Ha.163900	ESTs	1.41	0.52	upregulated stage	
	442593	A000386	Ha.130313	ESTs	1	0.36	upregulated stage	
	442597	AW39214	Ha.130926	ESTs	1	1	upregulated stage	
	442611	BE071155	Ha.177537	ESTs	4.35	0.15	upregulated stage	
	442612	A005233	Ha.130631	ESTs	1	0.28	upregulated stage	
	442619	AA447492	Ha.20183	ESTs. Weakly similar to AF164753 1 provi	7.85	0.09	upregulated stage	
	442642	R01653	Ha.226429	ESTs	1	1	upregulated stage	
	442650	AW138174	Ha.130651	ESTs	4.1	0.09	upregulated stage	
	442696	BE069562	Ha.7063	Human sapless cDNA: FLJ20913 fs, clone A	2.65	0.16	upregulated stage	
	442712	BE485168	Ha.131011	ESTs	2.51	0.23	upregulated stage	
	442760	BE076397	Ha.10067	ESTs. Weakly similar to KIAA1205 protein	8	0.1	upregulated stage	
	442795	AW243558	Ha.131155	ESTs	1	0.3	upregulated stage	
	442785	AW29825	Ha.131188	ESTs	1	0.27	upregulated stage	
	442805	AW294522	Ha.145991	ESTs	3.6	0.08	upregulated stage	
	442836	H56735	Ha.282558	Human sapless cDNA FLJ13611 fs, clone PL	4.3	0.11	upregulated stage	
	442861	AA243837	Ha.57787	ESTs	3.9	0.12	upregulated stage	
	442875	BE023003	Ha.23525	Human sapless clone TCCTA00142 mRNA sequ	3.65	0.15	upregulated stage	
	442879	AF032922	Ha.8813	synthasin binding protein 3	3.95	0.14	upregulated stage	
	442883	AW156774	Ha.253199	ESTs	1	1	upregulated stage	
	442951	BE014474	Ha.280074	Human sapless cDNA FLJ13395 fs, clone Y7	11.55	0.07	upregulated stage	
	442936	A034026	Ha.132327	ESTs. Weakly similar to dist specificity	2.99	0.16	upregulated stage	
	442980	AA067025	Ha.85678	kinasin-like 1	1	0.24	upregulated stage	
	442992	A031469	Ha.13297	ESTs	6.1	0.14	upregulated stage	
	442994	A026718	Ha.16554	ESTs	6.9	0.07	upregulated stage	
	443004	A0145186	Ha.85339	ves-associated protein 65 kDa	5.7	0.11	upregulated stage	
	443113	A040686	Ha.132303	ESTs	3.9	0.14	upregulated stage	
	443119	AA312264	Ha.7980	ESTs. Moderately similar to ALUAF1.HUMAN	8.73	0.08	upregulated stage	
	443171	BE281128	Ha.5030	TOMDU	3.18	0.22	upregulated stage	
	443211	A0130380	Ha.143555	ESTs	6.55	0.08	upregulated stage	
	443242	BE243910	Ha.5900	melanoprotein p54	11.05	0.08	upregulated stage	
	443243	AA52496	Ha.132065	ESTs	8.9	0.09	upregulated stage	
	443247	BE814387	Ha.47378	ESTs. Moderately similar to hypotheical	10.95	0.05	upregulated stage	
	443270	NM_004272	Ha.9195	Home, neuronal immediate early gene, 1B	3.75	0.2	upregulated stage	
	443295	A073842	Ha.133342	ESTs	1	0.69	upregulated stage	
	443328	A053464	Ha.166506	ESTs	2.9	0.16	upregulated stage	
	443383	A0792453	Ha.166507	ESTs	5	0.14	upregulated stage	
	443411	AW134650	Ha.65320	ESTs	1	0.59	upregulated stage	
	443426	AF038158	Ha.5322	chromosome 20 open reading frame 1	2.68	0.21	upregulated stage	
	443447	A054222	Ha.165572	ESTs	1	0.38	upregulated stage	
	443542	A0327065	Ha.146040	ESTs	5.65	0.13	upregulated stage	
	443557	AW646987	Ha.145691	ESTs	1	1	upregulated stage	
	443584	A087035	Ha.101619	ESTs	1	0.36	upregulated stage	
	443605	A0716654	Ha.180424	ESTs	1	1.15	0.23	upregulated stage
	443634	H73972	Ha.134460	ESTs	3.05	0.16	upregulated stage	
5	443640	A072643	Ha.134218	ESTs	2.65	0.12	upregulated stage	
	443715	A0583187	Ha.95700	cydin E1	5.65	0.11	upregulated stage	
	443789	AA150220	Ha.5900	protein kinase Nmu-R1	1.6	0.19	upregulated stage	
	443869	AA042283	Ha.79593	cydin I	4.65	0.13	upregulated stage	
	443917	AW653739	Ha.72325	Human DNA sequence from clone RP1-187A11	1	1	upregulated stage	
	443919	A091284	Ha.135224	ESTs	8.05	0.07	upregulated stage	
	443967	AW294013	Ha.202042	ESTs	5.55	0.13	upregulated stage	
	443977	AL102986	Ha.150627	ESTs	4	0.14	upregulated stage	
	443979	AW647396	Ha.282305	ESTs	1	1	upregulated stage	
	444020	R02962	Ha.35052	ESTs	10.45	0.08	upregulated stage	
	444105	AW189357	Ha.166597	ESTs	6.29	0.1	upregulated stage	
	444129	AW294292	Ha.256512	ESTs	1	0.77	upregulated stage	
	444152	A0126594	Ha.149305	Human sapless cDNA FLJ14264 fs, clone PL	1.64	0.48	upregulated stage	
	444163	A0126098		gla:cs54g07.x1 Soares, placenta, 80w/week_	1.12	0.81	upregulated stage	
	444166	AW646429	Ha.262993	ESTs	1	1	upregulated stage	
	444270	A0136901	Ha.255325	EST	1	0.47	upregulated stage	
	444271	AW652269	Ha.1549804	ESTs	3.2	0.12	upregulated stage	
	444282	A0138955		gla:cs73h07.x1 Soares, testis, NHT Homo sap	1	1	upregulated stage	
	444333	A0262687	Ha.253861	Nmu-ncleof10 repeat containing 15	1	0.77	upregulated stage	
	444342	NM_014398	Ha.10887	similar to lysosome-associated membrane	9.9	0.06	upregulated stage	
	444378	R01335	Ha.12569	ESTs	1	0.32	upregulated stage	
	444381	BE387335	Ha.283713	ESTs. Weakly similar to CA54_HUMAN COLLA	2.85	0.26	upregulated stage	
	444431	AW513324	Ha.42280	ESTs	6.27	0.12	upregulated stage	

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5	444437	A/377961	Hs.44041	ESTs	9.9	0.07	upregulate stage
	444444	A/149332	Hs.14855	ESTs	1.16	0.47	upregulate stage
	444525	A/593778	Hs.25699	ESTs	1	0.5	upregulate stage
	444584	A/169432	gb:AC0611.11 Soares_NSF_F8_9W_CT_PA_P_S	ESTs	3.6	0.15	upregulate stage
	444599	A/174377	Hs.143396	ESTs	1	0.44	upregulate stage
10	444646	A/184665	gb:q50608.1 Soares_testis_NHT Homo sap	ESTs	1	1	upregulate stage
	444649	A/207193	Hs.197628	ESTs	9.35	0.06	upregulate stage
	444675	A/186360	Hs.244621	ESTs	9.00	0.06	upregulate stage
	444686	A/188139	Hs.147050	ESTs	1	0.5	upregulate stage
	444743	AA045648	Hs.11817	nucleix (nucleoside diphosphate linked moi	2.1	0.15	upregulate stage
15	444762	A/273700	Hs.143883	ESTs	3.9	0.14	upregulate stage
	444781	NM_014000	Hs.11950	GPI anchored metastasis-associated prote	1.44	0.33	upregulate stage
	444783	A/601448	Hs.22100	enilin (Drosophila Scrape homolog), act	6.65	0.07	upregulate stage
	444838	A/651680	Hs.200558	ESTs	4.84	0.14	upregulate stage
	444849	A/159436	Hs.146480	ESTs	3.05	0.17	upregulate stage
20	444950	A/600266	Hs.224875	ESTs	1	0.51	upregulate stage
	445027	A/652692	Hs.254358	ESTs	11.1	0.06	upregulate stage
	445091	A/602164	Hs.147594	ESTs	1	1	upregulate stage
	445098	AL050272	Hs.12205	DKFZP566B183 protein	9.75	0.07	upregulate stage
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZP566C109 f	10.9	0.07	upregulate stage
25	445250	A/597698	Hs.175621	ESTs	9.8	0.06	upregulate stage
	445258	A/635501	Hs.149613	ESTs	3.05	0.13	upregulate stage
	445300	A/222165	Hs.144923	ESTs	10.6	0.06	upregulate stage
	445356	B/181752	gb:CV1-HT0639-070500-193-g06 HT0639 Homo	ESTs	1	0.29	upregulate stage
	445413	AA151342	Hs.12677	CGA-147 protein	4.62	0.12	upregulate stage
30	445436	A/224105	Hs.151408	ESTs	1.35	0.22	upregulate stage
	445444	AA380676	Hs.270	electrin homology, Sec7 and collectin	10.7	0.07	upregulate stage
	445463	A/307150	Hs.146945	ESTs	1	1	upregulate stage
	445496	A/300780	Hs.12802	development and differentiation enhancin	12.06	0.06	upregulate stage
	445525	BE149866	Hs.14631	ESTs	10.65	0.06	upregulate stage
35	445527	V/35694	Hs.63306	ESTs	4.85	0.1	upregulate stage
	445537	A/245671	Hs.12844	EGF-like domain, multiple 6	9.7	0.06	upregulate stage
	445546	AW468821	Hs.150054	ESTs	4.2	0.13	upregulate stage
	445576	A/179323	Hs.145608	ESTs	1	0.31	upregulate stage
	445623	A/243366	Hs.145758	ESTs	1	1	upregulate stage
40	445640	AW986628	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.7	0.13	upregulate stage
	445668	A/557114	Hs.181591	EST	1	0.34	upregulate stage
	445766	A/623607	Hs.28277	Homo sapiens cDNA FLJ13450 fs, clone PL	1	0.23	upregulate stage
	445770	AL119499	Hs.33365	neuronal potassium channel alpha subun	1	1	upregulate stage
	445776	A/159443	Hs.88413	Homo sapiens cDNA FLJ13559 fs, clone PL	9.7	0.07	upregulate stage
45	445797	A/253167	Hs.145355	ESTs, Weakly similar to ALUC_HUMAN [H	3.1	0.13	upregulate stage
	445814	H62020	Hs.101824	ESTs	1	1	upregulate stage
	445818	BE043321	Hs.136017	ESTs	1	1	upregulate stage
	445825	A/452457	Hs.145528	ESTs	1	0.37	upregulate stage
	445832	A/261545	gb:q30607.x1 NCL_CGAP_Kid11 Homo sapien	ESTs	3.21	0.22	upregulate stage
50	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fs, clone L	5.25	0.12	upregulate stage
	445880	AW855474	Hs.131058	ESTs	1	0.67	upregulate stage
	445883	AF070559	Hs.13413	Homo sapiens clone 24493 mRNA sequence	1	1	upregulate stage
	445908	RT3580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.25	0.15	upregulate stage
	445936	BE019658	Hs.141003	Homo sapiens cDNA: FLJ21691 fs, clone C	8.85	0.06	upregulate stage
55	446019	A/382520	Hs.94133	ESTs	9.75	0.06	upregulate stage
	446034	A/601437	Hs.13034	KIAA0637 gene product	10.25	0.07	upregulate stage
	446062	A/211739	Hs.292574	ESTs, Weakly similar to transformation-	1	1	upregulate stage
	446080	A/221741	Hs.117777	ESTs	9.75	0.09	upregulate stage
	446082	A/274139	Hs.155452	ESTs	1.37	0.4	upregulate stage
60	446095	T30506	Hs.17128	ESTs	2.4	0.31	upregulate stage
	446119	D/25627	gb:U148W8567 Human epidermal keratinocyte	ESTs	1	1	upregulate stage
	446120	N/28080	Hs.43741	ESTs	1	0.31	upregulate stage
	446126	AW055050	Hs.47413	ESTs	9.35	0.08	upregulate stage
	446127	AA333908	Hs.13990	ubiquitously transcribed tetratricopepti	1	0.25	upregulate stage
65	446152	A/252036	Hs.150228	ESTs	4.7	0.12	upregulate stage
	446196	A/744886	Hs.146470	ESTs	1	0.23	upregulate stage
	446229	A/744984	Hs.14449	KIAA1509 protein	2.4	0.36	upregulate stage
	446248	A/283014	Hs.149638	ESTs	1	1	upregulate stage
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	10.65	0.07	upregulate stage
70	446303	X/7124	Hs.14732	malic enzyme 1, NAD(P)+-dependent, cytos	1	1	upregulate stage
	446312	BE087853	Hs.14638	gb:CV1-BT0681-290400-181-h5 BT0681 Homo	11.75	0.06	upregulate stage
	446332	AK001635	Hs.14638	hypothetical protein FLJ10773	6.45	0.1	upregulate stage
	446356	A/816726	Hs.14895	DHHC1 protein	9.9	0.06	upregulate stage
	446382	AW512481	Hs.150354	ESTs	7.6	0.1	upregulate stage
75	446398	A/891317	Hs.150074	ESTs	1	1	upregulate stage
	446411	A/298828	Hs.153439	ESTs	1	0.37	upregulate stage
	446474	A/301227	Hs.150166	ESTs	3.35	0.13	upregulate stage
	446501	A/302615	Hs.150819	ESTs	4.25	0.12	upregulate stage
	446507	A/352554	Hs.151504	nuclear DNA-binding protein	11.25	0.05	upregulate stage
	446526	H/89616	Hs.296290	Homo sapiens cDNA FLJ13357 fs, clone PL	10.25	0.07	upregulate stage
	446555	AW659046	Hs.201847	ESTs	1	1	upregulate stage

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446577	AB040833	Hs.15420	KIAA1500 protein	1	0.51	upregulate stage
446629	AI436046	Hs.159148	Homo sapiens cDNA: FLJ23062 lit, clone L	1	0.25	upregulate stage
446636	AC002553	Hs.15767	ctnnb (rho-interacting, semaphorin)	2.54	0.28	upregulate stage
446682	AW026362	Hs.111198	ESTs	4	0.18	upregulate stage
446701	AK001621	Hs.15921	hypothetical protein FLJ10759	1.32	0.69	upregulate stage
446718	AV860019	Hs.282676	ESTs	1	1	upregulate stage
447019	W39500	Hs.47050	ESTs, Weakly similar to LONX_HUMAN MITOC	9.65	0.07	upregulate stage
447020	AI439136	Hs.14305	ESTs	4.55	0.12	upregulate stage
447655	AV060345	Hs.382088	ESTs	4.51	0.51	upregulate stage
446771	AA129965	Hs.80679	TAT-A box binding protein (TEP) associate	11.2	0.06	upregulate stage
446821	W03766	Hs.301482	ESTs	6.9	0.09	upregulate stage
446830	BE117930	Hs.64239	Human DNA sequences from clone RP5-1174N9	10.65	0.07	upregulate stage
446839	BE091926	Hs.15244	mitotic spindle colocalized related prot	14.05	0.05	upregulate stage
446853	AV060630	Hs.87627	disruptor of silencing 10	9.7	0.09	upregulate stage
446880	AB11807	Hs.106646	Homo sapiens cDNA FLJ12534 lit, clone NT	11.05	0.06	upregulate stage
446922	BE175605	Hs.15244	glnCRS-HT0590-100590-022-H07 HT0590 Homo	2.75	0.16	upregulate stage
446950	AA305000	Hs.293454	ESTs, Weakly similar to Similarity to Ye	9.0	0.06	upregulate stage
446988	AW039338	Hs.272108	ESTs	1	0.29	upregulate stage
446989	AK001898	Hs.15740	hypothetical protein FLJ11036	1.75	0.51	upregulate stage
447052	AV061911	Hs.282735	ESTs	1	1	upregulate stage
447065	AB29014	Hs.159878	ESTs	1	0.25	upregulate stage
447069	A335927	Hs.157722	ESTs	1	0.4	upregulate stage
447078	AW885727	Hs.301670	ESTs	4.4	0.13	upregulate stage
447080	AI418781	Hs.300144	ESTs	1	0.31	upregulate stage
447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.55	0.12	upregulate stage
447115	A3314599	Hs.17411	KIAA0089 protein	10.15	0.07	upregulate stage
447153	AA355572	Hs.173512	eukaryotic translation initiation factor	6.2	0.12	upregulate stage
447154	H52284	Hs.293545	ESTs	1	0.24	upregulate stage
447159	AB685296	Hs.280396	EST	1.25	0.25	upregulate stage
447215	BE17056	Hs.263000	ESTs	2.4	0.15	upregulate stage
447228	AW092020	Hs.159188	ESTs	1	0.29	upregulate stage
447268	BE047911	Hs.173512	glut44a05.y1 NC2_CGA_P_Erm52 Homo sapien	1.15	0.23	upregulate stage
447286	AV197097	Hs.183558	transcriptional intermediary factor 1	1	1	upregulate stage
447289	AW247017	Hs.36578	melanoma antigen, family A, 3	1	1	upregulate stage
447334	AA150532	Hs.21159	ESTs	9.15	0.08	upregulate stage
447342	AI159268	Hs.19322	ESTs	5.95	0.09	upregulate stage
447343	AA256641	Hs.236894	ESTs, Highly similar to LRPI_HUMAN LOW-D	2.11	0.33	upregulate stage
447376	A375747	Hs.19442	glnCRS95.x1 Soares_tctat_tctat_Na2HFO	1	0.33	upregulate stage
447397	BEA7876	Hs.19442	E-1 enzyme	5.3	0.14	upregulate stage
447430	AI42269	Hs.206112	ESTs	3.65	0.13	upregulate stage
447444	AK000318	Hs.19816	hypothetical protein FLJ20311	9.2	0.08	upregulate stage
447519	AB42658	Hs.23448	ESTs	14.4	0.05	upregulate stage
447622	BE113889	Hs.136585	glnCRS-HT0765-081199-001-b04 HT0765 Homo	1.7	0.18	upregulate stage
447570	AA312347	Hs.170995	ESTs	1.5	0.3	upregulate stage
447608	A569854	Hs.170995	ESTs	2.7	0.16	upregulate stage
447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta s	4.55	0.12	upregulate stage
447701	BE019526	Hs.255527	ESTs, Weakly similar to unannoted protein	1.63	0.46	upregulate stage
447741	A421737	Hs.167253	ESTs	1	1	upregulate stage
447748	A4022023	Hs.161358	ESTs	3.9	0.11	upregulate stage
447827	U73727	Hs.17918	protein tyrosine phosphatase, receptor I	1.44	0.59	upregulate stage
447891	BE020898	Hs.23037	ESTs	12.15	0.06	upregulate stage
447963	A452373	Hs.166590	ESTs, Weakly similar to ALUC_HUMAN III	6.9	0.06	upregulate stage
447977	A467037	Hs.260508	ESTs	1	1	upregulate stage
447979	A467039	Hs.260548	ESTs	1	1	upregulate stage
447982	H22953	Hs.137551	ESTs	4.25	0.13	upregulate stage
448032	AW511770	Hs.240958	ESTs	1	1	upregulate stage
448045	A2287406	Hs.25166	prostate stem cell antigen	2.22	0.29	upregulate stage
448058	A459998	Hs.170424	ESTs	1	0.51	upregulate stage
448062	AW295923	Hs.255472	ESTs	5.9	0.08	upregulate stage
448138	AA342725	Hs.170736	ESTs	9	1	upregulate stage
448154	AL120320	Hs.203203	ESTs	0.85	0.07	upregulate stage
448165	NM_005591	Hs.202273	meloid recombination (S. cerevisiae) 11	7.3	0.09	upregulate stage
448168	AW060599	Hs.22549	hypothetical protein FLJ12793	1	0.77	upregulate stage
448236	AA590449	Hs.20766	oxysterol 7alpha hydroxylase	1	0.47	upregulate stage
448256	BE514149	Hs.20814	CD-27 protein	11.55	0.07	upregulate stage
448289	AW090251	Hs.202402	ESTs	1	0.47	upregulate stage
448356	AL120837	Hs.20093	high glucose-regulated protein 8	11	0.07	upregulate stage
448357	N20189	Hs.108923	ESTs	1.34	0.51	upregulate stage
448408	A4322986	Hs.21107	neurofilin	1.7	0.24	upregulate stage
448455	A252625	Hs.165890	ESTs	0.8	0.09	upregulate stage
448459	AW069636	Hs.171055	ESTs	1	0.27	upregulate stage
448464	A522053	Hs.196093	ESTs	10.35	0.06	upregulate stage
448488	BE550361	Hs.171072	ESTs	9	1	upregulate stage
448502	AW060266	Hs.219899	ESTs	9.3	0.08	upregulate stage
448552	AW973653	Hs.20704	hypothetical protein FLJ00052	4.75	0.13	upregulate stage
448556	AW885606	Hs.50564	ESTs	9.8	0.08	upregulate stage
448569	BE382857	Hs.21486	signal transducer and activator of trans	2.14	0.35	upregulate stage

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5	448632	BE614269	gb:5015043111 N1HL_MGC_71 Homo sapiens c	1	1	upregulate stage	
	448643	AI557331	gb:pt2.1-06.D06.r1 homo2 Homo sapiens cD	3.6	0.14	upregulate stage	
	448649	T94590	ESTs	1.95	0.21	upregulate stage	
	448653	BE614599	h1-sapiens gene from PAC 42618, similar t	4.3	0.12	upregulate stage	
	448680	AWA58900	Ha.21753	IM5 protein	0.97	0.93	upregulate stage
10	448725	AA193251	Ha.40289	ESTs	2.6	0.19	upregulate stage
	448729	BE614535	Ha.138580	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.25	0.16	upregulate stage
	448743	AB332962	Ha.21695	KIAA1136 protein	1.9	0.19	upregulate stage
	448826	AJ502262	Ha.293346	ESTs, Weakly similar to putative p150 [H]	1.78	0.44	upregulate stage
	448914	AB27656	Ha.195450	ESTs	2.75	0.19	upregulate stage
15	448946	AB62855	Ha.155796	ESTs	9.7	0.07	upregulate stage
	448958	AB520651	Ha.22653	KIAA0844 protein	1	0.16	upregulate stage
	448974	AL468390	Ha.22689	Homo sapiens mRNA; cDNA DKFZ66813-18 [H]	1.86	0.11	upregulate stage
	448979	AB11378	Ha.192610	ESTs	1	1	upregulate stage
	449008	AW578003	Ha.22826	topomodulin 3 [ubiquitous]	5.2	0.11	upregulate stage
20	449032	AA045573	Ha.22900	nuclear factor (erythroid-derived 2-like)	1	0.33	upregulate stage
	449053	AB52777	Ha.219344	ESTs	1.73	0.12	upregulate stage
	449057	AA037784	Ha.22941	KIAA1363 protein	9.25	0.07	upregulate stage
	449148	AW636677	Ha.287564	Homo sapiens cDNA FLJ13345 fs, clone OV	7.2	0.09	upregulate stage
	449203	AB34578	Ha.28721	ESTs	7	0.1	upregulate stage
25	449207	AL044222	Ha.23255	neuropilin 155kD	3.34	0.36	upregulate stage
	449219	AJ07581	Ha.195012	ESTs	1	1	upregulate stage
	449230	BE613348	Ha.23348	S-phase kinase-associated protein 2 [p45]	3.08	0.25	upregulate stage
	449246	AW411209	Ha.23363	hypothetical protein FLJ10083	4.79	0.16	upregulate stage
	449316	AW238621	Ha.108788	ESTs, Weakly similar to zeste [Drosophila]	2.8	0.10	upregulate stage
30	449326	AB564893	Ha.197647	ESTs	2.55	0.17	upregulate stage
	449343	AJ514118	Ha.272458	protein phosphatase 3 [flomerty 2B], cat	4.75	0.12	upregulate stage
	449344	AJ640355		gbwa1Toh1.x1 NCLCGAP_K011 Homo sapien	2.1	0.22	upregulate stage
	449351	AW016537	Ha.200790	ESTs	2.45	0.14	upregulate stage
	449370	AQ002114	Ha.22485	hypothetical protein FLJ11252	1.55	0.14	upregulate stage
35	449424	AW448937	Ha.197030	ESTs	4.05	0.12	upregulate stage
	449425	AW703433	Ha.195684	ESTs	4.6	0.12	upregulate stage
	449434	AW294858	Ha.197641	ESTs	1	0.29	upregulate stage
	449437	AJ702038	Ha.100057	Homo sapiens cDNA: FLJ22902 fs, clone K	2.38	0.34	upregulate stage
	449474	AJ021344	Ha.2055	ubiquitin-activating enzyme E1 (U159T an	6.9	0.12	upregulate stage
40	449523	NM_000679	Ha.54443	chemokine (C-C motif) receptor 5	6.45	0.1	upregulate stage
	449526	BE63337	Ha.38178	Homo sapiens cDNA: FLJ23458 fs, clone H	2.85	0.18	upregulate stage
	449565	AB24925	Ha.197066	ESTs	1	1	upregulate stage
	449566	AL157479	Ha.23740	KIAA1593 protein	10.15	0.06	upregulate stage
	449518	AJ076459	Ha.14386	Homo sapiens cDNA FLJ12819 fs, clone NT	11.7	0.06	upregulate stage
45	449639	AA021968	Ha.29956	ESTs, Highly similar to MGR7_HUMAN METAB	1	1	upregulate stage
	449666	AA002047		gb:zh64005.r1 Soares_fetal_liver_sapem...	1.55	0.33	upregulate stage
	449704	AQ000733	Ha.23900	GTPase activating protein	2.82	0.3	upregulate stage
	449722	BE230074	Ha.23960	cyclin B1	6.44	0.12	upregulate stage
	449764	NB3104	Ha.54895	ESTs, Weakly similar to ZNF91L [Hsapien	1	1	upregulate stage
50	449784	AW613119	Ha.12915	ESTs	6.25	0.11	upregulate stage
	449829	NS1440	Ha.47821	ESTs	1	0.57	upregulate stage
	449843	RB3337	Ha.24030	solute carrier family 31 [copper transpo	10.2	0.07	upregulate stage
	449892	N73608	Ha.53039	ESTs	6.5	0.1	upregulate stage
	449894	AQ001576	Ha.24129	hypothetical protein FLJ10716	4.55	0.12	upregulate stage
55	449919	AJ674685	Ha.200141	ESTs	5.3	0.11	upregulate stage
	450020	AJ666664	Ha.262219	ESTs	1	1	upregulate stage
	450033	RA3210	Ha.262462	ESTs, Weakly similar to JH0148 nucleolin	1	0.65	upregulate stage
	450063	AB81509	Ha.277133	ESTs	4.2	0.17	upregulate stage
	450083	AA131795	Ha.142001	ESTs	3.9	0.16	upregulate stage
60	450116	AQ003555	Ha.222862	ESTs	1	1	upregulate stage
	450121	AL049174	Ha.389327	Homo sapiens cDNA: FLJ22944 fs, clone K	1	1	upregulate stage
	450135	AB610816	Ha.201142	ESTs	4.95	0.14	upregulate stage
	450144	T33961	Ha.301851	ESTs	2.75	0.13	upregulate stage
	450149	AW665781	Ha.174840	ESTs, Moderately similar to ZIC2 protein	3.75	0.14	upregulate stage
65	450151	AB68159	Ha.266233	ESTs	2.51	0.28	upregulate stage
	450162	AV136315	Ha.22266	ESTs	2.45	0.15	upregulate stage
	450195	AQ007352	Ha.256042	ESTs	4.1	0.14	upregulate stage
	450221	AA328102	Ha.24641	cytochrome associated protein 2	1	0.3	upregulate stage
	450238	T96693	Ha.138777	ESTs	12.2	0.07	upregulate stage
70	450257	AW92013		gb:U2G150296-150220-028-d02 ST0296 Homo	1	1	upregulate stage
	450313	AJ03989	Ha.24009	hypothetical protein FLJ10625	4.35	0.15	upregulate stage
	450314	AA574309	Ha.283402	TGR eta	10.1	0.07	upregulate stage
	450350	T97817	Ha.174880	ESTs	3.65	0.1	upregulate stage
	450411	DB1187	Ha.302166	ESTs	1	0.67	upregulate stage
75	450447	AF212223	Ha.25010	hypothetical protein P15-2	10.75	0.07	upregulate stage
	450448	DS4269	Ha.35244	ESTs	1	1	upregulate stage
	450449	AB65599	Ha.202068	ESTs	1	1	upregulate stage
	450506	NM_004460	Ha.415	Fibroblast activation protein, alpha	11.45	0.05	upregulate stage
	450513	AW964334		gb:EST376407 MAGE resequences, MAGH Homo	1.2	0.2	upregulate stage
80	450626	AW982694	Ha.204715	ESTs	4.95	0.13	upregulate stage
	450636	AJ703076	Ha.201959	ESTs	1	0.69	upregulate stage

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	450655	A107846	Hs.279890	hypothetical protein FLJ29030	1	1	upregulate stage
	450654	AA080358	Hs.36950	ESTs	1	0.34	upregulate stage
	450656	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.51	0.05	upregulate stage
5	450722	A1073218	Hs.109120	ESTs	1	0.87	upregulate stage
	450751	A1073251	Hs.128653	ESTs, Weakly similar to J100333 hypothetical	1	1	upregulate stage
	450772	BE326391	Hs.280146	ESTs, Weakly similar to J100333 hypothetical	1	1	upregulate stage
	450800	BE396151	Hs.243953	ESTs, Weakly similar to ALU3_HUMAN ALU S	8.7	0.06	upregulate stage
	450824	R09055	Hs.259204	ESTs	3.03	0.22	upregulate stage
	450832	AW970602	Hs.105421	ESTs	6.15	0.08	upregulate stage
	450870	AA011471	Hs.25267	gcb20108.1 Soares fetal_liver_spleen	1.15	0.23	upregulate stage
	450937	R49131	Hs.25267	ATP-dependent interferon response protein	9.75	0.08	upregulate stage
	450983	AA308384	Hs.25740	EROT1 (S. cerevisiae)-like	3.32	0.26	upregulate stage
	451052	AA281504	Hs.24444	ESTs, Moderately similar to ALU2_HUMAN	0.25	0.08	upregulate stage
	451067	BE172186	Hs.180789	S194 protein	2.8	0.21	upregulate stage
	451068	AA015800	Hs.82415	ESTs	1	0.32	upregulate stage
	451094	A1949825	Hs.260395	ESTs	4.45	0.14	upregulate stage
	451096	BE383234	Hs.25925	Homo sapiens clone 23890 mRNA sequence	4.15	0.14	upregulate stage
15	451126	H30900	Hs.40910	ESTs	1	1	upregulate stage
	451161	AA211329	Hs.25006	hypothetical protein FLJ10559	2.15	0.16	upregulate stage
	451166	T08171	Hs.185675	ESTs	9.26	0.08	upregulate stage
20	451222	AA018386	Hs.24541	ESTs	1	0.35	upregulate stage
	451225	AA333954	Hs.263908	ESTs	9.19	0.08	upregulate stage
	451228	A167166	Hs.207025	ESTs	1	1	upregulate stage
	451246	AW189232	Hs.35140	cutaneous T-cell lymphoma tumor antigen	7.35	0.11	upregulate stage
	451266	AA016292	Hs.20849	ESTs	1	0.33	upregulate stage
	451276	AW024985	Hs.239533	ESTs, Highly similar to d3J42C10.2 B1aa	1	1	upregulate stage
	451277	AK001123	Hs.26176	hypothetical protein FLJ10281	11.7	0.06	upregulate stage
	451281	R39288	Hs.6702	ESTs	1	1	upregulate stage
	451326	AW26948	Hs.300607	ESTs	10.55	0.07	upregulate stage
	451347	A1288079	Hs.191139	ESTs	1	1	upregulate stage
	451350	H85334	gcb550605.1 Soares retina N2b5HR Homo	2.7	0.15	upregulate stage	
	451385	A1751783	gcb20010y5 NC1_CGAP_Co12 Homo sapiens	8.9	0.09	upregulate stage	
	451386	A1902006	Hs.26334	specific paralog 4 (autosomal dominant	2.45	0.16	upregulate stage
	451440	AA017559	Hs.233817	ESTs	1	1	upregulate stage
	451487	AA018072	gcb5510p02.1 Soares retina N2b4HR Homo	5.7	0.1	upregulate stage	
	451492	AA018119	Hs.297824	ESTs, Highly similar to CK1_HUMAN VOLTA	1	1	upregulate stage
35	451495	H86887	gcb5070a01.1 Soares retina N2b5HR Homo	4.25	0.13	upregulate stage	
	451535	AW570677	gcb53325858 IMAGE sequences, MAGK Homo	6.8	0.12	upregulate stage	
	451533	A1018454	Hs.269211	ESTs, Weakly similar to S34687 hypothetical	1	1	upregulate stage
	451562	H04150	Hs.107708	ESTs	4.65	0.11	upregulate stage
	451580	AW138195	Hs.184328	ODC10 (cell division cycle 10, S. cerevi	1	0.42	upregulate stage
	451592	A1805416	Hs.213897	ESTs	2.8	0.17	upregulate stage
	451651	A1007337	Hs.38977	hypothetical protein d3511E16.2	1	0.18	upregulate stage
	451658	AW195351	Hs.259520	ESTs	9.55	0.07	upregulate stage
	451684	AF216751	Hs.25813	CDA14	3.7	0.15	upregulate stage
45	451690	AW451499	Hs.205990	ESTs	10.86	0.07	upregulate stage
	451724	A193785	gcb1A-BT037-301298-102 BT037 Homo sapien	8.85	0.09	upregulate stage	
	451743	AW074295	Hs.23071	ESTs	2.17	0.35	upregulate stage
	451794	AA015799	Hs.111611	ESTs	1	1	upregulate stage
	451844	T81430	gcb506a02.s1 Stratagene lung G37210 H	6.5	0.11	upregulate stage	
	451903	W15617	Hs.261003	ESTs, Moderately similar to S34987 hypot	2.2	0.21	upregulate stage
	451914	A1822115	Hs.270018	ESTs, Weakly similar to KJ44862 protein	11.87	0.07	upregulate stage
	451938	A1354385	Hs.16667	down-regulator of transcription 1, TBP-	11.65	0.06	upregulate stage
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	1	0.95	upregulate stage
	451971	AA021165	Hs.232606	ESTs	1	1	upregulate stage
	451998	AW594129	Hs.213958	ESTs	1	0.26	upregulate stage
	452028	AK001859	Hs.27555	hypothetical protein FLJ10997	1	0.21	upregulate stage
	452036	NM_003996	Hs.27621	sera domain, seven thrombospondin repeat	1.76	0.41	upregulate stage
	452099	BE812952	Hs.27631	hypothetical protein FLJ10607 similar to	8.9	0.07	upregulate stage
60	452122	AF216833	Hs.17710	ATP-binding cassette, sub-family B (MDR)	1	0.47	upregulate stage
	452163	A1853143	gcb549412.s1 NC3_O3AP_Bm52 Homo sapien	1	0.2	upregulate stage	
	452179	H18725	Hs.27463	ESTs	3	0.13	upregulate stage
	452198	A1067550	Hs.81210	ESTs	1	0.28	upregulate stage
	452206	AA340281	Hs.53074	ESTs, Moderately similar to ALU1_HUMAN A	12.4	0.07	upregulate stage
	452234	AW084176	Hs.232356	ESTs	6.8	0.09	upregulate stage
	452240	A1591147	Hs.81232	ESTs	3.75	0.07	upregulate stage
	452247	AL137432	Hs.28564	hypothetical protein DKFZp761E1824	3.9	0.15	upregulate stage
	452250	BE818854	Hs.28907	hypothetical protein A-211C8.1	8.75	0.09	upregulate stage
	452265	AK000933	Hs.18621	Homo sapiens cDNA FLJ100711 fls, clone HE	5.2	0.09	upregulate stage
	452266	A1767259	Hs.165240	ESTs	10.45	0.06	upregulate stage
	452277	AL049013	Hs.28783	KOA1223 protein	8.9	0.05	upregulate stage
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fls, clone PL	8.2	0.04	upregulate stage
	452291	AF015592	Hs.28853	CDCA7 (cell division cycle 7, S. cerevisi	3.5	0.13	upregulate stage
	452328	AA056179	Hs.127171	ESTs	3.6	0.14	upregulate stage
75	452331	AA595906	Hs.25117	Hsapiens mRNA for per alpha extended 3'	11.75	0.07	upregulate stage
	452345	AA2383279	Hs.29173	hypothetical protein FLJ20515	1.08	0.73	upregulate stage
	452357	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.15	0.07	upregulate stage

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5	452401	NM_007115	Hs.26352	tumor necrosis factor, alpha-induced pro	1	0.17	upregulate stage
	452404	AF450676	Hs.212709	ESTs	3.63	0.2	upregulate stage
	452430	AF118083	Hs.25494	PXO1912 protein	1	0.41	upregulate stage
	452438	BE077546	Hs.31447	ESTs	10	0.07	upregulate stage
	452457	AW062459		gbl/R0-CT0065-100899-001.d02 CT0065 Homo	1	0.13	upregulate stage
10	452461	N78223	Hs.108106	transcription factor	8.1	0.06	upregulate stage
	452518	AA280722	Hs.24758	ESTs	9.3	0.08	upregulate stage
	452519	BE032701		gbl/R02-BM0132-270300-021.a03 BM0132 Homo	1	0.19	upregulate stage
	452524	AW136459	Hs.29796	Homo sapiens mRNA; cDNA DKFZ434D1319 (1	0.45	upregulate stage
	452531	AA42462	Hs.263546	ESTs	2.94	0.22	upregulate stage
15	452547	AA335295	Hs.74120	adipose specific 2	1.51	0.53	upregulate stage
	452550	BE077084		gbl/R05-CT00603-220200-013.C07 BT0603 Homo	5.35	0.11	upregulate stage
	452571	W31518	Hs.34865	ESTs	2.55	0.11	upregulate stage
	452597	AI160028	Hs.61438	ESTs	4.75	0.11	upregulate stage
	452597	BE187202	Hs.212065	ESTs	1	0.32	upregulate stage
20	452680	AW138410	Hs.45051	ESTs	1	1	upregulate stage
	452724	R94810	Hs.30964	cyclic E2	1	0.27	upregulate stage
	452738	AL133800		gbl/DKFZp761A0614_r1.761 (synonym: hamy2)	3.45	0.15	upregulate stage
	452741	BE382514	Hs.30503	Homo sapiens cDNA FLJ11344 fa, clone PL	3.05	0.16	upregulate stage
	452747	BE153855	Hs.61460	ESTs	2.54	0.28	upregulate stage
25	452761	BE244742	Hs.30532	CGI-77 protein	3.85	0.14	upregulate stage
	452825	AI021520		gbl/w26609.x1 NCL_CGAP_Gas4 Homo sapiens	1	1	upregulate stage
	452831	AW864089	Hs.135145	ESTs	2.4	0.19	upregulate stage
	452845	AA082150	Hs.204295	ESTs	8.9	0.08	upregulate stage
	452850	H23230	Hs.22481	ESTs	4.75	0.14	upregulate stage
30	452859	AI300255	Hs.288158	Homo sapiens cDNA: FLJ23591 fa, clone L	9.15	0.08	upregulate stage
	452862	AW378065	Hs.8687	ESTs	5.95	0.07	upregulate stage
	452899	M96739	Hs.30955	Human NSCL-1 mRNA sequence	1.04	0.9	upregulate stage
	452902	AI265001	Hs.249728	ESTs	6.8	0.1	upregulate stage
	452909	NM_015358	Hs.30955	pannexin 1	5.6	0.1	upregulate stage
35	452931	AW160011	Hs.158006	hypothetical protein	1	0.53	upregulate stage
	452934	AA581322	Hs.4213	ESTs	1.44	0.55	upregulate stage
	452958	AW003578	Hs.231672	ESTs	1	0.22	upregulate stage
	452974	BE008083	Hs.61506	ESTs	1.75	0.18	upregulate stage
	453011	BE2552	Hs.45473	ESTs	1	1	upregulate stage
40	453050	AW136476	Hs.224046	ESTs	1	0.39	upregulate stage
	453074	AA031813	Hs.271880	ESTs	1	1	upregulate stage
	453076	AB78583	Hs.222151	ESTs	3.75	0.14	upregulate stage
	453123	AB23718	Hs.221549	ESTs	6.6	0.11	upregulate stage
	453134	AA032211	Hs.18493	ESTs	1.68	0.42	upregulate stage
45	453135	T07866		Homo sapiens clone 25129 mRNA sequence	1	1	upregulate stage
	453137	AI954735	Hs.223540	ESTs	1	0.51	upregulate stage
	453144	AW266807	Hs.61546	ESTs	1	0.28	upregulate stage
	453153	NS3893	Hs.24360	ESTs	5	0.13	upregulate stage
	453158	BE483782	Hs.223764	ESTs	2.8	0.15	upregulate stage
50	453204	R10799	Hs.151990	ESTs	9.5	0.05	upregulate stage
	453228	AW628525	Hs.232327	ESTs	1	1	upregulate stage
	453274	AA018611	Hs.527859	Homo sapiens mRNA full length insert cDN	1	1	upregulate stage
	453293	AA382257	Hs.10653	ESTs	8.4	0.09	upregulate stage
	453321	AB84381	Hs.232521	ESTs	6.7	0.1	upregulate stage
55	453329	T19205	Hs.17598	ESTs	8.9	0.08	upregulate stage
	453339	BE223648	Hs.32963	caldesmon 5, type 2, K-cadherin (beta) ki	1	0.18	upregulate stage
	453347	HT0751	Hs.79981	Human clone 25560 mRNA sequence	1	0.83	upregulate stage
	453450	AW797827	Hs.89474	ADP-ribosylation factor 6	7.09	0.08	upregulate stage
	453459	BE047032	Hs.257788	ESTs	2.35	0.3	upregulate stage
60	453476	AB045030	Hs.24633	SAM domain, SH3 domain and nuclear local	2.75	0.16	upregulate stage
	453485	AA571098	Hs.159397	x 010 protein	8.55	0.08	upregulate stage
	453563	AW505554	Hs.300284	ESTs	4.8	0.1	upregulate stage
	453775	NM_002916	Hs.35120	regulator factor C (activator 1) 4 (37	3.4	0.1	upregulate stage
	453778	R15749	Hs.31677	ESTs	1	1	upregulate stage
65	453846	AL157585		gbl/DKFZp761H02116_r1.761 (synonym: hamy2)	1	0.95	upregulate stage
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.25	0.06	upregulate stage
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALLU_HUMAN ALLU S	4.75	0.12	upregulate stage
	453913	AW004883	Hs.233502	ESTs	3.65	0.14	upregulate stage
	453926	AW021088	Hs.151814	ESTs	3.7	0.13	upregulate stage
70	453951	AL121278	Hs.25144	ESTs	3.45	0.18	upregulate stage
	453945	NM_005171	Hs.36008	activating transcription factor 1	6.35	0.12	upregulate stage
	454022	W31790	Hs.194293	ESTs	6.15	0.07	upregulate stage
	454046	AW022885		gbl/AB0563.y1 Morlon Fetal Cochlin Homo	2.8	0.15	upregulate stage
	454081	AW025190	Hs.34161	ESTs, Moderately similar to ALLU1_HUMAN A	1	0.32	upregulate stage
75	454099	AW052974		gbl.U1-S10041-020899-001.H08 ST0041 Homo	1	1	upregulate stage
	454111	AW081681	Hs.269004	ESTs	2.8	0.18	upregulate stage
	454218	X50542	Hs.44313	w-rat avian reticulocytoblastosis virus	9.4	0.05	upregulate stage
	454259	AL110135	Hs.47679	Homo sapiens mRNA; cDNA DKFZ566H112 (r	8.2	0.11	upregulate stage
	454327	BE064057		gbl/CH3-BT0297-331199-002.H06 BT0297 Homo	1	1	upregulate stage
	454331	AW372837		gbl/CH3-BT0381-151299-042.H09 BT0381 Homo	1	0.43	upregulate stage
	454380	AW858722		gbl/RC3-CT0347-281199-011.c04 CT0347 Homo	1	0.29	upregulate stage

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454524	AW057101	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
454592	AW061012	gdc-R2C124-100403-006-007 S1024 H0264	1	0.37
454648	AW181990	gdc-R2C S10162-24300-017-09 S1016 H0810	1	0.4
454687	AW181473	gdc-R2C S10243-03200-01-01 S1024 H0810	1	0.4
454701	AW183550	gdc-R2C S10123-180104-001-01 S1012 H0810	4.45	0.14
454702	BE145191	gdc-MR0E H0262-221299-204-00 H0208 H0810	0.05	0.08
454720	AW187003	gdc-QVW S10247-040100-081-003 S1024 H0264	1	0.8
454789	BE158314	gdc-QVW H0367-154020-114-002 H0367 H0367	1	0.31
454801	BE151158	gdc-QVW H010425-170100-040-01 H010425 H0810	4.1	0.14
454853	AW033510	gdc-QVW L0016-100200-100-02 T0015 H0810	1	1
454893	AW037753	gdc-QVW L100423-010100-112-003 L00423 H0810	4.45	0.18
454908	AW038125	gdc-QVW L2105-24300-007-01 T2051 H0810	1	0.37
454951	AW047721	gdc-R2C T0268-270909-012-12 T0268 H0810	7.4	0.23
454967	AW047723	gdc-R2C L3-CT013-180201-01-01 CT013 H0367	1	0.37
455047	AW082530	gdc-QVW PM1-CT027-0709-01-01 QVW CT024 H0810	4.25	0.13
455128	AW086155	gdc-QVW CT0321-112000-005-00 CT0321 H0810	2.9	0.13
455201	AW047884	gdc-R2C M0210-100300-001-008 M0210 H0810	3.15	0.16
455209	AW049394	gdc-R2C B00035-650401-01-01 B00035 H0810	2.9	0.13
455331	AW087222	gdc-QVW NN0057-15400-335-002 NN0057 H0810	1	0.27
455351	AW091942	gdc-QVW N0222-100400-190-001 N0222 H0264	1	0.36
455390	SE190188	gdc-QVW H1-RT013-02200-055-00 H1 RT013 H0367	1.98	0.33
455414	AW036969	gdc-R2C T03029-160203-01-01 T03029 H0810	1	0.37
455428	AW039260	gdc-QVW CT0147-170201-24-001 CT0147 H0810	1	0.37
455573	SC004393	gdc-MR2-BN0114-100500-020-00 BN0114 H0810	1	0.37
455586	BE067074	gdc-R2C B10501-1301010-01-01 B10501 H0810	1	1
455595	BE030343	gdc-QVW B00154-00400-325-01 B00154 H0810	1	0.37
455610	BE011703	gdc-QVW B00225-165000-01-01 B00225 H0810	2.05	0.12
455615	BE064615	gdc-QVW B00131-241109-010-01 B00131 H0810	1	0.37
455650	BE064655	gdc-R2C B1031-301229-012-009 B1031 H0810	1	0.67
455657	BE066528	gdc-R2C B1031-410300-015-01 B1031 H0810	1.87	0.4
455669	BE066803	gdc-R2C B1031-241109-014-001 B1031 H0810	2.85	0.2
455670	BE066907	gdc-QVW B1015-120300-014-01 B1015 H0810	1.8	0.18
455781	BE060895	gdc-QVW CT01951-200200-00-00 CT01951 H0810	1	0.48
455799	BE149951	Ha.14570 Homo sapiens cDNA FL223.308, clone H	5.71	0.11
455831	SE086619	gdc-R2C H0107-07-201003-01-01 H0107 H0810	1	0.37
455832	SE122833	gdc-QVW B1015-151109-05-00 B1015 H0810	1	0.37
455903	BE165185	gdc-QVW PM1-H0350-212200-005-00 H0350 H0810	1	0.31
455938	SE158432	gdc-MR0E H02047-14000-005-006 H02047 H0810	2.4	0.15
455939	BE181004	gdc-PVW H02425-170100-002-003 H02425 H0810	1	0.44
455951	BE181001	gdc-PVW H02425-170100-002-010 H02425 H0810	1	0.38
455952	BE181014	gdc-QVW CT01502-140300-008-008 H01502 H0810	1	0.37
455981	BE177900	gdc-MR0E BE1657-07400-01-007 H0267 H0810	1	0.57
456004	AW0450079	gdc-UH-B185-act-02-00-0151 NCL_GCAP_Su	0.29	0.05
456046	RS1494	Ha.71818 ESTs	3.15	0.17
456052	RS1513	gdc-QVW3041.1 Source flint brain INCH	1	0.31
456122	N51636	gdc-QVW301.1 Source, multiple species	4.45	0.14
456205	A058201	Ha.173523 ESTs	1	0.34
456215	RS9515	Ha.268748 ESTs	1	0.83
456320	AT534064	Ha.136212 ESTs	1	0.34
456330	AT242350	Ha.87120 ESTs	1	0.37
456358	AA876544	Ha.17 ESTs	1	0.37
456403	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456404	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456405	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456406	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456407	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456408	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456409	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456410	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456411	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456412	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456413	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456414	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456415	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456416	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456417	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456418	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456419	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456420	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456421	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456422	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456423	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456424	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456425	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456426	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456427	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456428	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456429	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456430	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456431	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456432	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456433	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456434	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456435	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456436	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456437	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456438	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456439	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456440	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456441	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456442	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456443	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456444	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456445	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456450	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456451	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456454	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456455	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456456	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456457	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456458	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456459	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456460	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456461	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456462	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456463	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456464	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456465	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456466	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456467	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456468	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456469	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456470	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456471	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456476	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456478	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456479	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456480	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456481	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456482	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456484	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456485	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456486	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456487	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456488	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456489	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456490	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456492	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456493	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456500	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456502	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456503	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456504	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
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456507	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08
456508	AA761830	gdc-R2C T0304-080100-01-01 T0304	10.55	0.08

[illegible]

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457474	AW972635		gb:EST385031 MAGE sequences, M/AGM Homo	1	0.29	upregulated stage
457530	AW973713	Hs.253699	ESTs	1	0.39	upregulated stage
457637	A268373	Hs.146875	ESTs	1	1	upregulated stage
457643	A375469	Hs.237975	ESTs	3.25	0.19	upregulated stage
457650	AA849152	Hs.238448	ESTs	0.85	0.08	upregulated stage
457661	AA917801	Hs.126596	ESTs	0.06	0.5	upregulated stage
457692	AA744048	Hs.133359	ESTs	1	1	upregulated stage
457697	AW814852	Hs.273104	ESTs	1	1	upregulated stage
457692	AA744396		ghy951e10.s1 NCLGAP_P118 Homo sapiens	8.7	0.06	upregulated stage
457502	AB24875	Hs.75882	MAD (mothers against decapentaplegic, D)	2.2	0.21	upregulated stage
457543	AA755525	Hs.155930	ESTs	3.55	0.1	upregulated stage
457548	AA96880	Hs.193534	ESTs	2.65	0.19	upregulated stage
457554	NM_015353	Hs.5943	ESTs	1.5	0.17	upregulated stage
458004	AW976642	Hs.153057	ESTs	1	0.87	upregulated stage
458027	L60504	Hs.85105	ESTs, Highly similar to I(35)(q25.1)p34	3.45	0.12	upregulated stage
458079	A756870	Hs.54277	ESTs	11.5	0.05	upregulated stage
458158	AA206718	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.s]	1	1	upregulated stage
458171	AA920116	Hs.192090	ESTs	0.69	1.09	upregulated stage
458172	BE007237		gb:PM6-0N013-05050-003-g06 BN0139 Homo	3	0.15	upregulated stage
458186	AA904244	Hs.153035	ESTs	4.6	0.16	upregulated stage
458242	BE295688	Hs.28485	Homo sapiens cDNA: FLJ21895 fls, clone H	3.1	0.15	upregulated stage
458270	T61139	Hs.113631	ESTs	1	0.97	upregulated stage
458282	AA584075	Hs.22590	alpha-ylcerone phosphate synthase	1	1	upregulated stage
458287	AA987555	Hs.12897	ESTs	5.05	0.13	upregulated stage
458296	Z30718	Hs.237593	ESTs, Moderately similar to unnamed prot	1	0.23	upregulated stage
458385	AB83479	Hs.53500	ESTs	8.2	0.07	upregulated stage
458608	AA444832	Hs.202247	ESTs	1	0.27	upregulated stage
458632	A744445	Hs.24650	Homo sapiens cDNA FLJ13047 fls, clone NT	1.05	0.23	upregulated stage
458653	AV358444	Hs.280779	Homo sapiens cDNA FLJ13584 fls, clone PL	5.05	0.13	upregulated stage
458670	A3301387	Hs.233308	ESTs	8.9	0.08	upregulated stage
458680	N7773	Hs.282580	ESTs	0.51	0.23	upregulated stage
458720	AV952037	Hs.124740	ESTs	1	0.3	upregulated stage
458722	AA741545	Hs.282832	ESTs	3.2	0.11	upregulated stage
458747	BE183595	Hs.257391	ESTs, Weakly similar to GTPase-activat	3.3	0.14	upregulated stage
458760	AA689311	Hs.111334	keratin, type I, polypeptide	11	0.07	upregulated stage
458761	AA444821		gb:RET407 subcloned retina cDNA library	6.05	0.12	upregulated stage
458801	N68548	Hs.279880	ESTs	4.45	0.13	upregulated stage
458880	AA045742		gb:Z48059.1 Soares retina N2R-H48 Homo	9	0.08	upregulated stage
458886	AQ247487	Hs.103277	ESTs	1	0.3	upregulated stage
458943	AA905718	Hs.42311	ESTs	8.7	0.08	upregulated stage
459023	AA598226	Hs.80798	ESTs	2.95	0.15	upregulated stage
460028	AB405777		gb:IL5-4TT0039-120759-001-G07 HT0006 Homo	2.6	0.17	upregulated stage
460300	HB8858	Hs.107899	ESTs, Weakly similar to hypothetical pro	1	1	upregulated stage
460558	HB8539	Hs.203935	ESTs	1	1	upregulated stage
461128	AI902169		gb:IL-3T002-21119-051 ST002 Homo sapien	1	0.26	upregulated stage
461822	BE178517		gb:PM1-HT063-090300-001-e09 HT0903 Homo	1	1	upregulated stage
462904	AW194901	Hs.13219	ESTs	2.85	0.15	upregulated stage
462556	AW857406	Hs.59621	Homo sapiens mRNA: cDNA DKFZ564C046 (fr	10.95	0.07	upregulated stage
463319	NM_000059		glioHomo sapiens breast cancer 2, early o	1	1	upregulated stage
463385	Z30300	Hs.281935	ESTs	4.05	0.14	upregulated stage
463429	AA460445		gb:z36911.1 Soares_t0tal_t0tal_N02F35	4.8	0.13	upregulated stage
463494	AA854847		gb:z77602.1 Soares_parietoyd_tamo_N	1	0.39	upregulated stage
463492	AL118919		gb:CKF2p781E2410_r1761 (cytochrome hamp2)	1	1	upregulated stage
463530	AW708111		gb:z45607.x1 NCL_GCAP_Cov17 Homo sapiens	1	1	upregulated stage
461519				12.65	0.06	upregulated stage
462474				25.55	0.03	upregulated stage
462727				8.25	0.05	upregulated stage
462411				12.95	0.05	upregulated stage
468535	L12054		glioHomo sapiens (clone WR4.12VL) anti-th	14.42	0.03	upregulated stage
468685	M18728		glioHuman nonspecific crossreacting anti	15.75	0.03	upregulated stage
467151	H35336	Hs.301527	ESTs, Moderately similar to unknown [Ls	16.3	0.04	upregulated stage
467242	M18728		glioHuman nonspecific crossreacting anti	12.55	0.03	upregulated stage
467347	AA875847	Hs.167347	ESTs, Weakly similar to ALU8_HUMAN ALU S	12.91	0.06	upregulated stage
467798	AA195509	Hs.272239	lymphocyte activation-associated protein	4.2	0.06	upregulated stage
468243	T01671	Hs.624	interleukin 8	6.52	0.02	upregulated stage
468390	AF123060	Hs.44532	dibucetin	16	0.03	upregulated stage
468818	AK000837	Hs.46624	HSPC043 protein	12.8	0.06	upregulated stage
468741	M73720	Hs.646	carboxypeptidase A3 (trast cell)	15.5	0.03	upregulated stage
468417	AA155247	Hs.269308	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.55	0.04	upregulated stage
410515	AB83871	Hs.17625	ESTs	14	0.05	upregulated stage
410324	AW225339	Hs.301177	ESTs	15.85	0.05	upregulated stage
412420	AL035668	Hs.73853	bone morphogenetic protein 2	12.6	0.05	upregulated stage
412430	AW903564	Hs.268850	Homo sapiens cDNA: FLJ25228 fls, clone H	18.45	0.03	upregulated stage
413281	AA851271	Hs.343459	ESTs	12.55	0.04	upregulated stage
414004	AA473703	Hs.7155	ESTs, Weakly similar to Z115357A TYK1 pr	15.25	0.04	upregulated stage
414161	AA136106	Hs.184852	KIAA1553 protein	13.25	0.06	upregulated stage
414217	A3305298	Hs.279858	Homo sapiens cDNA: FLJ23165 fls, clone L	12.5	0.05	upregulated stage

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414219	W20010	Hs.75823	ALL1-tused gene from chromosome 1q	12.71	0.05	upregulate stage
414403	AL133921	Hs.76372	refinoblastoma-binding protein 2	13.05	0.05	upregulate stage
414522	AW518944	Hs.76335	Homo sapiens cDNA: FLJ23125 fls, clone L	35.45	0.02	upregulate stage
414602	AW520088	Hs.76520	Homo sapiens mRNA: cDNA: D62765fl21264 fl	21	0.02	upregulate stage
414761	AL077728	Hs.77256	enhancer of zeste (Drosophila) homolog 2	13.2	0.05	upregulate stage
415114	AB65540	Hs.183868	glucuronidase, beta	14.7	0.04	upregulate stage
416179	R19015	Hs.75067	MAD (mothers against decapentaplegic, D)	13	0.06	upregulate stage
416391	AB02927	Hs.75284	mesoderm specific transcript (muscle) hom	13.3	0.04	upregulate stage
416815	U1514	Hs.76020	UDP-N-acetyl-sulfol-D-galactose-4-epimerase	15.55	0.04	upregulate stage
416980	AA361133	Hs.82064	high-mobility group (nonhistone chromoso	23.85	0.03	upregulate stage
417258	NS6885	Hs.294040	ESTs	15.05	0.06	upregulate stage
417274	NQ235	Hs.81848	RAD21 (S. pombe) homolog	23.05	0.04	upregulate stage
417353	AA317532	Hs.75362	general transcription factor 1A, 2 (TfA)	13	0.05	upregulate stage
417615	BE548641	Hs.82314	Pyruvate kinase phosphatase 1	19.45	0.04	upregulate stage
417696	BE241824	Hs.82401	CD68 antigen (p50, early T-cell activat	12.45	0.03	upregulate stage
417777	AB023763	Hs.70555	ESTs	12.58	0.06	upregulate stage
417821	BE25145	Hs.70545	protein tyrosine kinase 9	20.8	0.04	upregulate stage
417928	AB203444	Hs.763973	ESTs	14.65	0.05	upregulate stage
418699	BE536639	Hs.173030	ESTs, Weakly similar to ALUR_HUMAN ALU S	13	0.05	upregulate stage
418791	AA035633	Hs.194628	ESTs	12.35	0.06	upregulate stage
421878	AA259662	Hs.111496	Homo sapiens cDNA FLJ11645 fs, clone HE	12.6	0.05	upregulate stage
422150	AB87118	Hs.2383	ribosomal protein S15a	13.55	0.05	upregulate stage
422363	T55079	Hs.115474	replication factor C (activator 1) 3 (8	15.7	0.05	upregulate stage
424673	AA345051	HA.20492	ESTs	16.9	0.04	upregulate stage
424848	AP26321	Hs.146807	ESTs	15.2	0.05	upregulate stage
424865	AF011333	Hs.153563	lymphocyte antigen 75	12.85	0.04	upregulate stage
425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	13.25	0.06	upregulate stage
425257	AA363867	Hs.155029	ESTs	17.55	0.05	upregulate stage
426252	BE170890	Hs.28917	ESTs	12.35	0.05	upregulate stage
426329	AL389561	Hs.271623	nucleophan 50KD	13.6	0.05	upregulate stage
427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	13.85	0.05	upregulate stage
427351	AA042993	Hs.123253	Homo sapiens cDNA: FLJ22009 fs, clone H	12.8	0.06	upregulate stage
427979	BE379776	Hs.181309	non-kinase Cdc42 effector protein SPEG	16.95	0.05	upregulate stage
428044	AA063322	Hs.182225	DNA binding motif protein 3	14.65	0.05	upregulate stage
428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	17.15	0.05	upregulate stage
428840	V15990	Hs.194148	v-vex-1 Yamaguchi sarcoma viral oncogene	16.8	0.05	upregulate stage
430191	AA149880	Hs.188809	ESTs	14.5	0.05	upregulate stage
430269	AJ022744	Hs.246315	UDP-N-acetyl-alpha-D-galactose-4-epimerase	14.9	0.05	upregulate stage
430353	AT034179	Hs.105976	ESTs	13.55	0.06	upregulate stage
431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	16.2	0.04	upregulate stage
431211	AB6849	Hs.5596	gap junction protein, beta 2, 26KD (conn	27	0.01	upregulate stage
431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	13.45	0.06	upregulate stage
431639	AV020890	Hs.289176	phosphoprotein associated with GEFs	21.2	0.03	upregulate stage
431770	BE221580	Hs.268555	5'-3' exonuclease 2	13.05	0.06	upregulate stage
431863	AA181815	Hs.271871	spindlin	15.6	0.05	upregulate stage
434263	N34895	Hs.44648	ESTs	14.25	0.06	upregulate stage
434651	BE516802	Hs.265313	core promoter element binding protein	17.95	0.05	upregulate stage
436286	AA004442	Hs.3450	Homo sapiens cDNA: FLJ22003 fs, clone H	14.35	0.05	upregulate stage
436385	BE551618	Hs.144097	ESTs	13.85	0.06	upregulate stage
437192	AAW97596	Hs.75355	ubiquitin-conjugating enzyme E2N (homolog	12.75	0.06	upregulate stage
438030	AB15580	Hs.6855	non-kinase Cdc42 effector protein SPEG	15.3	0.04	upregulate stage
439441	AB32640	Hs.18272	ESTs	17.42	0.05	upregulate stage
440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	12.59	0.05	upregulate stage
440116	AV178851	Hs.9403	ESTs	14.5	0.05	upregulate stage
440120	W75293	Hs.35952	ESTs	12.4	0.04	upregulate stage
441633	AW558444	Hs.112242	ESTs	15.85	0.03	upregulate stage
441980	AK001441	Hs.8055	hypothetical protein FLJ10579	13.8	0.05	upregulate stage
442043	BE567820	Hs.99210	ESTs	12.5	0.06	upregulate stage
442953	R35343	Hs.14968	Human DNA sequence from clone RP1-233G16	12.65	0.06	upregulate stage
442271	AF033652	Hs.8010	synuclein binding protein (synanin)	15.15	0.05	upregulate stage
443303	U87319	Hs.92116	caspase 7, apoptosis-related cysteine pr	13.4	0.05	upregulate stage
445033	AW62402	Hs.155145	ESTs	13.3	0.05	upregulate stage
446619	AU070643	Hs.313	secreted phosphoprotein 1 (osteopontin,	30.5	0.02	upregulate stage
446744	TS1454	Hs.42845	Human clone 33615 mRNA sequence	13.8	0.04	upregulate stage
446971	AB012113	Hs.187820	small inducible cytokine subfamily A (Cy	15.15	0.04	upregulate stage
446712	W01048	Hs.151634	Homo sapiens cDNA: FLJ23602 fs, clone L	13.2	0.05	upregulate stage
446772	AW390822	Hs.24639	ESTs	12.75	0.06	upregulate stage
446926	AT781614	Hs.140903	ESTs, Moderately similar to neuronal tr	13.35	0.06	upregulate stage
446962	AA048478	Hs.187820	small inducible cytokine subfamily A (Cy	12.79	0.05	upregulate stage
450139	AK001838	Hs.236323	Homo sapiens cDNA FLJ10678 fs, clone PL	14.76	0.06	upregulate stage
451035	AU076785	Hs.430	plestin 1 (I isoform)	17.65	0.04	upregulate stage
451334	AI122691	Hs.13268	ESTs	14.7	0.05	upregulate stage
452557	307123	Hs.23862	perforin-like cytotoxic protein	12.45	0.06	upregulate stage
453268	AW261344	Hs.32557	ring finger protein (CSH2C3) type 6	13.4	0.05	upregulate stage
453331	AT240665	Hs.8895	ESTs	12.6	0.05	upregulate stage
453365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.2	0.17	upregulate stage

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401256			2	0.16	upregulate stage
402075			1	0.1	upregulate stage
403029			1.75	0.16	upregulate stage
403341			3.3	0.1	upregulate stage
403426			1.7	0.18	upregulate stage
403754			2.8	0.12	upregulate stage
403822			1.2	0.14	upregulate stage
407635	Has.40337	hypothetical protein	1.9	0.15	upregulate stage
407693	AA046392	gcr11201.s1 Soares_fetal_NB#119W	1.35	0.14	upregulate stage
408061	AAW41597	ESTs	2.3	0.18	upregulate stage
408068	AF070571	Homo sapiens clone 24739 mRNA sequence	1.65	0.12	upregulate stage
408920	AL120071	fibronectin leucine rich transmembrane p	1	0.2	upregulate stage
409510	AAW09895	gb33-HF-EP9-pin-024-3J11 HFR_MJC_5	2.25	0.2	upregulate stage
410094	BE147857	general transcription factor IIF, polype	4.05	0.12	upregulate stage
410603	AA086219	ESTs	1.9	0.16	upregulate stage
410763	AF279145	tumor endothelial marker 8	4.15	0.13	upregulate stage
411416	BE241670	gcr1CAAP223047 Psediotic scale myelogeno	1.6	0.22	upregulate stage
411681	AAW57199	gcr1CC-CIT304-080-100-0114-06 CIT304 Homo	1.45	0.24	upregulate stage
411750	BE562256	KIAA0112 proteik, homolog of yeast ribos	2.2	0.2	upregulate stage
411880	AAW72477	gchrn3003.x1 NC1_CGAP_Thy4 Homo sapiens	1.75	0.06	upregulate stage
412102	H59435	KIAA0377 protein	1.7	0.2	upregulate stage
412303	AAW36336	gcr01A-DT021-2B1299-070-g11 DT021 Homo	1	0.17	upregulate stage
412312	AAW36686	gcr01A-DT023-080308-004-g01 DT023 Homo	3.4	0.16	upregulate stage
412598	AI661997	ESTs	2.25	0.2	upregulate stage
413363	AA128976	Homo sapiens cDNA FLJ13594 fls, clone PL	2.3	0.17	upregulate stage
413505	AAW45263	ESTs	3.52	0.14	upregulate stage
413516	BE154076	gcr01A-DT035-200404-010-F04 HT0339 Homo	1	0.18	upregulate stage
416661	AA634543	IGF-I mRNA-binding protein 3	1.05	0.12	upregulate stage
417708	N74392	ESTs	2	0.16	upregulate stage
417974	AA210765	gchrn9006.r1 NC1_CGAP_GCB1 Homo sapiens	3.75	0.13	upregulate stage
418044	AA225532	ESTs	1.75	0.2	upregulate stage
418631	AA225921	ESTs	3.6	0.09	upregulate stage
418630	BE513731	Human DNA sequence from clone 967N21 on	2.35	0.14	upregulate stage
418893	N32264	ESTs	2.15	0.19	upregulate stage
418990	T76517	ESTs	1.85	0.15	upregulate stage
419504	AT798135	Homo sapiens cDNA FLJ14201 fls, clone Y7	3.8	0.14	upregulate stage
420082	N43741	ESTs	2.05	0.16	upregulate stage
420553	A1224532	ESTs	3.5	0.13	upregulate stage
421112	AW243675	ESTs	2	0.14	upregulate stage
421683	AT147636	ESTs	2.35	0.15	upregulate stage
421799	AAW72292	ESTs	3.3	0.14	upregulate stage
422177	AA720876	ESTs	3.45	0.12	upregulate stage
422429	AA310527	gcrEST181333 Jurkat T-cells V Homo sapie	2.15	0.11	upregulate stage
422595	BE451972	hypothetical protein FLJ10461	3.6	0.14	upregulate stage
424028	AT956295	ESTs	1	0.09	upregulate stage
425650	NM_001944	desmoglein 3 (pemphigus vulgaris antigen	2	0.19	upregulate stage
425761	AAW64214	ESTs	2.1	0.16	upregulate stage
426427	M86959	TK protein kinase	2.15	0.14	upregulate stage
427558	D43453	growth differentiation factor 10	3.9	0.11	upregulate stage
429335	BE397986	tumor protein p53-binding protein	3.6	0.12	upregulate stage
429768	AA477958	ESTs	1.9	0.17	upregulate stage
429781	AT217680	ESTs	5.05	0.11	upregulate stage
430132	AA254686	hypothetical protein FLJ20647	3.55	0.15	upregulate stage
430253	AK001614	hypothetical protein FLJ10652	2.5	0.14	upregulate stage
430386	AA356523	nuclear cap binding protein subunit 2, 2	3.95	0.13	upregulate stage
431167	AW971146	ESTs	1.6	0.15	upregulate stage
431364	AW713382	ESTs, Weakly similar to alpha-1(XVII)c	1.65	0.22	upregulate stage
431401	AA504626	ESTs, Weakly similar to FYVE finger-cont	1.45	0.16	upregulate stage
431419	AL041844	ESTs	2.15	0.14	upregulate stage
432361	A378562	ESTs	3.7	0.08	upregulate stage
432810	AA863400	ESTs	2	0.2	upregulate stage
432929	AA070416	hypothetical protein FLJ10846	2.35	0.14	upregulate stage
433106	AA002448	gcr:Homo sapiens mRNA from chromosome 5q2	1	0.14	upregulate stage
434163	AF118072	Homo sapiens PRD1716 mRNA, complete cds	1.25	0.16	upregulate stage
435202	AW971313	KIAA0651 protein	2	0.18	upregulate stage
435313	AT809400	ESTs	3.6	0.11	upregulate stage
435359	T66843	ESTs	2.2	0.22	upregulate stage
435468	H57554	ESTs	1.4	0.19	upregulate stage
435683	AAW23909	ESTs	3.2	0.12	upregulate stage
435682	A1821540	ESTs, Moderately similar to ALU8_HUMAN A	2.05	0.22	upregulate stage
437465	AT149570	ESTs	2.75	0.15	upregulate stage
437854	AL119723	gcr:CKF2p76:A2124_r1 761 (synonym: hamy2)	2.45	0.13	upregulate stage
438316	AA785045	gcr:a27g6.s1 Soares_fetal_NHT Homo sap	3.1	0.13	upregulate stage
438390	AAZ20017	gcr14G12.x1 NC1_CGAP_Bm23 Homo sapien	1.35	0.12	upregulate stage
438515	AA3280174	ESTs	4	0.13	upregulate stage
439563	AA858394	ESTs	5.55	0.09	upregulate stage
442048	AA974603	gcrp34005.s1 Soares_NFL_T_GDC_S1 Homo s			

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	442369	A0565071	Hs.159983	ESTs	3.85	0.14	upregulate stage
	442748	A016713	Hs.135787	ESTs	2.35	0.23	upregulate stage
	443717	BE163884	Hs.282331	ESTs	2.5	0.18	upregulate stage
	445935	AA267537	Hs.197595	ESTs	1	0.2	upregulate stage
5	446078	AS35982	Hs.159081	ESTs	2.25	0.24	upregulate stage
	446139	H77365	Hs.39749	ESTs	2.15	0.18	upregulate stage
	446163	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (f)	3.45	0.14	upregulate stage
	448283	H26999	Hs.201591	ESTs	1.65	0.18	upregulate stage
	44866	A0001674	Hs.29030	cofactor required for Sp1 transcription	2.2	0.14	upregulate stage
10	449199	AW90122	Hs.196988	ESTs	1.25	0.23	upregulate stage
	449568	AA001765	Hs.157079	KIAA1227 protein	1	0.16	upregulate stage
	449676	AW014631	Hs.225068	ESTs	2.3	0.19	upregulate stage
	449859	T8077	Hs.16214	ESTs	5.3	0.07	upregulate stage
	450434	AA166650	Hs.15645	ESTs, Weakly similar to partial CDS (Ca	1.65	0.22	upregulate stage
	450625	AW870197	gb:EST382183 MAGE-resonances, MAGK Homo	1.35	0.19	upregulate stage	
	451337	AA000209	Hs.80787	ESTs	1.6	0.16	upregulate stage
	451686	AA356246	Hs.110253	ESTs	3.4	0.14	upregulate stage
	452079	AA832908	Hs.15205	ESTs	1.9	0.23	upregulate stage
	452220	BE158006	Hs.212296	ESTs	3.1	0.17	upregulate stage
20	453916	AW005123	Hs.231975	ESTs	1	0.21	upregulate stage
	455300	AW501919	gb:CDV-NN1020-7040C-155-02 NN1020 Homo	2	0.2	upregulate stage	
	456511	AA282300	Hs.145568	ESTs	1.15	0.12	upregulate stage
	456966	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	1.85	0.18	upregulate stage
	457427	AW971287	gb:EST383376 MAGE-resonances, MAGL Homo	2.35	0.16	upregulate stage	
25	402988	AA335827	Hs.135358	ATP-binding cassette, sub-family C (CFTR	2.33	0.27	upregulate stage
	402439	AF153341	Hs.283954	Homo sapiens winged helix/loop helix	7.45	0.09	upregulate stage
	402471				0.71	0.31	upregulate stage
	402641				7.25	0.1	upregulate stage
30	402749				5.35	0.09	upregulate stage
	402781				5.9	0.1	upregulate stage
	402843				5.85	0.07	upregulate stage
	401045				2.42	0.17	upregulate stage
	401049				1.2	0.19	upregulate stage
35	401192				2.47	0.3	upregulate stage
	401223				6.73	0.08	upregulate stage
	401205				6.63	0.1	upregulate stage
	401276				6.95	0.1	upregulate stage
	401581				2.2	0.13	upregulate stage
40	401604				1	0.19	upregulate stage
	422445				7.65	0.09	upregulate stage
	422286				1	0.33	upregulate stage
	422530				5.1	0.13	upregulate stage
	422812				1.65	0.17	upregulate stage
45	422820				1	0.34	upregulate stage
	422892				1	1	upregulate stage
	433444				6.5	0.08	upregulate stage
	434158				3.7	0.11	upregulate stage
50	434250				4.45	0.09	upregulate stage
	434538				8.38	0.09	upregulate stage
	434676				6.3	0.09	upregulate stage
	434677				0.9	0.25	upregulate stage
	435003				1.52	0.31	upregulate stage
55	435109	N47812	Hs.81380	CGI-35 protein	6.2	0.1	upregulate stage
	435654				1.95	0.06	upregulate stage
	436381				3	0.07	upregulate stage
	436270				6.09	0.13	upregulate stage
	436399				1.55	0.41	upregulate stage
60	436475				6.2	0.12	upregulate stage
	436485				1	0.48	upregulate stage
	437411	AA358357	Hs.74496	carcinoembryonic antigen-related cell ad	5.4	0.07	upregulate stage
	436987	AA157857	Hs.182265	keratin 19	2.28	0.37	upregulate stage
	437173	T64349	gb:ycr000c.s1 Stralagene lung (93721Q) H	3.35	0.11	upregulate stage	
65	437230	AA157857	Hs.182265	keratin 19	2.15	0.38	upregulate stage
	437286	AJ235954	gb:Homo sapiens mRNA for immunoglobulin	2.1	0.09	upregulate stage	
	437783	AW566372	Hs.172238	a disialogin and metalloproteinase domain	3.25	0.11	upregulate stage
	437825	NW_008152	Hs.42322	lymphocyte-restricted membrane protein	6.25	0.08	upregulate stage
	437870	AB032990	Hs.40719	hypothetical protein KIAA1164	4.5	0.12	upregulate stage
70	437877	AW116811	Hs.234478	Homo sapiens cDNA: FLJ22648 fls, clone H	3.3	0.15	upregulate stage
	437968	NW_004063	Hs.59403	zincine polynucleotide, long chain	7.35	0.1	upregulate stage
	438152	AA563833	Hs.118527	ESTs	6.2	0.09	upregulate stage
	438353	NW_003389	Hs.43396	corexin, actin-binding protein, 2A	5.35	0.14	upregulate stage
	438576	NW_003542	Hs.46423	H4 histone family, member G	7.28	0.1	upregulate stage
75	438673	BE208517	Hs.194109	fibronectin protein L37s	2.53	0.24	upregulate stage
	438684	HS1377	Hs.172727	hypothetical protein FLJ21610	1	0.3	upregulate stage
	439381	NW_005082	Hs.54416	stine oculis homeobox (Drosophila) homolo	7.7	0.06	upregulate stage
	439592	BE280951	Hs.55068	E11-domain containing 4	3.95	0.1	upregulate stage

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499744	AW675258	He 56265	Homo sapiens mRNA; cDNA DKFZp586P3221 (1.55	0.16	upregulate stage
410141	R07775	He 287657	Homo sapiens cDNA: FLJ121291 fls, clone C	4.1	0.18	upregulate stage
410322	AW372451	He 61184	CGI-79 protein	3.65	0.14	upregulate stage
410288	AW815957	He 61184	gltc1h75g12x1 NCL_GCAP_GLI1 Homo sapiens	7.55	0.09	upregulate stage
410297	AA148710	He 159441	ESTs	3.8	0.1	upregulate stage
410337	M83822	He 62364	cell division cycle 4-like	4.35	0.19	upregulate stage
410418	D31382	He 63325	transmembrane protease, serine 4	1.42	0.4	upregulate stage
410541	AA066003	He 64179	hypothetical protein	1.61	0.48	upregulate stage
410724	AW702629	He 65479	gltc1C0-UM0051-210300-012-017 UM0051 Homo	0.65	0.12	upregulate stage
410785	AW805341	He 67397	gltc1C2-UM0079-090300-050-D03 UM0079 Homo	1.4	0.16	upregulate stage
410988	AA195907	He 67397	homoeb box A1	3.65	0.1	upregulate stage
411162	AW819544	He 67397	gltc1C0-5T0294-240300-172-a03 5T0294 Homo	2	0.23	upregulate stage
411173	R81571	He 69319	gltc1G0294-011 Spores plasencia Hb2HP Homo	7.2	0.1	upregulate stage
411243	AE036886	He 69319	CAT1	0.38	0.53	upregulate stage
411407	R03903	He 69319	gltc1e7a07.r1 Spores fetal liver spleen	8	0.00	upregulate stage
411704	AA99220	He 71573	hypothetical protein FLJ10074	1.75	0.22	upregulate stage
412121	AE033361	He 73287	KIA11235 protein	5.3	0.11	upregulate stage
412132	BE251329	He 73291	hypothetical protein FLJ10881	6.9	0.1	upregulate stage
412129	M21964	He 73454	Itoporin T3, skeletal, test	0.27	1.06	upregulate stage
412354	AW935148	He 74126	gltc1QV1-0T0069-110200-067-005 0T0069 Homo	8.9	0.11	upregulate stage
412610	XG3908	He 74126	fatty acid binding protein 6, testis	2.88	0.21	upregulate stage
412700	BE222433	He 761262	ESTs	2.85	0.15	upregulate stage
412706	R97106	He 167546	ESTs	3.75	0.16	upregulate stage
412935	BE267045	He 75064	tubulin-specific chaperone c	7	0.09	upregulate stage
413042	T24058	He 75355	gltc1ae2245 HbMSW7K Homo sapiens cDNA clo	6.3	0.12	upregulate stage
413321	AA245428	He 75355	ubiquitin-conjugating enzyme E2N (bromio	3.45	0.11	upregulate stage
413465	BE141022	He 75355	gltc1WRD-3T0195-002-410 HbT0067 Homo	3.09	0.13	upregulate stage
413687	AA158194	He 771833	Homo sapiens cDNA FLJ13473 fls, clone PL	7.63	0.00	upregulate stage
413800	AI129238	He 192235	ESTs	3.2	0.18	upregulate stage
413859	AW922355	He 63364	pyruvate dehydrogenase kinase, isoenzyme	2.54	0.33	upregulate stage
413930	M88153	He 75918	RAB11A, member RAS oncogene family	1.75	0.21	upregulate stage
413991	HA4725	He 71300	ESTs	1.3	0.21	upregulate stage
414023	AW578849	He 263552	ESTs, weakly similar to unnamed protein	8.1	0.07	upregulate stage
414202	BE26710	He 75914	gltc1B1150419F1 NH_MGC_19 Homo sapiens c	1.45	0.14	upregulate stage
414343	AL028166	He 75914	scated vesicle membrane protein	4	0.23	upregulate stage
414684	AA587775	He 66295	Homo sapiens HSPC311 mRNA, partial cds	1	0.36	upregulate stage
414687	AA524394	He 165544	ESTs	1.51	0.51	upregulate stage
414993	AW819403	He 77724	KIA0586 gene product	2.72	0.23	upregulate stage
415276	U88666	He 76353	SFRS3 protein kinase 2	6.55	0.1	upregulate stage
415303	R11813	He 119174	gltc1E334041 Spores infant brain NBH 8	6.1	0.09	upregulate stage
415392	Z44067	He 76981	gltc1SIC1RF061 normalized infant brain cDN	5.59	0.11	upregulate stage
415572	F12294	He 76981	gltc1SIC8D051 normalized infant brain cDN	5.7	0.11	upregulate stage
415773	R21651	He 76981	gltc1h19602.r1 Spores placenta Hb2HP Homo	5.3	0.11	upregulate stage
416012	AF061569	He 20981	protein phosphatase 1, regulatory (p1b)	2.19	0.28	upregulate stage
416074	RA0714	He 21209	ESTs	7.61	0.11	upregulate stage
416182	NM_004354	He 75089	cyclin G2	1	0.39	upregulate stage
416518	H60730	He 16917	ESTs	6.6	0.1	upregulate stage
416702	L30335	He 75986	thiose 5-phosphate isomerase A (thiose 5	3.9	0.17	upregulate stage
416987	D69957	He 87012	KIA02022 protein	2.54	0.31	upregulate stage
417004	NM_006895	He 81182	histamine N-methyltransferase	4.26	0.12	upregulate stage
417275	X63578	He 81849	parvalbumin	1	0.12	upregulate stage
417395	BE564246	He 82084	myosin beta 3 binding protein (beta-3	8.4	0.08	upregulate stage
417683	AW596208	He 239154	Homo sapiens cDNA FLJ12514 fls, clone NT	2.2	0.17	upregulate stage
417759	R13567	He 12548	ESTs	6.18	0.00	upregulate stage
417848	AA206881	He 35457	ESTs	8.6	0.08	upregulate stage
417985	AA187345	He 83114	cytochrome, zeta (cytochrome reductase)	0.1	0.11	upregulate stage
418073	R39789	He 119174	ESTs	6.3	0.11	upregulate stage
418354	AF132818	He 84728	Kruppel-like factor 5 (intestinal)	1.63	0.46	upregulate stage
418406	X73501	He 84005	cytochrome 20	3.5	0.02	upregulate stage
418555	AM17215	He 87159	Homo sapiens cDNA FLJ12577 fls, clone NT	7.65	0.06	upregulate stage
418596	AW148865	He 87159	gltc1C04-5T0334-281295-053-05 5T0334 Homo	4.1	0.11	upregulate stage
418766	AT79817	He 203594	Homo sapiens undifferentiated gastric pro	7.5	0.08	upregulate stage
418827	BE227311	He 47166	HT021	5.6	0.13	upregulate stage
418948	AZ17097	He 87159	gltc1d43h07.x1 Spores_fetal_heart_NBH-H19W	1.5	0.22	upregulate stage
419551	AW582258	He 51071	anterior gradient 2 (Xenopus laevis) hom	2.44	0.29	upregulate stage
419590	AF035443	He 51350	poly (ADP-ribose) glycohydrolase	6.08	0.1	upregulate stage
419663	AA133749	He 53223	FXFD domain-containing ion transport reg	1.64	0.48	upregulate stage
419712	AA360838	He 179909	Homo sapiens cDNA: FLJ22995 fls, clone K	5.4	0.11	upregulate stage
419713	AW396503	He 53281	nucleic (nucleoside diphosphate linked mol	7.9	0.06	upregulate stage
419720	AA291331	He 143637	hypothetical protein FLJ11056	2.95	0.15	upregulate stage
419751	AI579009	He 105104	ESTs	2.45	0.2	upregulate stage
419872	AA22951	He 146162	ESTs	4.25	0.17	upregulate stage
419903	T16038	He 87002	ESTs	2.5	0.22	upregulate stage
419932	AZ211594	He 87002	gltc1A3501.r1 NCL_GCAP_GCB1 Homo sapiens	6.1	0.12	upregulate stage
420026	AB311190	He 166676	ESTs	3.4	0.4	upregulate stage
420187	AK007114	He 35744	hypothetical protein similar to ankyrin	4.03	0.18	upregulate stage
420193	AA60080	He 202889	ESTs	1	0.28	upregulate stage

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420281	AI623693	Hs.191533	ESTs	6.6	0.11	upregulate stage
420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fls, clone C	6	0.00	upregulate stage
420370	Y13645	Hs.97234	uroplakin 2	1.2	0.45	upregulate stage
420393	T85154	Hs.144880	ESTs	3.8	0.12	upregulate stage
420450	AW886860	Hs.177728	ESTs	2.75	0.14	upregulate stage
420588	AF000982	Hs.147916	DEAD/HD (Asp-Glu-Ala-Asp/His) box polypep	8.1	0.09	upregulate stage
420763	AA419092	Hs.179354	ESTs	8	0.09	upregulate stage
420838	AW118210	Hs.5244	ESTs	6.65	0.07	upregulate stage
420981	L40024	Hs.100724	peroxisome proliferator activated recep	1.98	0.32	upregulate stage
421013	M62397	Hs.1345	mutated in colorectal cancers	1	0.29	upregulate stage
421072	AU215069	Hs.89113	ESTs	5.8	0.12	upregulate stage
421110	AJ280717	Hs.1355	cathespain E	5.45	0.03	upregulate stage
421141	AW117261	Hs.122914	ESTs	2.75	0.16	upregulate stage
421338	AJ327443		gluc2c010.1 NCL_GCAP_GCB1 Homo sapiens	7.45	0.09	upregulate stage
421508	NM_048433	Hs.105115	absent in melanoma 2	4.21	0.19	upregulate stage
421834	AA437414	Hs.106283	hypothetical protein FLJ10262	7.79	0.06	upregulate stage
421874	T10707	Hs.256356	neuronal PAS domain protein 2	7.5	0.1	upregulate stage
421810	AQ007118	Hs.105530	hypothetical protein FLJ10855	6.45	0.08	upregulate stage
421865	P06504	Hs.27384	ESTs	2.9	0.16	upregulate stage
421898	AA259011	Hs.109266	hypothetical protein FLJ12552	7.06	0.11	upregulate stage
422156	H34524	Hs.300853	ESTs, Weakly similar to envelope protein	3.78	0.16	upregulate stage
422225	BC145822	Hs.111681	zinc finger protein 268	2.95	0.17	upregulate stage
422243	AW803733	Hs.253655	prothymosin, alpha (gene sequence 28)	6.18	0.08	upregulate stage
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.21	0.17	upregulate stage
422634	NM_016010	Hs.118821	CGI-52 protein	1.3	0.29	upregulate stage
422988	AW673847	Hs.173721	ESTs	4.15	0.11	upregulate stage
423081	AF282002	Hs.123159	open associated antigen 4	2.82	0.3	upregulate stage
423696	AA326195	Hs.234101	ESTs, Weakly similar to CTL1 protein (H	2.75	0.19	upregulate stage
423872	AB020316	Hs.134015	urovyl 2-sulbotransferase	1.96	0.13	upregulate stage
423973	AF229181	Hs.136844	CS box-containing WD protein	7.12	0.11	upregulate stage
424005	AB033411	Hs.141215	protein KIAA1215	1.71	0.37	upregulate stage
424014	AA333853	Hs.24790	KIAA1573 protein	4.86	0.12	upregulate stage
424028	AF065084	Hs.153682	KIAA0086 protein	6.5	0.07	upregulate stage
424194	BE245833	Hs.163954	hypothetical protein SP152	6.1	0.1	upregulate stage
424308	AW875331	Hs.154543	myochromosome maintenance deficient (S	6.59	0.11	upregulate stage
424540	AB65641	Hs.115298	ESTs	3.25	0.12	upregulate stage
424631	AA688021	Hs.178908	ESTs	5.45	0.11	upregulate stage
424659	AW891298	Hs.301877	ESTs, Weakly similar to hSUAH2 (H.sapien	3.55	0.15	upregulate stage
424704	AZ653263	Hs.152098	cytochrome P450, subfamily 1U (arachido	6.45	0.06	upregulate stage
424775	AB014540	Hs.153526	SWAP-70 protein	6.65	0.11	upregulate stage
424800	AL035598	Hs.153203	MyoD family inhibitor	1.94	0.3	upregulate stage
425086	M82882	Hs.154355	ET4-like factor 1 (ets domain transcript)	2.85	0.19	upregulate stage
425236	AL043280	Hs.155357	Homo sapiens mRNA; cDNA DRFZP664K143 (H	5.2	0.1	upregulate stage
425277	NM_001241	Hs.155478	cyclin T2	6	0.13	upregulate stage
425508	AA391551	Hs.97013	ESTs	5.87	0.1	upregulate stage
425689	W16480	Hs.24283	ESTs	4.55	0.13	upregulate stage
425721	AC020215	Hs.155939	uroplakin 1A	0.71	0.8	upregulate stage
426069	H11907	Hs.30296	ESTs	2.4	0.17	upregulate stage
426668	AF038007	Hs.166196	ATPase, Class I, type 6B, member 1	6.84	0.09	upregulate stage
428110	NM_002913	Hs.165583	replication factor C (pactivator 1) 1 (14	6.7	0.1	upregulate stage
428227	U87058	Hs.185102	Human proteinase activated receptor-2 mR	3.05	0.14	upregulate stage
428603	AA362291	Hs.177371	gdc3T53563 Testis 1 Homo sapiens cDNA 5	1.6	0.26	upregulate stage
428657	NM_015885	Hs.171731	solute carrier family 14 (sua transport	0.98	0.36	upregulate stage
428716	NM_005379	Hs.171921	sema domain, immunoglobulin domain (Hf,	1.32	0.49	upregulate stage
428922	A1125334	Hs.97408	ESTs	5.06	0.07	upregulate stage
428931	NM_003418	Hs.2078	zinc finger protein 7 (PCX 4, clone HF.1	2.65	0.12	upregulate stage
429171	NM_004482	Hs.173135	dual-specificity kinase (Y)-phosphoryl	4.5	0.12	upregulate stage
429707	BE073913	Hs.173515	uncharacterized hypothalamus protein H10	0.57	0.86	upregulate stage
429798	AW290020	Hs.20415	chromosome 21 open reading frame 11	1.86	0.31	upregulate stage
429799	NM_014883	Hs.177864	KIAA0914 gene product	5	0.13	upregulate stage
429790	AB014526	Hs.178121	KIAA0026 gene product	6.37	0.13	upregulate stage
429800	Z95152	Hs.178605	multigene-activated protein kinase 13	6.7	0.11	upregulate stage
429747	AA139888	Hs.178066	ESTs, Weakly similar to AF068289 5 HDGME	5.7	0.11	upregulate stage
428042	AA411923		gluc2c03212.1 Source: NIH/NCPU_S1 Homo sapi	1.55	0.14	upregulate stage
428536	AA580315	Hs.183752	microseminoprotein, beta	5.37	0.05	upregulate stage
428537	AA644088		gluc2c0301.1 Source: NIH/NCPU_S1 Homo sapi	3.4	0.13	upregulate stage
428565	AA259331	Hs.183661	Homo sapiens cDNA: FLJ20042 lis, clone CO	1	0.17	upregulate stage
428471	X57348	Hs.184510	estratin	1.81	0.39	upregulate stage
428583	AA430689	Hs.301374	ESTs, Moderately similar to ALLUS_HUMAN A	7.55	0.11	upregulate stage
428670	AA116892	Hs.134531	ESTs	6.06	0.1	upregulate stage
428785	AD115953	Hs.125265	ESTs	1.55	0.15	upregulate stage
429332	AF030403	Hs.199253	Ste-20 related kinase	2.64	0.26	upregulate stage
429543	AK000705	Hs.199480	epim 3	3.18	0.27	upregulate stage
429556	AW139399	Hs.98086	ESTs	1.87	0.31	upregulate stage
429693	M68874	Hs.211587	phosphatase A2, group IVA (cytosolic,	0.61	1.02	upregulate stage
429824	AA226362	Hs.121520	Human BAC clone A21-59186	2.03	0.39	upregulate stage
429988	BE081342	Hs.226799	HSPC039 protein	7.86	0.06	upregulate stage

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5	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1	0.61	upregulate stage
	430042	AB023170	Hs.227850	KIAA0953 protein	2.5	0.17	upregulate stage
	430168	AB684343	Hs.300896	ESTs, Highly similar to AF128113 1 proni	1.98	0.4	upregulate stage
	430306	BC540865	Hs.236950	cyclic-dependent kinase inhibitor 1E (p2	6.7	0.09	upregulate stage
	430399	A016294	Hs.108571	ESTs	8.08	0.08	upregulate stage
10	430763	AA484548	Hs.105558	ESTs	3.18	0.24	upregulate stage
	431474	AL133990	Hs.190642	ESTs	0.37	0.51	upregulate stage
	431587	N51357	Hs.205855	Homo sapiens mRNA, cDNA DKFZp761G2311 #	1.74	0.39	upregulate stage
	431585	BE142803	Hs.263823	hypothetical protein FLJ10326	3.55	0.15	upregulate stage
	431683	AK001749	Hs.267604	hypothetical protein FLJ10450	8.55	0.08	upregulate stage
15	431700	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	7.95	0.1	upregulate stage
	431846	BE019624	Hs.271580	uroplakin 1b	1.33	0.5	upregulate stage
	431912	A1602652	Hs.154063	ESTs, Weakly similar to A56154 Abi subcl	4.15	0.12	upregulate stage
	432050	NX_205865	Hs.174407	protein, serine, 16 (Thyru)	3.7	0.13	upregulate stage
	432520	A075978	Hs.188007	ESTs	2.05	0.22	upregulate stage
20	432624	A458020	Hs.283287	ESTs	5.15	0.14	upregulate stage
	432640	A021517	Hs.105896	ESTs	5.5	0.11	upregulate stage
	432623	AA573521	Hs.152448	ESTs, Moderately similar to PUR1_HUMAN	8.43	0.09	upregulate stage
	432632	AW973801	Hs.134656	ESTs	2.45	0.16	upregulate stage
	432820	A554057	Hs.152477	ESTs	8.29	0.09	upregulate stage
25	432945	AL043983	Hs.271357	ESTs, Weakly similar to unnamed protein	3.22	0.23	upregulate stage
	433027	AF151016	Hs.279523	putative nucleotide binding protein, est	2.15	0.39	upregulate stage
	433037	NM_014158	Hs.279938	HSPC067 protein	5.1	0.11	upregulate stage
	433156	R55208	Hs.175519	Homo sapiens cDNA: FLJ22539 fts, clone H	7.9	0.1	upregulate stage
	433171	AA579425		gbm16708.s1 NCL_CGAP_P2 Homo sapiens	3.54	0.14	upregulate stage
30	433311	AA686149		hypothetical protein FLJ10326	6.6	0.08	upregulate stage
	433383	AF034557	Hs.192731	double-stranded RNA specific adenosine d	2.45	0.21	upregulate stage
	433409	A278802	Hs.25581	ESTs	4.75	0.1	upregulate stage
	433560	AA603472	Hs.284556	ESTs	1.6	0.18	upregulate stage
	433675	AW975653	Hs.110771	Homo sapiens cDNA: FLJ21594 fts, clone II	3.88	0.17	upregulate stage
35	434328	DE564957	Hs.15584	pc11 homolog	3	0.15	upregulate stage
	434476	AW868520	Hs.271825	ESTs	4.6	0.1	upregulate stage
	434683	AW280724	Hs.202839	ESTs	2.1	0.19	upregulate stage
	434726	AF062719	Hs.139053	ESTs	1.76	0.34	upregulate stage
	435124	AA253562	Hs.120458	ESTs	7.7	0.09	upregulate stage
40	435683	AF103117	Hs.56457	schell carrier family 2 (facilitated g'u	5.8	0.09	upregulate stage
	435899	N89093	Hs.188974	ESTs	1.32	0.42	upregulate stage
	436026	A345784	Hs.217081	ESTs	1	0.22	upregulate stage
	436154	AA764550	Hs.119850	ESTs	8.4	0.05	upregulate stage
	436263	A011188	Hs.120910	ESTs	2.42	0.2	upregulate stage
45	436381	AA825814	Hs.149065	ESTs	6.95	0.09	upregulate stage
	436455	A027959	Hs.132300	ESTs	3.25	0.15	upregulate stage
	436577	W64774	Hs.17643	ESTs	6.3	0.05	upregulate stage
	436684	AW976919	Hs.54806	KIAA1052 protein	4.75	0.12	upregulate stage
	437036	A1571514	Hs.133022	ESTs	1.4	0.13	upregulate stage
50	437146	AA730677		gbm5505.s1 NCL_CGAP_Ew1 Homo sapiens	1	0.37	upregulate stage
	437282	B2250537	Hs.174838	Homo sapiens cDNA FLJ14192 fts, clone NT	3.25	0.17	upregulate stage
	437277	AA748018	Hs.123310	ESTs	0.75	0.09	upregulate stage
	437862	A243203	Hs.131572	ESTs	8.12	0.09	upregulate stage
	438392	AA806395	Hs.123205	ESTs	1	0.34	upregulate stage
55	438418	N78398	Hs.211187	Homo sapiens cDNA: FLJ23058 fts, clone L	8.1	0.1	upregulate stage
	438739	AA815391		gbm1607.s1 Source_blasts, NIH Homo sap	4.89	0.12	upregulate stage
	439211	A1803417	Hs.271923	Homo sapiens cDNA: FLJ22785 fts, clone H	6.65	0.11	upregulate stage
	439354	AA149250	Hs.58105	ESTs, Weakly similar to WDMN RAT WDMN: P	3.19	0.11	upregulate stage
	439544	W26354	Hs.28881	hypothetical protein FLJ11360	2.3	0.34	upregulate stage
60	439589	AW602168	Hs.222339	CECP1 protein	0.73	0.51	upregulate stage
	439588	AA522506	Hs.111009	ESTs	4.3	0.1	upregulate stage
	439706	AW672527	Hs.59761	ESTs	1	0.14	upregulate stage
	439897	NM_015310	Hs.8763	KIAA0942 protein	8.4	0.08	upregulate stage
	439988	AA505814	Hs.205661	ESTs, Weakly similar to C05E11.1 gene pr	7.35	0.1	upregulate stage
65	439949	AW979197	Hs.252073	ESTs	6.55	0.08	upregulate stage
	440035	BC261548	Hs.261262	hypothetical protein FLJ21839	8	0.11	upregulate stage
	440019	AAW06886	Hs.91052	ESTs, Moderately similar to ALLUS_HUMAN A	7.95	0.07	upregulate stage
	440635	AW610331		gb:RC4-ST0316-190100-011-c08 ST0316 Homo	5.95	0.11	upregulate stage
	440787	AW920243	Hs.209433	ESTs	5.05	0.12	upregulate stage
70	441253	AA972855	Hs.135598	ESTs	1.7	0.12	upregulate stage
	441528	A005797	Hs.130815	hypothetical protein FLJ21870	7.2	0.09	upregulate stage
	441670	AW974069	Hs.127392	ESTs, Moderately similar to p30ING1 [Hs	2.45	0.19	upregulate stage
	441843	BC584214	Hs.102946	ESTs	5.9	0.13	upregulate stage
	441847	AZ155684	Hs.220872	ESTs	6.95	0.11	upregulate stage
75	442145	A022650	Hs.81177	erbB2-interacting protein ERBIN	3	0.19	upregulate stage
	442299	AAW67791	Hs.155561	ESTs	5.05	0.13	upregulate stage
	442315	AA173992	Hs.7556	ESTs	3.97	0.17	upregulate stage
	442528	AF150317	Hs.134217	ESTs	1.4	0.34	upregulate stage
	442571	C05358	Hs.165464	ESTs	8	0.08	upregulate stage
	442607	AA50576	Hs.288361	Homo sapiens cDNA: FLJ22696 fts, clone H	6.7	0.1	upregulate stage
	442652	A005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	7.15	0.11	upregulate stage

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	442947	R40800	Hs.21303	ESTs	8.5	0.08	upregulate stage
	442993	BE018682	Hs.44343	ESTs	1.51	0.24	upregulate stage
	443015	R33261	Hs.6614	ESTs	8.5	0.09	upregulate stage
	443086	A032660	Hs.164711	ESTs	4	0.13	upregulate stage
5	443228	W24781	Hs.293798	ESTs	1.61	0.47	upregulate stage
	443367	AW071349	Hs.215937	ESTs	1.75	0.29	upregulate stage
	443371	A1792888	Hs.145489	ESTs	5.85	0.11	upregulate stage
	443504	A1921685	Hs.1469713	ESTs	1.4	0.18	upregulate stage
	443538	AW028096	Hs.1456705	ESTs	3.25	0.15	upregulate stage
10	443677	AV646006	Hs.293776	ESTs, Weakly similar to 120728H.revenue	6.45	0.11	upregulate stage
	443861	AW449462	Hs.134743	ESTs	6.72	0.09	upregulate stage
	444069	AW517412	Hs.150757	ESTs	4.25	0.11	upregulate stage
	444171	AE013249	Hs.10458	small inducible cytokine subfamily A (Cy	8.46	0.09	upregulate stage
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	8.1	0.1	upregulate stage
15	444386	BE278664	Hs.11085	CGI-111 protein	8.6	0.09	upregulate stage
	444624	AV650476	Hs.282936	ESTs	7.52	0.1	upregulate stage
	444631	AW595395	Hs.84520	ESTs	1.25	0.21	upregulate stage
	444707	A198613	Hs.143868	ESTs	2.1	0.21	upregulate stage
	444735	BE019923	Hs.243122	hypothetical protein FLJ13067 similar to	6.8	0.1	upregulate stage
20	444779	A192105	Hs.147170	ESTs	0.94	0.6	upregulate stage
	444823	BE262969	Hs.12045	putative protein	8.08	0.1	upregulate stage
	444859	A1197336	Hs.202275	ESTs, Weakly similar to unnamed protein	4.5	0.09	upregulate stage
	444875	A1200789	Hs.44737	ESTs	6.85	0.11	upregulate stage
25	444888	A1651039	Hs.148569	ESTs	3.15	0.18	upregulate stage
	445076	A0206886	Hs.154131	ESTs	7.81	0.09	upregulate stage
	445182	AW189787	Hs.147474	ESTs	2	0.07	upregulate stage
	445189	A1934649	Hs.147482	ESTs	2.65	0.12	upregulate stage
30	445320	AA503887	Hs.167011	Human sapiens cDNA: FLJ21362 fa, clone C	1.47	0.46	upregulate stage
	445394	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.2	0.07	upregulate stage
	445674	BE410347	Hs.13063	transcription factor CA150	3.8	0.15	upregulate stage
	445817	HA_009442	Hs.12340	isoleucine acyl-transferase 1	6.6	0.1	upregulate stage
	445871	A702901	Hs.145582	ESTs	2.3	0.33	upregulate stage
	446140	AA356170	Hs.26750	Human sapiens cDNA: FLJ21908 fa, clone H	2.15	0.18	upregulate stage
35	446563	AB021179	Hs.15259	HMBA-inducible	2.55	0.18	upregulate stage
	446611	AA339027	Hs.27179	ESTs	6.05	0.07	upregulate stage
	447088	AA421397	Hs.161321	ESTs	6.9	0.1	upregulate stage
	447290	A1476732	Hs.263912	ESTs	2.35	0.18	upregulate stage
	447379	A1564946	Hs.150794	ESTs	6.3	0.09	upregulate stage
40	447393	X53354	Hs.18425	translational inhibitor protein p14.5	7.25	0.08	upregulate stage
	447533	NA_004786	Hs.18702	thioredoxin-like, 32kD	1	0.24	upregulate stage
	447548	NE3388	Hs.7222	ESTs	8.6	0.07	upregulate stage
	447731	AA373527	Hs.19385	CGI-58 protein	7.3	0.08	upregulate stage
	447853	A1434204	Hs.164285	ESTs, Weakly similar to Alp1p [S. cerevisiae]	6.75	0.11	upregulate stage
45	447857	A4081218	Hs.35958	Human sapiens cDNA: FLJ14295 fa, clone NT	2.2	0.24	upregulate stage
	447965	AW292577	Hs.94445	ESTs	3.6	0.19	upregulate stage
	448072	A169306	Hs.24908	ESTs	5.8	0.11	upregulate stage
	448474	A792014	Hs.13809	ESTs	2.72	0.28	upregulate stage
	448513	AA344741	Hs.17173	Human sapiens cDNA: FLJ11648 fa, clone HE	4.9	0.12	upregulate stage
50	448601	RI1666	Hs.235690	ESTs	2.65	0.2	upregulate stage
	448625	AW970786	Hs.178470	Human sapiens cDNA: FLJ22662 fa, clone H	1.68	0.44	upregulate stage
	448875	AW473830	Hs.171442	ESTs	2.95	0.19	upregulate stage
	448970	A1971940	Hs.7548	ESTs	0.14	0.34	upregulate stage
	448920	AW080009	Hs.22690	ethylglyoxane phosphate synthase	8.6	0.08	upregulate stage
	449448	D60730	Hs.27471	ESTs	1	0.13	upregulate stage
55	449517	AW600106	Hs.23843	serine/threonine protein kinase MASK	6.4	0.11	upregulate stage
	449585	A1653321	Hs.17963	ESTs	0.1	0.16	upregulate stage
	449619	A165992	Hs.200447	ESTs	8.35	0.09	upregulate stage
	449685	BE00031	Hs.198699	eukaryotic translation initiation factor	6.65	0.11	upregulate stage
	449689	AF228421	Hs.201309	Human DNA sequence from clone: RP1-132P21	8.35	0.06	upregulate stage
60	449901	A1674072	Hs.273163	gbw1501.x1 Scanes_NFL_T_GBC_S1 Homo s	5.8	0.1	upregulate stage
	449904	AW001741	Hs.273163	hypothetical protein FLJ15706	8.7	0.09	upregulate stage
	450170	A165336	Hs.32775	ESTs	6.77	0.12	upregulate stage
	450193	A1916071	Hs.224623	ESTs	5.79	0.1	upregulate stage
	450336	AA046814	Hs.288928	Human sapiens cDNA: FLJ23298 fa, clone H	8.2	0.08	upregulate stage
65	450341	N160566	Hs.17230	hypothetical protein FLJ22387	4.2	0.16	upregulate stage
	450353	A1944661	Hs.103206	ESTs	4.71	0.15	upregulate stage
	450737	AW007152	Hs.203330	ESTs	2.14	0.25	upregulate stage
	450795	AW173371	Hs.60435	ESTs	6	0.1	upregulate stage
	450928	A744417	Hs.26999	gbr1-0h12.x1 NCL_C2AP_Ov23 Homo sapiens	1.75	0.18	upregulate stage
70	451134	AA318315	Hs.25999	hypothetical protein FLJ22105	4.3	0.1	upregulate stage
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	4.75	0.16	upregulate stage
	451553	AF151879	Hs.26706	CGI-121 protein	5.8	0.11	upregulate stage
	451618	AA115639	Hs.26794	KIA06345 protein	5.8	0.13	upregulate stage
	451658	Z43948	Hs.26794	hypothetical protein FLJ10320	6.73	0.25	upregulate stage
75	451790	AA027403	Hs.43927	ESTs, Weakly similar to P2CA_HUMAN PROTE	3.2	0.25	upregulate stage
	452001	A1827675	Hs.297735	Human sapiens cDNA: FLJ22094 fa, clone H	3.7	0.13	upregulate stage
	452039	A1822988	Hs.172510	ESTs	1	0.65	upregulate stage

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5	452045	AB018345	Hs.27657	KIA0802 protein	1.13	0.39	upregulate stage
	452092	BE245374	Hs.27842	hypothetical protein FLJ_1210	3.2	0.15	upregulate stage
	452218	AL037715	Hs.26336	Homo sapiens cDNA: cDNA: DNFZ688F0219 g	8.29	0.07	upregulate stage
	452381	H23323	Hs.25080	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.34	upregulate stage
	452420	BE564871	Hs.25463	centrin, EF-hand protein, 3 [CDC31 yeast	4.97	0.13	upregulate stage
	452714	AW770894	Hs.30340	hypothetical protein KIA1165	7.6	0.09	upregulate stage
	453078	AF053551	Hs.21584	metalin 2	5.3	0.09	upregulate stage
	453370	AW02023	Hs.18256	ESTs, Moderately similar to translation	3.78	0.13	upregulate stage
	453765	BE275901	Hs.35091	hypothetical protein FLJ_0775	3.96	0.11	upregulate stage
10	453972	AW137224	Hs.245869	ESTs	6	0.09	upregulate stage
	454044	AW02293	Hs.28923	gbc357h12 y1 Morkon Fetal Cochlea Homo	1.15	0.18	upregulate stage
	454286	AL_37554	Hs.49927	Hs.28923	7.06	0.1	upregulate stage
	454314	AW364844	Hs.251928	gbc-QV3-DT0044-22:1299-045-d3 DT0044 Homo	1	0.37	upregulate stage
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	2.7	0.13	upregulate stage
15	454775	BE160229	Hs.251928	gbcQV1-HT0413-16:0200-062-a12 HT0413 Homo	8.5	0.09	upregulate stage
	454790	AW02052	Hs.251928	gbcQV1-HT0413-16:0200-062-a12 HT0413 Homo	1.15	0.14	upregulate stage
	454792	AW02052	Hs.251928	hypothetical protein FLJ_12296 similar to	3.65	0.12	upregulate stage
	455170	AW080972	Hs.251928	gbcQV3-CT0387-18:0300-167-007 CT0387 Homo	5.7	0.07	upregulate stage
	455511	BE144762	Hs.288761	gbcQV3-CT0387-18:0300-167-007 CT0387 Homo	1	0.26	upregulate stage
20	456141	A0751357	Hs.288761	Homo sapiens cDNA: FLJ22595 s6, clone H	8.35	0.09	upregulate stage
	456268	AW076410	Hs.288761	Homo sapiens cDNA: FLJ21016 s6, clone C	4.95	0.14	upregulate stage
	456279	AW006783	Hs.6686	ESTs	7.25	0.1	upregulate stage
	457518	AA025350	Hs.143805	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.84	0.11	upregulate stage
	457570	AW175426	Hs.150226	ESTs	2.6	0.2	upregulate stage
	457882	AW050693	Hs.183617	ESTs	1	0.25	upregulate stage
25	458090	BE142728	Hs.121583	gbcMR0-4:10157-02:1255-004-038 HT0157 Homo	2.05	0.27	upregulate stage
	458340	AA07102	Hs.121583	Human glucose transporter pseudogene	2.25	0.18	upregulate stage
	458440	A085468	Hs.135254	ESTs, Weakly similar to thrombospondin I	2.35	0.13	upregulate stage
	458771	AW255151	Hs.163612	ESTs	1	0.19	upregulate stage
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TABLE 10

Play: Unique Eas project identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

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	408241	1048867_1	AW176546 AW178565 BE141057
	408268	104987_1	AL135247 AA053529 BE173373
	408277	10501_31	AW177555 AW177560 AW175066 AW178022
	408306	1050863_1	BE141991 AW178855 BE141990 BE141993 BE141994 BE062405 BE062404 AW178850
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	408566	11407_2	AW078859 AA078762 AW075788
	408700	115373_1	AA032845 TS0916 TS2890 AA077551
	408794	1154785_1	AW886981 BE183699 BE185540 AW803322 H10082
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	410266	1189983_1	AW613557 BE080235 BE080168
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	410534	1207247_1	AW906138 AW753008 R138118 243519
	410537	1207336_1	AW753108 AW862909 N39993 AW894327 AW903629
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	410973	1228236_1	AW812278 AW812286 AW812274
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	415114	1523035_1	D60468 D60950 D61218 H89936
	415178	1527354_1	D60503 D61739 H95691
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	415303	1533602_1	R11813A4 H4376 T59632
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	415364	1535008_1	F06771 H04895 Z42778
	415371	1535066_1	R15239 Z45189 F08036
	415382	1535146_1	Z4087 F07617 R34555
	415689	1539611_1	Z43030 F12170 H10881 T65261
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	415600	1540373_1	F12694 T74312 N80318 Z20039
	415626	1540758_1	Z43847 F13068 T75331
	415635	1540852_1	F13168 R21290 T77628
	415760	155216_1	AA167712 AW530024 AW364428 AW364445
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	415948	156264_1	AA202226 AB94175 AA17307
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	419807	188282_1	R77402 AA252452 AA250868 R07694
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	419996	185766_1	AA252891 AW298355 AA680333
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	448632	77303_1	DE614265
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	451365	887325_1	A751793
	451573	887533_1	N792030 AW386116 AW875145
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	452636	921149_1	DE063380 DE063346 A905097
	452650	92108_1	AA020735 DE340405 AL003023 AA323059
	452690	922216_1	DE077094 AW135953 AW353127 AW306209 AW306204 AW306205 AW306206 AW306211 AW306212 AW306207 AW306208 AW306210
50			A807487
	452738	929686_1	AL133800 A916209
	452825	930306_1	A912153 AW503197 AW303587
	453472	958371_1	AL337526 AL47951 AL037957
	453877	977149_1	AL079386 AL079390
55	453725	978780_1	V028543 AL119531
	453846	983043_1	AL175366 AL175790
	454044	995485_1	AW323933 AW322678
	454049	996858_1	AW322895 AW323054
	454059	1007650_1	AW062974 AW859625 DE081356
60	454314	110815_1	AW364844 AW364847 AW507534 AW507593 AW507569
	454327	1114267_1	DE365057 DE364124 DE364087 AW371617
	454331	1115276_1	AW372337 AW372043 AW377370 DE145850 AW377853 AW377954 AW378040
	454380	1152648_1	AW688722
	454471	1213795_1	AW502125 AW752853 AW337703 AW837710
	454524	1221840_1	AW867151 AW867152 AW869450
	454594	1223892_1	AW817636 AW817192 DE051442 DE061433 AW847506 AW809599 AW806996 AW806998 DE061436 DE061430 DE142460 DE142465 AW806954
			AW801195 AW806951 AW814082 AW806992 DE061659 AW807002 DE146559 AW806956 AW807000 AW845743 AW845747 AW847504
			DE142458 DE061431 DE061435 AW847607 DE146550 DE142470 AW814096 AW807012 DE061438 AW807011 AW806993 BE142465 DE142455
			BE142462 AW854330 AW854331 BE061434 DE061731 BE142464 AW847501 AW807001 DE142463 AW811800 DE061457 AW811802 DE061440
70			AW806997 AW806958 DE061145 DE061753
	454592	1226500_1	AW810112 AW810114 AW810032 AW809531 AW810183 AW810178
	454622	1226951_1	U70071 AW883715 AW810701
	454637	1227707_1	AW811513 AW811511 AW811510
	454648	1227876_1	AW811503 AW811507 AW811505
75	454687	1229077_1	AW811473 AW811517 AW815956 AW813298 AW813315 AW816100 AW813389 AW813338 AW813342 AW816108 AW813318 AW816105
	454692	1229118_1	AW816100 AW816153 AW814480 AW813392 AW816053 AW813399
			AW813350 AW816082 AW813476 AW813383

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75 TABLE 1C

Pisec: Unique number corresponding to an Eos probe set

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Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:485-495.

Strand: Indicates DNA strand from which exons were predicted.

NL position: Indicates nucleotide positions of predicted exons.

5

	Play	Ref	Strand	NL position
10	430471	9931670	Minus	106629-106750
	430485	9714773	Minus	61902-62137
	430528	6981624	Plus	472381-472528,474170-474277,475326-475542,476875-476900
	430577	7990401	Plus	101635-101881
	430606	8667666	Minus	96756-97556
15	430641	6117653	Plus	4786-4992
	430644	8117653	Plus	27682-27840
	430666	8116496	Plus	179621-16115,20297-20405
	430749	7331445	Minus	9166-9293
	430750	8119067	Plus	196991-199166,199316-199548
20	430751	7331445	Minus	35395-35533
	430761	6131639	Minus	114220-115164
	430762	8131616	Plus	7225-7995
	430773	8131629	Minus	44116-44236,48208-48321
	430843	9166605	Plus	5863-5970,7653-7784,6892-9023,9673-9607,10634-10789,15254-15440,23827-23958
25	430844	9166605	Plus	24746-24872,25035-25204
	430845	9166605	Plus	34426-34612
	430846	9166605	Plus	39319-39474
	430960	9757499	Minus	151830-152104,152645-152744
	430960	9931121	Plus	29235-29336,36393-36890
30	430987	9956187	Plus	119239-121542
	430988	9956187	Minus	199600-199757
	430937	7652890	Minus	68519-69905
	430977	8072510	Plus	73950-74364
	431002	6117281	Minus	77698-78050
35	431024	6117469	Plus	60851-60892
	431045	8117618	Plus	90044-90194,91111-91345
	431048	7232177	Plus	132436-132761
	431049	7232177	Plus	149157-150692
	431086	9959712	Plus	84561-84894
40	431093	6516137	Minus	22335-23166
	431101	6596122	Plus	77051-77226
	431192	9719502	Minus	69659-70101
	431197	9719503	Plus	176341-176452
	431203	9743367	Minus	172861-173066,173666-173826
45	431205	9743369	Plus	167573-167430,167536-168031
	431258	9796573	Minus	45482-45620
	431262	9796963	Plus	35662-35799
	431271	9797373	Minus	61252-61911
	431278	6564274	Minus	15915-16096
50	431279	9801082	Minus	13535-13669
	431342	9908992	Plus	3096-3242
	431365	9796180	Minus	119572-119972
	431395	7327642	Minus	11502-11771,46357-46489,58720-58916
	431420	7452669	Plus	141362-141502
55	431439	6245737	Minus	92993-94026
	431451	6634068	Minus	119926-121272
	431508	7554110	Minus	110778-110963
	431519	6646315	Plus	157515-157590
	431537	7963396	Minus	166796-167029,190607-190779,198218-198348
60	431561	8224660	Plus	10652-10838,19915-20018
	431566	8469090	Minus	96277-96420,96979-97100
	431604	7666593	Minus	119635-120186
	431619	8516761	Minus	141336-143576
	431689	9801805	Plus	25414-26310
65	431691	5882311	Plus	162333-162715
	431694	3504702	Minus	64059-64168
	431757	9799672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131666-131832,132451-132575,133580-134011
	431759	9929699	Plus	59611-60665
	431780	7249190	Minus	28297-28617,28920-29045,29135-29296,29411-29667,29705-29787,30024-30573
70	431866	6016106	Plus	73126-73623
	431905	8671966	Plus	153965-154441,156599-156819
	431994	4153889	Minus	429004-43124,43211-43336,44607-44763,45199-45281,46337-46732
	432001	5901618	Plus	68052-68223
	432075	8117407	Plus	121907-122035,122604-122921,124019-124161,124455-124610,125672-126076
75	432076	8117408	Plus	128316-128627
	432089	7249194	Plus	101610-101819
	432110	8131678	Minus	173889-174062

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	402176	7543687	Minus	10-750
	402220	5600312	Minus	26782-25532
	402245	7690231	Minus	88253-86417
	402265	6598624	Plus	22387-25723
5	402325	7635348	Minus	60059-50738,61677-61903
	402407	3962498	Minus	115812-116187
	402408	9796239	Minus	110025-110491
	402430	9796372	Minus	62362-62552
	402435	9796462	Plus	114553-115589
10	402472	9797116	Plus	53716-54470
	402474	7547175	Minus	63526-63268,65755-55920,57530-57757
	402480	9797375	Plus	59708-59599
	402490	9797548	Plus	145567-150529
	402522	5798493	Plus	20656-20731
15	402530	7630937	Minus	1524-2000
	402546	7637348	Plus	24573-25170
	402553	9863565	Plus	46592-46398,49654-49944
	402604	9600420	Plus	20363-20707
	402716	8989263	Minus	84065-84242
20	402727	9211324	Plus	54506-54777
	402812	6016110	Plus	25026-25061,25844-26520
	402820	6455863	Minus	8227-82443
	402846	9408716	Minus	5726-5850
	402889	9531133	Plus	85392-86498,90358-90571
25	402892	8089844	Minus	154394-154545
	402901	8894222	Minus	175426-176587
	402922	8215669	Minus	159356-15401,15689-15849,15961-20102
	402938	8963442	Plus	22365-22473
	402985	2596043	Minus	6552-6216
30	403005	6791501	Minus	19945-1763,20619-20463
	403020	6584114	Minus	56944-57023,57402-67898
	403029	7758593	Minus	44568-44765
	403047	3540153	Minus	66793-66568
35	403073	8954241	Plus	142564-143350
	403085	8954241	Plus	150035-163394,165420-165713
	403092	8954241	Plus	174720-175016,175104-175408,175508-175813
	403105	7331404	Plus	77162-77550,81338-81511
	403172	7464784	Minus	64007-54275
	403212	7630897	Minus	150371-152010
40	403214	7630945	Minus	70723-77027,75317-75484
	403277	8072697	Minus	27494-27542
	403331	8507536	Plus	189793-189566
	403344	8509726	Plus	70323-70390
	403382	8571772	Plus	94056-64280
45	403381	9438267	Minus	26009-26178
	403426	9719529	Minus	157156-158183
	403485	9955528	Plus	2888-3001,3195-3532,3555-4117
	403587	8101141	Plus	33349-35674
50	403588	8101227	Minus	197672-197944
	403590	8101229	Plus	405-1295
	403615	8507954	Plus	107671-107866
	403687	7387384	Plus	8708-9534
	403764	7225815	Minus	163890-164725
55	403776	7770611	Minus	1414-1513,1624-1756
	403822	6366510	Minus	142803-142922
	403851	7706872	Plus	22733-23007
	403900	7706660	Minus	56755-56545
	403954	7381715	Minus	1442-2224
	403903	7710671	Minus	161185-162897
60	403959	8224359	Minus	170353-174747
	404015	9835548	Minus	387651-1580222
	404059	3548785	Plus	104335-106788
	404113	5688571	Minus	13446-13046
	404148	9863703	Plus	78218-78418,79671-79709
	404152	5884757	Plus	11111-11241,45495-45716,47801-47910
65	404155	9886577	Plus	127319-127754
	404229	7159766	Plus	16807-16841
	404232	8218045	Minus	71900-71956
	404268	9711362	Plus	30236-33463
70	404274	9685189	Plus	104127-104318
	404288	2755644	Plus	3512-3591
	404290	2769644	Plus	36651-36813
	404336	9839028	Plus	157851-158129
	404403	7272157	Minus	72033-72239
75	404410	7529551	Plus	80430-81581
	404488	8113285	Minus	64635-84994
	404498	8151554	Plus	13252-13457

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	424507	8151803	Plus	146359-146739
	404516	8151967	Plus	1141531-14322
	424536	8247059	Minus	192746-192945
	424534	8938262	Minus	15310-15510
5	424636	8769776	Plus	5776-14381
	424653	8796999	Plus	164997-65230
	424676	8797204	Minus	56167-55342,58066-58189,58891-59048,60452-60028
	424684	8797033	Minus	110361-111150
	424685	8797137	Minus	153217-153316,154043-154124,155185-155353,161290-161420,163544-163669,166127-166207,167654-167734
10	424704	8802728	Minus	88841-89018
	424819	4678240	Plus	16223-16319,16427-16513,16738-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	424829	6624702	Minus	4913-5063,7310-7469,9472-9621,9951-10082
	424850	8673555	Plus	65862-65981
	424874	8656223	Minus	90666-96152
15	424881	5931510	Minus	35360-36608
	424894	6880447	Plus	102822-103127
	424939	6862697	Plus	175318-175476
	424977	3736341	Minus	43081-43229
20	425033	7107731	Minus	142356-142646
	425059	7659583	Plus	349-822
	425094	7658416	Plus	81207-81416
	425071	7708797	Minus	11115-11552
	425122	8078881	Minus	120222-121296
25	425167	5968316	Plus	43766-43981,46245-48427,54141-54317
	425170	9968524	Plus	37047-37198
	425177	7139395	Minus	118406-118663
	425186	7229763	Plus	161447-161581,162630-163067
	425268	7329310	Plus	129930-130076
30	425281	6139376	Minus	34202-34351,35194-35336,45412-45473,45473-45958,47296-47457,49549-49658,49790-49904,50231-40342,53683-53687,54111-54279
	425308	3638954	Plus	40778-41004,41353-41573
	425346	2514717	Minus	85652-85806
	425379	6513908	Minus	22332-22473,24333-24436
35	425390	6626264	Minus	54007-94177
	425411	3451305	Minus	17503-17778,18021-18250
	425463	7715830	Minus	123097-123260
	425494	8050262	Minus	70264-70518
	425520	5454943	Plus	69849-69891
	425526	9588586	Minus	132704-133277
40	425580	45112957	Plus	165232-169647
	425590	5926240	Plus	26962-27225
	425654	4855155	Minus	53624-53769
	425720	9797144	Plus	13409-13861
	425725	9838026	Minus	106147-106521
45	425736	9931101	Minus	22984-22976
	425738	9943998	Plus	44370-45410
	425806	5304520	Minus	6655-6883,8887-8889
	425838	5086575	Plus	2480-3717
	425863	7637810	Plus	45410-46600
50	425867	6758731	Minus	74553-75173
	425906	7705124	Minus	10835-11066
	425922	6758735	Plus	120021-120071
	425958	6247785	Plus	14853-15149
55	426017	8272561	Minus	46271-46874
	426036	6758919	Plus	17942-18163
	426081	9123661	Minus	38115-38651
	426137	9168422	Minus	30467-31058
	426187	7283992	Plus	8044-8877
60	426243	7417725	Plus	38869-35369
	426270	7534217	Plus	13136-13591
	426320	9211754	Minus	20170-20511
	426322	9212102	Minus	150230-150418
	426380	9256107	Minus	7513-7673
65	426387	9256126	Minus	58313-58469
	426387	9256263	Minus	127317-127454
	426399	9256288	Minus	63446-63554
	426434	9256951	Minus	17803-17931
	426457	9795551	Plus	182212-182958
70	426471	9795566	Plus	87353-87389
	426475	9797684	Plus	126117-126463,128052-128180
	426495	7711305	Plus	125036-125422
	426511	7711412	Plus	177277-177384
	426588	8189273	Minus	135629-136848

TABLE 2A: 485 GENES UP-REGULATED IN BLADDER CANCER

	Prkey:	ExAcon:	UnigeneID:	Unigene Title:	R1:
	Unique Ecd probe/seq identifier number	Exon/Accession number, Genbank accession number	Unigene number	Unigene gene title	Ratio of mRNA expression in bladder tumors compared to normal bladder
5					
10	Prkey	ExAcon	UnigeneID	Unigene Title	R1
	418818	AA228859	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	3.473
	418841	AT151157	Hs.101355	hypothetical protein MGC11352	2.779
	421066	AU076725	Hs.101408	branched chain aminoketolase 2, mlec	3.052
15	435136	R27259	Hs.10172	ESTs	4.717
	440424	NM_004515	Hs.10237	ATP-binding cassette, sub-family G (WHIT)	0.003
	421307	BE535576	Hs.103353	Homo sapiens mRNA; cDNA DKFZp43450425 (f	188.231
	421318	UE30173	Hs.103501	rhodopsin kinase	1.381
	421359	AK001589	Hs.103816	hypothetical protein FLJ10727	1.000
20	459462	AA481366	Hs.105167	ESTs	1.000
	430134	BE380145	Hs.105223	ESTs, Weakly similar to T33788 'hypotheti	1.000
	433227	AB043023	Hs.105808	hsh (Drosophila-like 1	1.000
	421742	AIW970004	Hs.107928	androgen induced protein	1.514
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comitin)	2.782
25	444342	NM_014358	Hs.10887	similar to lysosome-associated membrane	20.064
	451686	AA592446	Hs.110253	ESTs	0.033
	454417	A244459	Hs.110305	trivucleotide repeat containing 9	56.751
	458760	AI48631	Hs.111334	lentin, light polypeptide	2.512
	422119	AI277828	Hs.111862	KIAA0590 gene product	2.634
30	422170	AT781945	Hs.112452	anti-Müllerian hormone	0.055
	441877	AIW273032	Hs.113340	hypothetical protein FLJ23047	0.039
	459598	BE326257	Hs.114536	ESTs	0.002
	434288	AIW183075	Hs.118265	litrin3	11.401
	435347	AIW014873	Hs.119563	ESTs	0.003
35	453134	AI332211	Hs.119493	ESTs	262.962
	444781	NM_014430	Hs.11950	GPI-anchored metastasis-associated prote	5.336
	436154	AA764550	Hs.119868	ESTs	103.154
	438246	AIW453963	Hs.119931	ESTs	0.071
	436253	AB011188	Hs.120910	ESTs	25.129
40	433078	AIW015168	Hs.121675	Homo sapiens cDNA FLJ12231 fls, clone MA	274.769
	438181	AIW978608	Hs.122121	ESTs, Weakly similar to 130722 'hypotheti	0.024
	449399	AA760881	Hs.122408	ESTs	1.000
	437722	AIW252847	Hs.122872	ESTs, Weakly similar to J00333 'hypotheti	4.314
	457465	AIW01344	Hs.122938	DNA replication factor	0.264
45	408757	NM_001898	Hs.123114	cystatin SN	1.390
	439907	AA653978	Hs.124577	ESTs	0.010
	437181	AI308615	Hs.125343	ESTs, Weakly similar to KIAA0758 protei	0.344
	440304	BE159804	Hs.125386	ESTs	0.025
50	423248	AA380177	Hs.125845	thiostone-5-phosphate-3-epimerase	0.014
	441495	AIW254603	Hs.127039	ESTs	0.198
	435376	AIW770956	Hs.127280	ESTs	0.028
	427685	AT751124	Hs.127311	ESTs	3.244
	423419	AF010258	Hs.127428	tonno box A9	0.134
	445457	AF188793	Hs.12743	carbamate O-octanoyltransferase	7.255
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fls, clone HE	1.000
	441875	AI435973	Hs.128056	ESTs	0.013
	441940	AIW288115	Hs.128152	ESTs	6.075
	445537	A2445671	Hs.12844	EGF-like domain, multiple 6	0.137
	429963	W92820	Hs.128856	ESTs	162.590
60	445600	AF034803	Hs.12923	PTPRF interacting protein, binding prote	0.959
	437553	AA629578	Hs.130457	ESTs, Weakly similar to MAT5_HUMAN CHLOR	9.163
	459204	AIW194031	Hs.130215	ESTs	1.000
	439642	AI510896	Hs.132413	ESTs	1.000
	443113	AI040666	Hs.132508	ESTs	0.009
65	423853	AB011537	Hs.133456	shl (Drosophila) homolog 1	1.881
	420792	AA286321	Hs.13352	heparin binding factor SEC34	0.100
	427719	AI039122	Hs.134726	ESTs	0.667
	443861	AIW449462	Hs.134743	ESTs	5.100
70	447578	AA912347	Hs.135586	ESTs, Weakly similar to J05314 CDC72-like	1.881
	445550	AA24754	Hs.137305	ESTs	0.006
	454284	AIW287935	Hs.138453	ESTs, Moderately similar to ALU7_HUMAN A	0.003
	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	0.042
	424058	AF077374	Hs.139322	small proline-rich protein 3	1.347
75	453370	AI473523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.186
	424059	AF071202	Hs.139335	ATP-binding cassette, sub-family C (CFTR	47.949
	426900	AIW163564	Hs.142376	ESTs	0.404
	439337	AA448718	Hs.142525	ESTs	0.012

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	427961	AIW293155	Hs.143134	ESTs	0.073
	419888	AI243493	Hs.144049	ESTs	11.959
	413943	AIW294416	Hs.144887	Human sapiens cDNA FLJ12861 1s, clone NT	77.269
	445971	AI702261	Hs.145582	ESTs, Weakly similar to FCMB MOUSE FCBM	183.782
5	445911	AI985387	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.382
	424395	AA185082	Hs.145838	microhecto-associated protein 7	203.038
	424411	NM_005209	Hs.146548	crystallin, beta A2	1.868
	444517	AI503519	Hs.146585	ESTs	0.004
	445200	AI208665	Hs.147221	ESTs	0.307
10	422109	S73265	Hs.1473	gastin-releasing peptide	1.000
	445352	AI221087	Hs.147761	ESTs	0.015
	444444	AI149332	Hs.14855	ESTs	140.859
	444152	AI125594	Hs.148505	hypothetical protein IMGC2503	2.697
	448248	AI280014	Hs.148638	ESTs	0.016
15	439159	AB035898	Hs.150597	kinase-like protein 2	0.110
	428004	AA448563	Hs.151353	glutamate-cysteine ligase, catalytic sub	3.179
	458840	H03754	Hs.152213	siniglossa-type MMTV integrase alpha band	0.005
	458944	A2954155	Hs.152591	CDP-diacylglycerol synthase (phosphatidyl	1.111
	425205	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	257.949
20	448392	AI274139	Hs.155452	ESTs	0.779
	444948	AIY193025	Hs.155457	hypothetical protein FLJ22638	1.519
	448336	AC022553	Hs.157187	clonin (rho-interacting, serine/threonin	0.417
	447073	AIW204821	Hs.157728	ESTs	10.349
	422785	AIW429701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	1.839
25	448673	NM_018361	Hs.15971	LPAR for lysophosphatidic acid phosphat	1.591
	447475	AI380797	Hs.159932	ESTs	44.841
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	0.340
	418943	AA218372	Hs.163501	ESTs	0.023
	441143	AK027804	Hs.163590	ESTs	0.280
30	442917	AA309551	Hs.163725	ESTs	1.000
	416965	AW014345	Hs.161693	ESTs	0.055
	431639	AW020280	Hs.162025	ESTs	0.005
	448639	BE031925	Hs.16244	mitotic spindle coiled-coil related prot	0.005
	438617	AK023799	Hs.163242	ESTs	2.232
35	432441	AIW29425	Hs.163484	ESTs	2.335
	442577	AA292998	Hs.163930	ESTs	688.388
	435212	AIW300100	Hs.164195	ESTs	0.002
	426048	H05658	Hs.164502	ESTs	0.063
	442063	R53192	Hs.165382	ESTs	3.444
40	425235	L22015	Hs.16588	guanine nucleotide binding protein (G pr	0.157
	418678	NM_001327	Hs.167373	cancer/testis antigen	260.487
	448989	AK001899	Hs.16740	hypothetical protein FLJ11036	0.208
	458667	AW004058	Hs.168355	F-box 2	160.397
	447973	AI457197	Hs.170348	ESTs	0.018
45	458914	AI498957	Hs.170951	ESTs, Weakly similar to Z195_HUMAN ZINC	1.035
	446312	BE087853	Hs.171802	ESTs, Weakly similar to T08729 RING zinc	1.334
	426783	Z19384	Hs.172210	MUP1 protein	1.554
	423015	AIY934926	Hs.172215	Human sapiens clone TCCOIA0175 mRNA sequ	154.294
	429002	AI735283	Hs.172809	ESTs	0.007
50	429853	U32674	Hs.172777	baculoviral IAP repeat-containing 4	0.009
	429698	U07615	Hs.173204	amphiphysin (SH3-Mann syndrome with br	0.002
	407581	R84602	Hs.173508	PDE3C	0.086
	427239	BE223447	Hs.174070	ubiquitin carboxyl protein	15.708
	427269	X78520	Hs.174139	chloride channel 3	207.935
55	438577	W84774	Hs.17643	ESTs	82.333
	422675	AA919425	Hs.177744	ESTs	32.393
	427529	AI077143	Hs.178565	mitochondriome maintenance deficient (S	1.171
	427585	D31152	Hs.178729	collagen, type X, alpha 1 (Schmid mal'aph	1.000
	427747	AIW41425	Hs.180565	serine/threonine kinase 12	12.445
60	423813	AKW135678	Hs.180791	ESTs	0.013
	433806	AA454924	Hs.180806	ESTs	0.591
	427878	C05785	Hs.181022	Oca-27 protein	0.002
	440284	AA912032	Hs.181059	ESTs, Weakly similar to 2108276A setDNA-b	0.000
	427822	AK001594	Hs.181112	HSPC123 protein	0.009
65	427572	AA658870	Hs.181304	putative gene product	0.004
	428771	AF212848	Hs.182339	olef homologous factor	4.321
	428338	AA503115	Hs.183702	microsomemicroprotein, beta-	145.128
	428450	NM_014791	Hs.184339	KACAT175 gene product	0.370
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	0.032
70	432745	AB989815	Hs.184727	ESTs	0.338
	420557	AA980944	Hs.185579	Homo sapiens, clone IMAGE408143, mRNA	0.005
	431014	W67730	Hs.187573	ESTs	0.344
	428651	AF119478	Hs.188401	annexin A10	1.459
	416275	AA577330	Hs.188684	ESTs, Weakly similar to PC4259 ioninin	0.002
75	423487	AA551104	Hs.189048	ESTs, Moderately similar to ALUIC_HUMAN I	2.489
	431474	AI133990	Hs.190542	ESTs	0.044
	427742	AA411890	Hs.190889	ESTs	0.158

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5	428058	AJ821526	Hs.191602	ESTs	0.006
	431245	AA495933	Hs.191687	ESTs	0.006
	453204	R10799	Hs.191990	ESTs	1.754
	436008	AA526980	Hs.192371	down syndrome critical region protein DS	115.000
	447342	AI195268	Hs.193222	Homo sapiens, similar to 154374 cDNA 2010	0.162
10	454032	W31790	Hs.194263	ESTs, Weakly similar to 154374 gene NF2	60.163
	449121	AB15858	Hs.194980	ESTs	0.003
	478727	U73727	Hs.19716	protein tyrosine phosphatase, receptor I	305.974
	429401	ALJ43621	Hs.197484	ESTs, Weakly similar to J4C495 ring lig	0.002
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.011
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3)	9.390
	425257	AF168799	Hs.198365	2,3-bisphosphoglycerate mutase	178.436
	429276	AF055086	Hs.198612	G protein-coupled receptor 51	0.729
	449818	AIW54395	Hs.193965	ESTs	1.000
	429045	R11141	Hs.191685	hypothetical protein	7.339
20	443664	AB21085	Hs.199710	ESTs	0.001
	445847	AN204447	Hs.199720	organic anion transporter polypeptide-mr	1.000
	445551	AW010637	Hs.200760	ESTs	0.005
	428322	J05069	Hs.2012	transcobalamin I (vitamin B12 binding pr	381.474
	434111	AA632649	Hs.201372	ESTs	0.039
25	448045	AJ297435	Hs.20165	prostate stem cell antigen	2.337
	446555	AF059046	Hs.201847	ESTs	0.024
	450411	DB1157	Hs.202156	ESTs	0.004
	442282	AW451095	Hs.202390	ESTs	1.000
	427587	BE548244	Hs.202528	ESTs, Weakly similar to 178885 serine/th	228.705
30	429486	AF155027	Hs.203953	hypothetical protein FLJ10339	0.133
	426992	AF081038	Hs.20395	UDP-glucose-6-phosphate 1 family, polype	2.070
	426745	J03625	Hs.2057	uridine monophosphate synthetase (protal	0.528
	448275	BE514234	Hs.20830	kinesin-like 2	19.718
	440368	H69539	Hs.230905	EST	0.006
35	441795	BB1115	Hs.21137	A0024 protein	1.000
	451692	AB05416	Hs.213897	ESTs	0.012
	443307	AW071349	Hs.215937	ESTs	0.003
	415949	H10592	Hs.21691	ESTs	0.072
	444208	BE544855	Hs.220785	ESTs, Weakly similar to SFRA1_HUMAN SPLIC	213.962
40	425248	AW973399	Hs.22133	hypothetical protein FLJ20121	0.250
	427867	NM_005073	Hs.2217	solute carrier family 15 (oligopeptide 1	0.010
	453123	AB63718	Hs.221849	ESTs	0.596
	439569	AF1602106	Hs.222399	CEP1 protein	10.525
	429227	AA321548	Hs.2248	small inducible cytokine subfamily B (Cy	27.803
45	436965	AF269255	Hs.22604	lysosomal apyrase-like protein 1	127.564
	453883	AB38616	Hs.22620	cofactor required for Sp1 transcription	2.216
	431253	R03428	Hs.226351	ESTs	0.023
	439300	AW020692	Hs.227414	ESTs, Weakly similar to ALUS_HUMAN ALU S	0.103
	430394	X50165	Hs.227757	zinc finger protein 41	1.000
50	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	0.024
	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fls, clone K	1.635
	441382	BE514410	Hs.23044	RA251 (S. cerevisiae) homolog (E coli Ra	125.167
	452956	AW003578	Hs.231672	ESTs	1.000
	445009	AF98885	Hs.231926	ESTs	4.000
55	430499	AW993408	Hs.231991	ESTs	0.014
	446650	BE15105	Hs.23213	ESTs	285.090
	441638	AW015203	Hs.232327	ESTs	0.281
	463228	AW628325	Hs.232327	ESTs	1.000
	442167	H18740	Hs.23248	hypothetical protein from EUROIMAGE 2005	0.240
60	463321	AB94391	Hs.232621	ESTs	0.809
	445907	AL044222	Hs.23265	nucleoporin 159D	0.422
	430152	AB001325	Hs.234542	aquaporin 3	1.040
	439239	AW01540	Hs.235331	ESTs	0.598
	435087	AW975241	Hs.23567	ESTs	0.007
65	451276	AW284185	Hs.236533	ESTs, Highly similar to dJ74G19.2 (H.s	0.012
	447343	AA26541	Hs.236894	ESTs, Highly similar to S02282 alpha-2-m	1.280
	431011	AA400631	Hs.23783	ESTs	0.016
	433007	BE513442	Hs.239944	hypothetical protein FLJ10531	284.526
	444371	BE545274	Hs.239	toricoid box M1	3.891
70	424284	DB0423	Hs.239388	Human DNA sequence from clone RP1-304E14	0.265
	449722	BE280074	Hs.23960	cyclin B1	0.467
	430486	BE052109	Hs.241551	chloride channel, calcium activated, lam	13.419
	430168	AW998043	Hs.24265	DKFZP434I735 protein	1.192
	452282	AW135868	Hs.243369	ESTs	1.000
75	412651	N32590	Hs.24611	ESTs, Weakly similar to 154374 gene NF2	2.500
	456582	AW50321	Hs.246766	Homo sapiens cDNA FLJ12360 fls, clone MA	0.014
	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	0.233
	437678	U53683	Hs.248162	olfactory receptor, family 1, subfamily	1.000
	431320	AF378784	Hs.248235	caspases 14, apoptosis-related cysteine p	5.866
	431070	AF408184	Hs.249184	transcription factor T5 (SCF)	1.838
	431098	AW501485	Hs.249230	ribonuclease L (2'-5'-oligoadenylate	0.004

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5	454170	AW177225	Ha.250158	ESTs	0.243
	439223	AW238299	Ha.250518	UL16 binding protein 2	0.516
	439081	H49545	Ha.251391	claudin 16	0.090
	451347	AI133461	Ha.251654	Insulin-like growth factor 2 (somatomedin)	0.000
	450553	H43540	Ha.25222	fibronectin H1, large subunit	5.525
	450684	AA872605	Ha.25333	interleukin 1 receptor, type II	1.000
	413054	H24184	Ha.25413	TOLLIP protein	258.865
	450796	NM_001588	Ha.25482	seaxipodin	1.543
	409827	AW177310	Ha.254925	ESTs	0.008
10	444129	AW284292	Ha.25512	ESTs	0.002
	430637	BE160081	Ha.255290	S100 calcium-binding protein A11 (calgiz)	3.240
	436138	H53323	Ha.25717	Human sapiens cDNA: FLJ23454 It, clone H	0.879
	450993	AA305384	Ha.25740	EPD1 (S. cerevisiae)-like	259.1231
	453459	BE047032	Ha.257789	ESTs	2.133
15	456536	AW135986	Ha.257859	ESTs	98.755
	438424	AI812498	Ha.25895	hypothetical protein FLJ14595	1.852
	451161	AA211329	Ha.26006	hypothetical protein FLJ10559	0.012
	430534	AB80181	Ha.26066	cyclophilin	9.561
	435582	AL046988	Ha.26077	ESTs, Moderately similar to ALU7_HUMAN A	0.957
20	417964	R71449	Ha.26270	ESTs	0.004
	445703	AV554845	Ha.27	glycine dehydrogenase (decarboxylating);	1.124
	411845	BE15924	Ha.271650	viroplakin 1B	303.679
	453074	AA031613	Ha.271680	ESTs	0.004
	431890	X17033	Ha.271866	integrin, alpha 2 (CD45B, alpha 2 subunit)	1.528
25	435162	AA693386	Ha.272035	ESTs, Weakly similar to gonadotropin ind	0.013
	430791	AA465283	Ha.272098	ESTs, Weakly similar to ALU3_HUMAN AU S	5.578
	432136	AA157352	Ha.272630	vesicular proton pump, delta polypeptide	0.316
	451939	U80455	Ha.27311	single-minded (Drosophila) homolog 2	0.014
	451982	F13038	Ha.27373	Homo sapiens cDNA: DKFZ564O1763 (f	26.348
30	420331	AZ78995	Ha.27457	ESTs	53.228
	455512	BE040895	Ha.274448	ESTs	21.013
	452045	AB018345	Ha.27557	KIAA602 protein	129.013
	435557	AM52680	Ha.276904	ESTs	0.007
	458005	AM28631	Ha.27721	Wied-Hirschhorn syndrome candidate 1-like	0.531
35	430157	BE347008	Ha.278543	ESTs	95.144
	452012	AA307703	Ha.278786	klafsin family member 4A	0.405
	433001	AF217513	Ha.278905	clone H00310 PRO0310p1	1.721
	456883	AV558444	Ha.280776	tenkynase, TRF1-interacting ankyrin-rela	38.231
40	450020	AB58594	Ha.282210	ESTs	0.003
	436898	AF254260	Ha.283029	h/ah11	1.516
	430733	AW575920	Ha.283361	ESTs	1.000
	446024	AB040946	Ha.284227	KIAA1513 protein	9.424
	433957	AF113016	Ha.284302	PRO1821 protein	0.008
45	435915	AA280174	Ha.285681	Williams-Scott syndrome chromosome regi	0.030
	431558	X53629	Ha.2877	cadherin 3, type 1, P-cadherin (placenta	1.059
	414555	AA541725	Ha.288015	hypothetical protein MGC4171	273.013
	432057	X51730	Ha.2905	progesterone receptor	0.002
	452345	AA252279	Ha.291173	hypothetical protein FLJ20515	4.010
50	457733	AW574812	Ha.291571	ESTs	1.000
	441398	AA932398	Ha.292036	ESTs, Weakly similar to B34087 hypothei	1.000
	428182	BE386042	Ha.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	0.008
	452401	NAL_007115	Ha.293352	tumor necrosis factor, alpha-induced pro	0.000
	452385	AF102644	Ha.293707	ESTs	0.045
	417151	AA194055	Ha.293858	ESTs	6.593
55	424242	AA337475	Ha.293964	hypothetical protein MGC13102	1.555
	423875	BE535089	Ha.2952	S100 calcium-binding protein P	17.254
	422424	AI184431	Ha.295538	prostate differentiation factor	2.045
	432410	X58551	Ha.2982	Sp1 transcription factor	0.007
	426467	S78723	Ha.298823	5-hydroxytryptamine (serotonin) receptor	0.005
60	454054	AA358329	Ha.301619	Homo sapiens cDNA FLJ12535 It, clone HT	0.498
	452142	AG026947	Ha.301654	KIAA1024 protein	0.005
	445773	R76204	Ha.302893	ESTs	0.001
	438366	AA805780	Ha.303567	ESTs	1.000
	452724	R84810	Ha.304054	cyclin E2	1.000
65	428343	AB000785	Ha.307036	Homo sapiens. Similar to apelin 3, clone	0.494
	454546	H38075	Ha.309	arrestin 2, neural (K-arrestin)	0.022
	430694	AA810624	Ha.30935	ESTs, Weakly similar to H2BH_HUMAN HISTO	16.744
	432789	D26361	Ha.3104	KIAA0042 gene product	0.302
70	422655	AW204059	Ha.312715	ESTs, Weakly similar to unnamed protein	0.001
	453208	AB000532	Ha.314412	Hsc70 protein-like 1	13.252
	433051	Y12542	Ha.3165	lymphocyte antigen 6 complex, locus D	2.765
	427122	AW057736	Ha.323910	HER2 receptor tyrosine kinase (c-erb-b2,	553.782
	453216	AL137556	Ha.32405	Homo sapiens cDNA: cDNA DKFZ568G0321 (f	84.115
	423247	BE514387	Ha.333653	c-Myc target JPC1	79.355
75	429532	AW410714	Ha.334437	hypothetical protein MGC4248	337.474
	431448	AL137517	Ha.334473	hypothetical protein DKFZp564O1278	0.842
	411248	AA551538	Ha.334605	Homo sapiens cDNA FLJ14409 It, clone HE	402.500

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5	433958	AIW043909	Hs.334707	aminooxylase 1	191.179
	432842	AIW674053	Hs.334822	hypothetical protein MGC4485	313.402
	457282	AI521270	Hs.334882	hypothetical protein FLJ14251	21.744
	451359	H85334	Hs.335623	ESTs	0.038
10	404249	AI246590	Hs.337275	ESTs	0.432
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S95657 alpha	1.102
	447437	U07225	Hs.339	putative receptor P2Y, G-protein coupl	0.483
	447519	UK6288	Hs.339665	ESTs	1.022
15	434192	AIW387314	Hs.34371	ESTs	0.003
	453765	BE279601	Hs.35091	hypothetical protein FLJ10775	0.056
	441020	W19283	Hs.35962	ESTs	75.141
	453884	AA359825	Hs.36232	KIAA0186 gene product	0.138
20	453922	AF063305	Hs.36708	building uninhibited by benzimidazoles 1	0.008
	453945	NM_005171	Hs.36908	activating transcription factor 1	0.044
	447289	AIW247017	Hs.36978	melanoma antigen, family A, 3	0.002
	407626	US9156	Hs.37169	potassium inwardly-rectifying channel, s	0.009
25	428820	NT1320	Hs.38938	ESTs	1.000
	450227	AI864053	Hs.39972	ESTs, Weakly similar to 138588 reverse t	0.042
	407846	AA425022	Hs.40403	Cbly/COO-interacting transactivator, vit	1.810
	443133	AI033878	Hs.41379	ESTs	0.534
30	424534	H09477	Hs.41407	ESTs	0.013
	452934	AA581322	Hs.4213	hypothetical protein MGC15207	3.679
	434562	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.885
	422227	AK001925	Hs.44143	polyomino 1	0.070
35	423800	AL046533	Hs.44269	ESTs	10.435
	408522	AI641214	Hs.45320	Small proline-rich protein SPRK (human,	3.393
	452699	AC004770	Hs.4755	flap structure-specific endonuclease 1	386.256
	431009	BE149762	Hs.48958	gap junction protein, beta 5 (connexin 5)	0.222
40	426847	AL080593	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564H1662 (f	0.005
	453847	AB822040	Hs.49522	ESTs	175.510
	435854	AJ278120	Hs.4959	putative ankyrin-repeat containing prote	2.584
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	0.610
45	458506	AA703584	Hs.5105	hypothetical protein FLJ10659	0.008
	436461	AF135997	Hs.51199	HSP-C150 protein similar to ubiquitin-con	1.095
	405287	AL082213	Hs.52792	Homo sapiens mRNA; cDNA DKFZp56H1823 (f	16.910
	455047	AA454985	Hs.54073	cadherin-like protein VR20	0.612
50	439750	AL359553	Hs.57684	Homo sapiens mRNA full length insert cDN	5.508
	439452	AA916317	Hs.57687	B-cell CLL/lymphoma 116 zinc finger pro	1.000
	439462	W17045	Hs.58069	ESTs	0.116
	439606	W79123	Hs.58561	G protein-coupled receptor 87	0.095
55	433706	AW872527	Hs.59751	ESTs, Weakly similar to DAP1_HUMAN DEATH	0.055
	452240	AS91147	Hs.61232	ESTs	0.221
	452316	AA290484	Hs.61265	ESTs, Moderately similar to G785_HUMAN P	2.595
	452747	BE153855	Hs.61460	Ig superfamily receptor LMR8	3.577
60	424675	AF180477	Hs.61450	Ig superfamily receptor LMR8	7.587
	444783	AK001468	Hs.62180	anilin (Drosophila Scraps homolog), act	0.046
	428779	NM_003787	Hs.6414	nuclear protein 4	0.030
	429453	BE254974	Hs.65596	thyroid hormone receptor interactor 13	12.016
65	440126	AA975145	Hs.65194	ESTs	0.008
	451291	R38288	Hs.6702	ESTs	0.012
	429983	AW247529	Hs.6730	platelet-activating factor acetylhydrola	1.553
	440006	AK005517	Hs.6844	hypothetical protein FLJ20510	8.826
70	427044	AL035864	Hs.69517	cDNA for differentially expressed CC16 g	140.508
	418107	R41728	Hs.7284	ESTs	0.146
	453626	BE085238	Hs.75313	aceto-keto reductase family 1, member B1	0.649
	433675	AW971653	Hs.75719	ribonucleotide reductase M2 polypeptide	0.237
75	444418	AW403985	Hs.76394	hypothetical protein MGC2721	2.242
	414430	AI345201	Hs.75118	ubiquitin carboxyl-terminal esterase L1	0.202
	414582	AL021154	Hs.75894	inhibitor of DNA binding 3, dominant neg	2.318
	414907	AT75816	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	246.564
80	414507	X90725	Hs.77597	zoia (Drosophila-like kinase	1.000
	451575	AA767622	Hs.78893	KIAA0244 protein	4.552
	403303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.228
	416496	US3552	Hs.79351	potassium channel, subfamily K, member 1	0.246
85	458921	AB522088	Hs.79375	holocarboxylase synthetase (beta)-prp	7.249
	489235	AA188827	Hs.7988	ESTs, Weakly similar to 138022 hypothetical	0.792
	440371	BE268550	Hs.80449	Homo sapiens, clone IMAGE3035294, mRNA,	350.782
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE3035294, mRNA,	60.550
90	417033	AL033170	Hs.80758	benzine homocysteine methyltransferase	9.986
	427594	W25945	Hs.81373	hypothetical protein FLJ110803	402.705
	417312	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (10.805
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.051
95	428839	AT67755	Hs.82302	Homo sapiens cDNA FLJ14814 ts, clone NT	0.225
	438315	R55145	Hs.82419	ESTs	26.260
	417900	BE260127	Hs.82905	CDCC20 (cell division cycle 20, S. cerevi	221.050
	417933	X02308	Hs.82962	thymidylate synthetase	2.956
100	418057	AT127958	Hs.83393	cystathionase	2.956

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5	438086	AA335519	Hs.83523	nuclear receptor subfamily 1, group 1, m	1.000
	418205	L21715	Hs.83760	lipocalin 1, skeletal, fast	0.159
	411385	M34455	Hs.840	iodoacetamide-lysozyme 2,3 deacetylase	0.490
	415322	AA284166	Hs.94113	cyclin-dependent kinase inhibitor 3 (CDK	3.527
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.077
10	458027	L45054	Hs.85195	myeloid leukemia factor 1	0.008
	418543	NM_005329	Hs.85962	hyaluronan synthase	1.813
	418583	AA450439	Hs.86211	hyaluronidase	125.769
	441801	AW242735	Hs.86366	ESTs	55.025
	414792	BE314949	Hs.87128	hypothelial protein FLJ23309	8.139
15	407246	S70348	Hs.87149	integrin, beta 3 (platelet glycoprotein	0.020
	433417	AA587773	Hs.88859	Homo sapiens, Similar to RIKEN cDNA 5830	313.141
	445080	AA330611	Hs.88808	ESTs	1.000
	453450	AW787627	Hs.89474	ADP-ribosylation factor 6	137.718
	419227	BE537383	Hs.89738	cholinergic receptor, nicotinic, beta po	0.005
20	401484	AF039241	Hs.90028	histone deacetylase 5	6.848
	443162	T49951	Hs.90709	DMP2P345032 protein	14.027
	431024	AA713666	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.507
	419559	Y07628	Hs.91096	ring finger protein	0.025
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	684.577
25	443428	AF090160	Hs.93229	chromosome 20 open reading frame 1	0.383
	424467	A294939	Hs.94292	hypothelial protein FLJ23311	175.567
	410348	AW152653	Hs.95469	ESTs	0.011
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (fg),	428.231
	421478	AB83243	Hs.97258	ESTs, Moderately similar to S29539 ribos	0.005
30	443787	BE552135	Hs.97395	proteasome (prosome, macrophage) 26S sub	1.168
	428902	A128334	Hs.97408	ESTs	37.467
	444874	A218495	Hs.97515	BRCA1-interacting protein 1; BRCA1-assoc	0.067
	427356	AW023462	Hs.97849	ESTs	1.000
	430000	AW205931	Hs.99598	hypothelial protein MGC5338	0.012
35	419445	AA408023	Hs.99007	ESTs, Weakly similar to unnamed protein	0.242
	420783	AB558338	Hs.99923	lectin, galactoside-binding, soluble, 7	19.785
	421934	AA300625		gbcEST13478 Testis tumor Homo sapiens cD	103.769
	431322	AW970522		gbcEST32704 MAGE, resequences, MAGEK Homo	0.268
	423400	AA334400		gbcEST33916 Embryo, 5 week Homo sapiens	0.011
40	433108	AB002445		gbcHomo sapiens mRNA from chromosome 5q2	0.023
	468829	A557388		gbcPTT2_1_s_G03.r1 tumor2 Homo sapiens cDN	1.000
	459189	AB05517		gbcRC-6T051-210169-105 BT051 Homo sapien	0.773
	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	468.462
	440012	AA591672		gbcRC-20065.c1 Scores, testis, JMIT Homo sap	0.002
45	412799	A267505		gbcgby1803.x1 Stanley Frontal SS pool 1	0.010
	412954	BE019688		gbcbb28g08.x1 NIH_MGC_5 Homo sapiens cDN	0.003
	405992	S82472		gbcbeta-polyDNA polymerase beta (lcnou a	0.005
	414589	C15195		gbc151955 Oocyte human acetyl poly mRNA	0.023
	413158	BE088098		gbcCM1-6T0369-061299-050-c09 BT0369 Homo	0.007
50	453823	AL137957		gbcDKFZp76102316_r1 781 (synonym: hamy2)	0.094
	453845	AL157586		gbcDKFZp76102316_r1 781 (synonym: hamy2)	0.004
	407055	X59211		gbc1-synopsis DNA for endogenous syovir	0.037
	415204	T27434		gbcbb2294 Human pancreatic islet1 Homo s	76.500
	434572	AF147340		gbcHomo sapiens full length insert cDNA	0.030
55	439990	AF005890		gbcHomo sapiens full length insert cDNA	1.000
	439700	AL106688		gbcHomo sapiens mRNA full length insert	0.255
	413391	Z43712		gbcHSC-1A121 normalized infant brain cDN	0.009
	425974	M57293		gbcHuman parathyroid hormone-related pep	0.004
	455797	BE091833		gbcIL2-BT0731-260400-076-F04 BT0731 Homo	2.816
60	455807	BE141140		gbcHNR6-HT0075-321299-059-c05 HT0075 Homo	0.413
	432189	AA627941		gbcgms3005.x1 NCL CGAP_Pr3 Homo sapiens	0.015
	443309	AB21874		gbcms5010.x5 NCL CGAP_Pr3 Homo sapiens	0.007
	437240	AA747537		gbcms505.s1 NCL CGAP_GC81 Homo sapiens	0.005
	455189	AB884178		gbcPM6-SN0014-250400-002-b08 SN0014 Homo	0.059
65	444163	AL126068		gbcgms507.x1 Scars, placenta, B6Hwiesc,	394.262
	455170	AB989372		gbcQV6-CT0367-180300-167-c04 CT0367 Homo	0.757
	454789	BE165314		gbcQV6-1T0367-150200-114-c02 HT0367 Homo	1.000
	433005	AB939074		gbcQV1-0T0065-010200-057-c12 DT0069 Homo	0.013
	455380	BE180188		gbcQV1-HT0143-010200-059-c05 HT0143 Homo	0.249
70	455650	BE064685		gbcRC1-BT0313-301250-012-c05 BT0313 Homo	1.000
	436383	BE065178		gbcRC1-BT0314-020200-012-b01 BT0314 Homo	1.000
	413100	BE065208		gbcRC1-0T0314-010300-015-b05 BT0314 Homo	271.372
	428436	BE080180		gbcRC4-0T0625-120200-011-b10 BT0625 Homo	0.002
	455321	BE144985		gbcRC6-HT0167-201099-011-c04 HT0167 Homo	0.011
75	424414	AY758375		gbc134507.x1 NCL CGAP_Ov23 Homo sapiens	293.654
	414221	AY450979		gbcUH-513-3la-a-12-04U.s1 NCL CGAP_Su	0.807
	409488	AY462825		gbcUH-HF-6K0-ax4-038-0-UL.r1 NIH_MGC_35	0.965
	427938	AY55087		gbcms5032.x1 NCL CGAP_NJ412 Homo sapien	2.852
	451385	AA917655		gbcms5001.r1 Scores refseq NZ04HR Homo	7.341
	445025	AA007162		gbcz84805.r1 Scores refseq NZ04HR Homo	0.004
	413316	W61931		gbcz847c01.r1 Scores_fetal_liver_spleen_	0.004

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	401016	0.342
	401335	0.256
	401555	1.000
5	401780	301.372
	401781	247.141
	401961	1.722
	402229	5.180
	402265	0.917
10	402424	551.141
	402777	153.231
	402778	0.006
	402837	0.367
	402948	154.103
	402952	17.038
15	403142	0.195
	403267	12.744
	403537	0.304
	403557	0.032
	404136	0.006
20	404249	0.065
	404675	1.105
	404917	69.590
	404983	1.000
	405236	1.000
25	405364	294.141
	405531	1.747
	405601	145.551
	405621	0.224
	405932	1.986
30	406117	0.353
	406354	1.000
	406546	0.002
	406599	0.010
35	459702	0.449

TABLE 2B

Play	CAT number	Unique Eco protease identifier number
Accession	Gene cluster number	Genbank accession numbers
40		
45		
50		
55		
60		
65		
70		
75		

Play	CAT Number	Accession
40	409466	1134791_1
	412799	132817_1
	412964	1328276_1
	413100	1348119_1
	413158	1351251_1
	413316	1350169_1
	413671	1352504_1
	414221	142695_1
50	414989	1510393_1
	415204	1529407_1
	421834	203338_1
	424040	204569_1
	428436	291472_1
60	431322	331543_1
	432188	342815_1
	433005	357346_1
	433108	35698_1
	434414	36595_1
65	434572	39011_1
	436363	14666_1
	437240	435139_1
	437938	44573_2
70		
75		

TABLE 2C

	Play	Ref	Struc	Nu_position
35	401016	8117441	Plus	126234-126356, 128050-128236
	401335	9684881	Plus	167366-163652
	401555	8092864	Minus	162526-162657
	401760	9229899	Plus	83126-83260, 86320-86540, 94719-95287
	401781	7248190	Minus	83215-83436, 83431-83956, 83740-83901, 84237-94393, 64955-66037, 66290-6814
40	402961	4581193	Minus	124054-124209
	402999	7690131	Plus	38175-38354, 42133-42266
	402905	7302728	Plus	40052-41362
	402124	5795344	Minus	64925-65073
	402777	9588235	Plus	126786-126948
45	402837	9399121	Minus	126560-126702
	402846	9398489	Minus	2013-2106, 9570-9736, 11136-11309, 19429-19717, 21210-21455, 23368-23562, 24342-24527, 29132-29320
	402952	9406724	Minus	143456-143626, 143806-143936
	403142	9444521	Plus	119452-119619
	403297	8090639	Minus	89286-90131
50	403637	8671636	Minus	16684-17264
	403657	8640996	Minus	142647-142771, 145631-145782
	404136	9061900	Minus	156223-156370
	404249	8555533	Plus	42638-46428
	404875	8601324	Plus	64270-64603
55	404917	7341681	Plus	95688-96732, 97722-97831
	404983	4422779	Minus	49330-49366
	405238	7249119	Minus	51178-51374, 52000-52173
	406364	2281075	Minus	51728-51836
	406531	9665194	Plus	48326-48431, 49136-49262
60	406601	5815482	Plus	35602-35803
	406621	6202911	Plus	147835-147835, 149222-149299
	406932	7767812	Minus	59362-59807
	406117	9142932	Minus	123526-123713
	406354	9226409	Minus	54304-54684
65	406546	7711514	Minus	2095-2377
	406599	8248616	Plus	26138-26792
			Plus	10933-11089

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Table 3A: Preferred liverspecific targets for bladder cancer

Key: Unique Eos probe/est identifier number
 ExAccess: L177660
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of bladder tumor Als divided by the 90th percentile of normal bladder sample Als
 R2: 90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als

Key	ExAccess	UnigeneID	Unigene Title	R1	R2
421948	L24283	Hs.334309	keratin 5A	14.20	1.20
439925	AW014675	Hs.137007	EST5	11.21	21.34
413324	V00571	Hs.75294	corticotropin-releasing hormone	9.15	45.75
421110	AJ267017	Hs.1355	cathespine E	5.07	45.35
417308	H80720	Hs.81892	KIAA101 gene product	8.50	1.99
431211	M85949	Hs.323733	gap junction protein, beta 2, 29kD (conn	8.35	1.28
418405	X73501	Hs.84905	cyclosterin 22	8.10	40.50
446619	AU075643	Hs.213	secreted phosphoprotein 1 (osteopontin,	7.98	1.38
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67	2.12
408243	Y00787	Hs.524	interleukin 8	7.58	4.85
417715	AW969897	Hs.38306	EST5	7.45	4.70
417720	AA205825	Hs.208067	EST5	7.34	9.18
423673	BE003054	Hs.1595	matrix metalloproteinase 12 (macrophage	7.30	28.07
418007	M13659	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12	35.60
413763	L177660	Hs.75517	keratin, beta 3 (p63a) (125kD), keratin	5.98	4.96
441633	AW958444	Hs.112242	normal mucosa of esophagus specific 1	6.42	0.89
422168	AA568694	Hs.112408	S100 calcium-binding protein A7 (psorias	5.08	3.49
407242	M18728	Hs.118728	gli3 human non-specific cross-reacting anti	5.96	0.96
405033			C1028552-gf644327hg304-799fRMO5_RABIT	5.84	18.22
442330	BE513348	Hs.211579	melanoma cell adhesion molecule	5.62	2.28
406865	M18728	Hs.118728	gli3 human non-specific cross-reacting anti	5.60	0.89
420159	AJ572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fs, clone C	5.77	28.85
416611	AJ722617	Hs.182362	EST5	5.65	29.25
426528	NM_001110	Hs.72628	alpha disintegrin and metalloproteinase doma	5.60	6.61
424008	R07240	Hs.137555	putative chemokine receptor: GTP-binding	5.59	2.33
426651	AF196478	Hs.198401	annexin A10	5.56	27.75
400843			NM_003108-Homo sapiens sorvile-related	5.51	4.92
402230			Target: Exon	5.38	21.44
467247	BE153865	Hs.61460	ly superfamily receptor LMR	5.33	2.80
416085	BE287931	Hs.78996	proliferating cell nuclear antigen	5.17	1.98
428450	NM_014791	Hs.194339	KAA0175 gene product	4.90	2.83
418322	AA284166	Hs.61113	cyclin-dependent kinase inhibitor 3 (CDK	4.77	2.35
412610	X30308	Hs.74126	allyl acid binding protein 6, liver (gas	4.77	3.71
418653	AQ001100	Hs.41590	desmoplakin 3	4.74	1.48
414683	S78296	Hs.76888	hypothetical protein MG212702	4.74	2.92
424242	BE093589	Hs.38178	hypothetical protein FLJ23465	4.68	1.61
424634	AQ001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT	4.65	11.53
431958	X50323	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.83	2.06
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55	3.35
401780			NM_005567-Homo sapiens keratin 16 (foca	4.49	1.62
424308	AW975551	Hs.154443	chromozome maintenance keratin (S-	4.43	2.36
401939			C1200348P-gf63301E16tg3f6A466477.1(A	4.40	12.94
417933	X02308	Hs.82952	thymidylate synthetase	4.35	2.29
418113	A272141	Hs.83484	SRV (sex determining region Y)-box 4	4.32	2.82
412140	AA219691	Hs.73525	RASGE interacting 1,heskin-like (rakubius	4.24	8.15
401781			Target: Exon	4.15	1.91
425234	AW152225	Hs.105909	EST5, Weakly similar to 180222 hypothet	4.14	7.39
432842	AW674093	Hs.334822	hypothetical protein MGCA485	4.12	2.51
408390	AF123050	Hs.44532	duoxin	4.11	3.28
449722	BE280074	Hs.23860	cylin D1	4.09	3.72
420344	BE463721	Hs.87101	putative G protein-coupled receptor	4.07	2.50
422809	AQ001379	Hs.121028	hypothetical protein FLJ10549	4.00	7.14
404977			insulin-like growth factor 2 (somatomedin	3.89	5.17
402409	AF153341		Homo sapiens winged helix/forkhead trans	3.88	7.29
429119	D08238	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	1.61
444371	BE540274	Hs.239	forkhead box M1	3.87	2.75
443171	BE281128	Hs.9030	TQNDU	3.83	9.48
441382	BE144410	Hs.23044	RALG1 (G, orexin-like) homolog (E. coli Re	3.82	2.98
435983	AW975529	Hs.8793	platelet-activating factor acetylcholin	3.77	3.83
401137	T97307		glyco-5S.05.s1 Scans fetal liver spleen	3.73	4.91
428088	AF038007	Hs.166195	ATPase, Class I, type BB, member 1	3.68	7.08
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.68	2.29
414781	AJ077228	Hs.72256	enhancer of zeste (Drosophila) homolog 2	3.67	3.68
413953	AJ035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67	1.18
421508	NM_004833	Hs.105115	aberrant in melanoma 2	3.67	3.05
443162	T49951	Hs.9029	DNAZP4363032 protein	3.66	3.21

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5	419478	U38945	Ha.1174	cyclin-dependent kinase inhibitor 2A (mo	3.66	3.57
	417771	AA604598	Ha.22547	retinoleic acid receptor responder (lazarol	3.62	2.73
	441495	AW294903	Ha.127039	ESTs	3.60	2.71
	422262	AF519225	Ha.11434369	spkspk protein L	3.57	3.92
	417079	U36590	Ha.81134	telodectin 1 receptor antagonist	3.55	0.80
10	417275	X63578	Ha.295449	parvalbumin	3.54	4.60
	440006	AKC00517	Ha.6844	hyposulfite protein FLJ20610	3.52	2.69
	416203	X64942	Ha.63758	CDC28 protein kinase 2	3.50	3.61
	422889	XJ7820	Ha.2258	matrix metalloproteinase 10 (stromelysin	3.50	17.59
	404875			NM_022819*Homo sapiens phospholipase A2	3.46	3.24
15	420005	AW271108	Ha.133294	ESTs	3.40	2.22
	407957	NM_001898	Ha.123114	cystatin SN	3.39	2.93
	427719	AJ051122	Ha.134726	ESTs	3.31	2.51
	406950	M05940	Ha.205229	cardiac embryonic antigen-related cell ad	3.28	0.42
	422283	AW41307	Ha.114311	CDC45 (cell division cycle 45, Sorensen	3.28	2.62
20	406081			Target Exon	3.25	13.54
	425514	BE516533	Ha.170195	bone morphogenetic protein 7 (osteogenic	3.25	2.45
	421009	BE145782	Ha.49596	gap junction protein, beta 6 (connexin 3	3.23	2.88
	429983	W92620	Ha.260855	ESTs	3.20	2.84
	422168	L1C343	Ha.112241	protease inhibitor 3, skin-derived (SKAL	3.18	1.54
30	426451	AJ981655	Ha.165946	GA1E-binding protein 3 (T-cell receptor	3.17	5.44
	411945	AL033527	Ha.92137	myc avian myxovirus surface viral onco	3.13	15.65
	415752	BE214524	Ha.78776	putative transmembrane protein	3.11	2.46
	408833	AW963372	Ha.45677	PRO2000 protein	3.11	3.30
	409556	AW103254	Ha.727	inhibin, beta A (activin A, activin AB a	3.09	1.52
35	412420	ALC33558	Ha.73863	bone morphogenetic protein 2	3.08	2.22
	422297	A1127076	Ha.265201	hyposulfite protein DKFZ564C1278	3.05	12.49
	437921	A249468	Ha.124434	ESTs	3.01	3.70
	421461	AA291377	Ha.80831	ESTs	2.99	14.95
	426682	AV980308	Ha.2036	UDP glycosyltransferase 1 family, polype	2.97	2.10
40	402229			Target Exon	2.97	3.37
	429345	R11141	Ha.199995	hyposulfite protein	2.96	2.61
	435904	AF261555	Ha.8910	1,2-alpha-mannosidase IC	2.93	2.13
	423961	C13656	Ha.130346	perlecan (DSF-2a)	2.93	1.44
	423923	AF597621	Ha.733231	differentially expressed in hematopoietic	2.92	0.95
45	436608	AA626980		down syndrome critical region protein DS	2.92	4.85
	447343	AA256841	Ha.258994	ESTs, highly similar to S02922 alpha-2-m	2.88	2.93
	439223	AW232899	Ha.260618	UL18 binding protein 2	2.88	2.15
	421747			Homo sapiens keratin 17 (KRT17)	2.88	3.44
	421002	AW248506	Ha.279727	ESTs; homologous to PED-3 (Ciona savignyi)	2.85	14.30
50	444444	A1149332	Ha.14855	ESTs	2.85	2.68
	421100	AW351839	Ha.124660	Homo sapiens cDNA: FLJ21753 fs, clone C	2.84	2.46
	421070	AW408154	Ha.249184	transcription factor 19 (TCF1)	2.78	2.26
	417889	BE250954	Ha.65045	midline (neutrite growth-promoting factor	2.77	2.34
	442994	A1029718	Ha.16594	ESTs	2.75	2.82
55	444581	BE387235	Ha.282713	ESTs, weakly similar to S64054 hypophelli	2.74	2.44
	434487	AF143887	Ha.337588	ESTs, moderately similar to S65657 alpha	2.72	3.27
	417065	AL638170	Ha.85736	betaine-homocysteine methyltransferase	2.69	2.70
	404440			NM_021048*Homo sapiens melanoma antigen,	2.69	13.45
	403844			NM_003105*Homo sapiens scrofin-related	2.69	13.45
60	428322	J05038	Ha.2012	transcobalamin II (vitamin B12 binding pr	2.69	1.36
	421448	AL137517	Ha.205201	hyposulfite protein DKFZ564C1278	2.69	12.68
	423381			ENSPP000C21844*Escherichia virus integr	2.68	13.40
	411248	AA551538	Ha.334605	Homo sapiens cDNA FLJ14408 fs, clone HE	2.68	2.43
	425206	NM_002153	Ha.155109	hydroxytolerol (17-beta) dehydrogenase 2	2.67	2.68
65	435959	ACC04770	Ha.4749	tap structure-specific endonuclease 1	2.67	1.79
	423551	NM_020982		zinc oxide hemolysin (Drosophila) hemole	2.65	0.73
	413281	AA651271	Ha.222024	transcription factor BMAL2	2.65	2.23
	446082	A1274139	Ha.156422	ESTs	2.65	2.65
	422424	A1185431	Ha.239638	prostate differentiation factor	2.64	2.68
70	407829	AA045144	Ha.161565	ESTs	2.64	1.08
	423441	AWP20425	Ha.163494	ESTs	2.64	6.14
	417312	AW988411	Ha.250811	leukemia-associated phosphoprotein p18 (2.64	1.31
	430157	BE348705	Ha.278543	ESTs	2.63	2.68
	435481	ACC37657	Ha.1919	HSPCH159 protein similar to ubiquitin-con	2.61	1.93
75	416565	Z38030	Ha.87268	anexin A8	2.60	1.62
	430485	BE052109	Ha.241551	chloride channel, calcium activated, lam	2.59	2.87
	425275	AF056085	Ha.198812	G protein-coupled receptor 51	2.57	3.09
	439738	BE449502	Ha.9198	serpin domain, immunoglobulin domain (Ig)	2.57	2.49
	406362	W74001	Ha.76384	serpin (for cysteine) proteinase inhibitor	2.56	1.43
80	414812	X27755	Ha.77367	merckine induced by gamma interferon	2.54	3.10
	451668	Z43948	Ha.206444	cartilage acidic protein 1	2.51	3.60
	421379	Y15221	Ha.103982	small inducible cytokine subfamily B (Cy	2.50	2.91
	414416	AW409895	Ha.76084	hyposulfite protein M5C2721	2.48	1.78
	429512	AF062646	Ha.262687	pituitary tumor-transforming 1	2.49	1.80
85	416558	UC0272	Ha.79432	filorilin 2 (congenital contractural ara	2.49	3.46
	437553	A1829935	Ha.130497	ESTs, weakly similar to MATS_HUMAN CHLOR	2.48	2.36

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5	418941	AA452970	Hs.239527	ElB-55kDa-associated protein 5	2.06	2.33
	414807	A1739616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.44	2.49
	450983	AA306384	Hs.26740	ER01 (5, cerevical) like	2.43	1.42
	47788	BE514982	Hs.8991	S100 calcium-binding protein A2	2.41	2.26
	449019	AB09095	Hs.57778	ESTs, Weakly similar to T23241 hypophyl	2.40	1.90
10	417386	BE165289	Hs.1076	small proline-rich protein 1B (cornutin)	2.40	0.49
	420370	Y13645	Hs.97234	urogastrin 2	2.39	3.81
	408000	L11990	Hs.19869	bullock porphyrinoid antigen 1 (23C24/ND)	2.38	1.45
	40389			HMA_003127-Homo sapiens sialin protease	2.36	4.20
	435563	AF210317	Hs.56497	solute carrier family 2 (facilitated glu	2.31	4.05
15	424217	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE-447	2.31	1.17
	432446	AW450963	Hs.119991	ESTs	2.30	11.50
	433078	AW015188	Hs.121575	Homo sapiens cDNA FL112231 fis, clone MA	2.29	2.40
	424012	AW388372	Hs.375955	tumor protein 53 kDa with strong homolo	2.29	1.89
	411263	CE297802	Hs.65360	kinesin-like 6 (mitotic centrosome-assoc	2.28	2.14
20	432829	WB0377	Hs.57772	ESTs	2.28	4.85
	415025	AW207091	Hs.72307	ESTs	2.28	11.40
	436293	AB01188	hs.120910	ESTs	2.27	3.80
	415989	AI267700		ESTs	2.27	11.35
	418067	AI127858	Hs.63393	cystatin E/M	2.26	1.54
25	436291	CE369452	Hs.344337	protein regulator of cytokinesis 1	2.25	2.45
	422278	AF072873	Hs.114218	fizzled (Drosophila) homolog 5	2.25	1.55
	428473	Y00272	Hs.334582	cell division cycle 2, G1 to S and G2 to	2.22	11.10
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.21	1.32
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G91763 atrophin-	2.21	1.52
30	405932			C15006.035-g8339612g8339619s.1 (AF0	2.20	1.55
	418741	NM_007019	Hs.93002	soluble carrier protein L2-c	2.19	1.99
	423271	W47225	Hs.126256	interferon-1, beta	2.19	2.01
	402305			C19000735-g814509027ef8[NP_003414.1] z	2.19	2.54
	421054	A1264342	Hs.101382	tumor necrosis factor, alpha-induced pro	2.19	2.15
35	427747	AW411425	Hs.180565	serine/threonine kinase 12	2.18	1.80
	437181	A1306615	Hs.126343	ESTs, Weakly similar to KIAA0758 protein	2.17	10.85
	431890	X17033	Hs.271988	integrin, alpha 2 (CD49, alpha 2 subunit	2.17	2.14
	434347	U26536	Hs.3280	cathepsin 6, apoptosis-related cysteine pr	2.16	1.37
	427581	R48402	hs.173939	PSECL	2.15	1.95
40	403845			NM_003105?-Homo sapiens sortilin-related	2.15	2.23
	415359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.14	1.70
	418526	BE019320	Hs.68838	solute carrier family 16 (monocarboxylic	2.13	1.83
	448045	AJ267438	Hs.21188	prostate stem cell antigen	2.13	3.48
	453459	BE247032	Hs.267189	ESTs	2.12	2.30
45	419183	U06069	Hs.69683	cytochrome P450, subfamily XXIV (vitamin	2.12	10.60
	436251	BE515085	Hs.266585	nuclear protein (90kD rpeal)	2.11	1.89
	445911	A1989587	Hs.145845	ESTs, Moderately similar to ALU1_HUMAN A	2.11	2.57
	423678	AA519435	Hs.177744	ESTs	2.09	2.30
	438817	AI023759	Hs.183242	ESTs	2.09	10.45
50	434293	NM_004446	Hs.3786	EphB6	2.08	2.42
	422785	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.08	2.10
	418216	AA622440	Hs.283569	AF15c14 protein	2.08	4.62
	437915	A1937553	Hs.222312	Homo sapiens clone N11 NTER201 Heratoca	2.08	10.40
	409420	Z15008	Hs.54461	laminin, gamma 2 (p60in (101kD), kalaf	2.06	5.39
55	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.05	1.20
	403773			NM_003105?-Homo sapiens sortilin-related	2.05	1.78
	414987	AA524394	Hs.294202	hypothetical protein FLJ14559	2.04	2.06
	424687	J03070	Hs.151738	marix metalloproteinase 9 (gelatinase B	2.04	1.70
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), sekb	2.03	2.26
60	447437	U07225	Hs.329	purinergic receptor P2Y, G-protein coupl	2.02	1.73
	445337	AJ248871	Hs.1294	EGF-like domain, multiple 6	2.02	2.30
	427651	ACC02300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	2.02	1.55
	441801	AW242799	Hs.86366	ESTs	2.01	10.05
	439780	AL119988		gltc-Homo sapiens mRNA full length insert	2.00	10.00
65	452752	BE300078	Hs.30449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.00	1.53
	434876	AF160477	Hs.61460	lyg superfamily receptor LNFR	2.00	1.91
	430152	AB001325	Hs.234642	inuprotein 3	1.99	1.74
	458134	AA032211	Hs.118403	ESTs	1.99	3.16
	412719	AWC16610	Hs.818	ESTs	1.99	0.34
70	442677	AJ292598	Hs.163300	ESTs	1.99	3.09
	409402	AF206234	Hs.695	cystatin B (beta2in B)	1.98	1.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.97	1.84
	439318	AW837045	Hs.6527	G-protein-coupled receptor 56	1.96	1.42
	447334	AA515032	Hs.61190	ESTs	1.96	2.53
75	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp686D0724 f1	1.94	9.70
	429002	AW248439	Hs.2340	junction plakoglobin	1.94	1.57
	410553	AW616824	Hs.255527	hypothetical protein MGCL1129	1.94	2.02
	420783	AB59838	Hs.99233	iodin, galactose-binding, soluble, 7	1.93	0.55
	427811	AW190922	Hs.03068	cystine bond superfamily 1, LIMP antago	1.92	1.01
	468988	Y08763	Hs.22785	gamma-aminobutyric acid (GABA) A recept	1.92	1.47
	403033	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.92	1.59

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419818	AI219207	Hs.72222	hypothetical protein FLJ13459	1.92	2.77
424522	AL134847	Hs.145997	ribosomal protein S5 kinase, 90kD, poly	1.92	1.21
413278	BE963085	Hs.433	interferon-stimulated protein 15 kDa	1.92	1.72
428924	BE409838	Hs.194567	cathepsin L, type 1, E-cadherin (epitheli	1.91	1.41
414655	AJ641726	Hs.295015	hypothetical protein MSC4171	1.90	1.51
			sortilin-related receptor, I (DLR class)	1.90	1.93
417409	BE272505	Hs.82109	syndecan 1	1.89	1.75
444781	NM_014400	Hs.11580	GPI-anchored metastasis-associated prote	1.88	1.15
419887	D31771	Hs.85404	erbb (Drosophila) homoeo box homolog 2	1.88	3.09
419092	J05581	Hs.89503	muscin 1, transmembrane	1.88	1.18
446673	NM_015381	Hs.15871	LPAP for lysophosphatidic acid phospholip	1.87	2.01
413347	A1133451	Hs.251864	insulin-like growth factor 2 (somatomedi	1.86	1.87
430158	AW958343	Hs.42455	DKFZP434H735 protein	1.85	2.11
412115	AK001753	Hs.73209	hypothetical protein FLJ10901	1.89	1.77
402901			NM_025205/Homo sapiens hypothetical pro	1.85	2.35
449027	AJ271216	Hs.22880	oleophilic/lepidicase III	1.85	1.59
410418	D31382	Hs.53325	transmembrane protease, serine 4	1.84	1.90
419870	AF147204	Hs.89414	chemokine (C-C motif), receptor 4 (fuc	1.84	1.03
414732	AW410976	Hs.77152	mei4 chromosome maintenance deficient (S	1.84	1.54
432210	A1557421	Hs.273330	Homo sapiens, clone IMAGE:3544552, mRNA,	1.83	1.74
425294	AA813322	Hs.4213	hypothetical protein MSC15207	1.82	1.84
431130	NM_002204	Hs.25529	inosiprin, alpha 3 (antipep CD45C, alpha	1.82	1.53
427239	BE270447	Hs.174670	ubiquitin carrier protein	1.82	1.74
402424			NM_024901/Homo sapiens hypothetical prot	1.81	1.51
419058	AW871155	Hs.29390	ESTs, Weakly similar to ISHUSK protein d	1.81	3.67
431645	BE119824	Hs.271560	uroguinlin 1B	1.80	4.11
410153	BE311528	Hs.15930	hypothetical protein FLJ12691	1.80	9.00
408522	A1641214	Hs.45320	Small proline-rich protein SPFRK (human,	1.80	1.02
428330	L22824	Hs.42256	matrix metalloproteinase 7 (matrilysin),	1.80	2.25
416141	BE279383	Hs.26557	plateletlin 3	1.79	1.16
415785	AW181985	Hs.275204	hypothetical protein FLJ13782	1.79	5.59
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.79	8.95
425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.79	2.08
437852	BE001836	Hs.256897	ESTs, Weakly similar to d395012.1 (Hsa	1.77	2.96
437344	AL036854	Hs.17611	differentially expressed in fibroblasts an	1.76	1.43
439808	W78123	Hs.85851	G protein-coupled receptor 57	1.76	8.80
424086	AF077374	Hs.139322	small proline-rich protein 3	1.76	0.57
430890	X54232	Hs.2659	glypican 1	1.73	1.39
422682	AW378365	Hs.2667	ESTs	1.73	1.99
427335	AJ446642	Hs.261677	G antigen 7B	1.73	0.65
426883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZP434K0322 (f	1.72	2.07
414907	X90725	Hs.77597	pole (Drosophila)-like kinase	1.72	1.85
428484	AF104032	Hs.164501	solute carrier family 7 (cationic amino	1.72	1.53
425953	AB36516	Hs.347524	cofactor required for Sp1 transcription	1.71	1.86
446993	AK71830	Hs.8127	KIAA0144 gene product	1.71	1.52
422405	AF025441	Hs.115206	Opa-interacting protein 5	1.71	5.52
428664	AK001666	Hs.183095	similar to SALL1 (rat (Drosophila)-like	1.71	8.55
443432	NM_014398	Hs.10867	similar to lysosome-associated membrane	1.71	0.55
428227	AJ321549	Hs.2246	small inducible cytokine subfamily B (C/	1.71	8.55
424736	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.71	13.98
447532	AK000814	Hs.16791	hypothetical protein FLJ23007	1.70	1.84
414053	BE001835	Hs.75725	trinegulin 2	1.69	1.51
447342	A192986	Hs.10322	Homo sapiens, Similar to RHEN cDNA 2010	1.69	8.45
425050	AF017307	Hs.166096	E74-like factor 3 (zeta domain transcript)	1.69	1.60
448252	AW880830	Hs.185273	ESTs	1.67	2.07
425316	AJ296454	Hs.81285	ESTs, Moderately similar to G785_HUMAN P	1.66	0.70
425240	AB91147	Hs.29358	ESTs	1.66	1.23
417151	AA194055	Hs.293858	transcription factor	1.65	8.25
425461	N78223	Hs.108105	integrin, beta 4	1.65	1.78
418482	BE001596	Hs.85266	CCD20 (mit division cycle 20, S. cerevis	1.64	1.59
417900	BE255127	Hs.82936	Human melanoma-associated antigen p97 (m	1.64	1.13
438746	AB56915	Hs.104727	downstream of cathepsin 6 (by 3.3kb)	1.63	1.81
423151	AL045227	Hs.124775	High mobility group (nonhistone chromoso	1.62	1.51
439585	AA347843	Hs.52711	C10Z6527 (p644327) (p644799) (MCS_	1.62	2.33
402777			glycylthione S-transferase M2 (muscle)	1.62	2.18
435659	BA635539	Hs.279837	atlasin-1/leptinectin D-associated	1.62	1.27
417515	L24203	Hs.82237	indoleamine-pyrole 2,3 dioxygenase	1.61	2.05
413385	M34455	Hs.840	carboxyl esterase IX	1.60	1.10
410407	X95535	Hs.53257	mesenchymal stem cell protein DSCD75	1.60	1.53
425335	AW343654	Hs.5326	guanine monophosphate synthetase	1.59	1.50
437015	AU075916	Hs.237373	Homo sapiens mRNA; cDNA DKFZP564O1763 (f	1.58	1.92
451932	F13036	Hs.113502	solute carrier family 1 (high affinity a)	1.57	1.79
422247	U18244	Hs.230822	serine/threonine kinase 15	1.56	7.80
408953	BE289227	Hs.120197	threidin-like protein 2	1.56	7.80
431155	AB036868		ESTs	1.56	7.80
443211	A1176388	Hs.439355	minichromosome maintenance deficient (S	1.55	1.44
408953	AW247090	Hs.57101			

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	426900	AW163564	Hs.142375	ESTs	1.54	1.93
	421066	AUX076725	Hs.101408	branched chain aminotransferase 2, mitochondrial	1.54	1.71
	413804	T64892	Hs.86947	glyco-6b02.r1 Stratagene liver (837224)	1.53	1.55
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase domain	1.53	1.59
	444783	AK01468	Hs.62180	ankir (Proteasome Scrape homology) act	1.52	2.50
5	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor	1.49	0.52
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.48	1.54
	425211	AF052693	Hs.195249	hlyc-54y07.x1 Soares, placenta, Streptococcus	1.48	1.39
	422260			NM_004357 Homo sapiens Bcl11a (BCL	1.47	1.48
10	424264	D8C400	Hs.239388	Human DNA sequence from clone RF-1-304/014	1.47	7.35
	433061	Y12642	Hs.31185	lymphocyte antigen E complex, locus D	1.47	1.37
	422164	NM_114312	Hs.112377	corbo at thymocyte receptor (X laevis	1.46	1.80
	444163	AF126096	Hs.62180	glyc-54y07.x1 Soares, placenta, Streptococcus	1.45	1.58
	452304	AAU25396	Hs.61311	ESTs, Weakly similar to S10590 cytosine	1.45	1.58
15	445182	AW169787		ESTs	1.43	7.15
	408930	AA146721	Hs.334586	hypothetical protein FLJ12188	1.43	1.53
	429359	W00482	Hs.2359	matrix metalloproteinase 14 (membranin-	1.42	1.34
	425467			Target Exon	1.42	7.10
20	424244	AV547184	Hs.143601	hypothetical protein hCLA-iso	1.42	1.32
	422094	AF126535	Hs.272027	F-box only protein 5	1.41	4.55
	421322	AW970522		gls-EST13627/04 MAGE resequences, MAGI Homo	1.39	10.35
	401760			Target Exon	1.37	1.16
	425247	NM_00940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.35	1.39
25	424420	BE614743	Hs.146588	prostaglandin E synthase	1.33	1.49
	421817	AF146274	Hs.10950	ATP-binding cassette, sub-family C (CFTR	1.31	1.44
	422119	AGZ77829	Hs.118182	RNA-0590 gene product	1.31	1.22
	418729	AB024449	Hs.8789	telomere-mid	1.30	0.84
	418599	AF131781	Hs.84763	hypothetical protein FLJ12442	1.30	1.32
	463208	AB005532	Hs.31442	RecQ protein-like 4	1.29	1.42
	431369	BE184565	Hs.261764	secretory leukocyte protease inhibitor 1	1.29	0.61
	453321	A094381	Hs.22521	ESTs	1.27	6.35
	421478	AI693243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.26	6.30
	425726	AF085908	Hs.159330	uroleptin 3	1.26	2.25
	409005	Z28424		gls-H.sapiens protein-serine/threonine ki	1.26	1.11
35	429415	NM_014058	Hs.261767	BESG1 protein	1.25	1.01
	418878	NM_001327	Hs.87225	oncogenic antigen (NY-ESO-1)	1.23	1.17
	431940	AA514908	Hs.2860	POU domain, class 5, transcription facto	1.22	1.59
	417433	BE272266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	1.20	1.38
40	422357	AJ223356	Hs.116051	Homo sapiens cDNA: FLJ22106 ts, clone H	1.19	1.23
	421903			S5001632/011645/0308g11AAGE1430.11A200	1.19	1.88
	425721	AD002115	Hs.159309	uroleptin 1A	1.17	2.30
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 ts, clone NT	1.17	5.85
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospho	1.17	1.39
	443599	NM_013409	Hs.9914	folistatin	1.17	1.17
45	419743	AW408782	Hs.5957	Homo sapiens clone 24416 mRNA sequence	1.13	2.83
	422330	D33783	Hs.115263	epiregulin	1.13	5.65
	420281	AK23893	Hs.23494	Predicted cationic efflux pump	1.11	5.65
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	1.08	5.40
	442304	BE159864	Hs.125386	ESTs	1.06	5.30
50	422170	A1791949	Hs.112432	anti-Mullerian hormone	1.06	1.55
	417999	AA264688	Hs.62954	ESTs	1.05	1.02
	411874	AA296105	Hs.20453	ESTs	1.04	7.20
	449961	AW225534	Hs.133100	ESTs	1.03	0.65
55	418505	AA093248	Hs.85339	G protein-coupled receptor 39	1.03	0.92
	422259	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	1.02	5.10
	463216	AL137566	Hs.22405	Homo sapiens mRNA; cDNA DKFZp68030221 f	1.02	0.60
	423634	AW865508	Hs.1610	serpin-thymosin growth factor binding pr	1.00	0.95
	420317	AW178761	Hs.227946	serine (or cysteine) proteinase inhibitor	1.00	0.25
60	453365	AA035211	Hs.17404	SOX7 GRY (sex determining region Y-ho	1.00	0.25
	453239	AA031940	Hs.235331	ESTs	1.00	0.27
	450084	AA872035	Hs.25333	interleukin 1 receptor, type II	1.00	0.45
	425590	NM_001644	Hs.1525	desmoglein 3 (epithelium vulgaris antigen	1.00	0.72
	404403			Target Exon	1.00	1.00
	406974	M57293		gls-Human parathyroid hormone-related pep	1.00	1.00
65	410348	AW166563	Hs.154569	ESTs	1.00	1.00
	412661	NC2660	Hs.14611	ESTs, Weakly similar to I54374 gene NF2	1.00	1.00
	415121	AA743732	Hs.86526	parathyroid hormone-like hormone	1.00	1.00
	425200	W47595	Hs.169300	transforming growth factor, beta 2	1.00	1.00
70	426968	U07616	Hs.172034	amphiphysin (Shi-Weiss syndrome with br	1.00	1.00
	425037	X51320	Hs.2605	tumor necrosis factor binding pr	1.00	1.00
	452401	NM_007115	Hs.23052	human necrosis factor, alpha-induced pr	1.00	1.00
	453389	BE275849	Hs.22063	cadherin 6, type 2, K-cadherin (Hes1 ki	1.00	1.00
	416078	M63119	Hs.85694	irradiation-associated 1	1.00	1.25
	420378	Z28372	Hs.2586	tumor necrosis factor receptor superfam	1.00	1.35
75	428182	UE38542	Hs.233317	ESTs, Weakly similar to GC1.1.HUMAN GANT	1.00	1.75
	451944	T61430		gls-5b0d3.s1 Stratagene lung (S37210) H	1.00	1.80
	415178	D61903	Hs.232850	ESTs	1.00	2.20

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410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	2.25
425048	H05469	Hs.164502	ESTs	1.00	2.25
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	1.00	2.60
480448	D08730	Hs.57471	ESTs	1.00	2.70
417791	AW965339	Hs.111471	ESTs	1.00	2.95
421373	AA806229	Hs.167771	ESTs	1.00	3.00
427366	AW023402	Hs.97849	ESTs	1.00	3.15
421070	AA263185	Hs.19327	ESTs	1.00	3.25
415542	RI1474	Hs.520263	ESTs, Weakly similar to 138022 hypophel	1.00	3.35
429486	AF155827	Hs.203963	hypophel protein FLJ10339	1.00	3.55
402075			ENSP00000251055* Plasma membrane calcium	1.00	3.95
419559	Y07828	Hs.91056	ring finger protein	1.00	4.00
415981	AA435443	Hs.79440	ICF1 mRNA binding protein 3	1.00	4.00
418738	AW389633	Hs.68682	solute carrier family 7, (calcicic amino	1.00	4.35
412723	AA646459	Hs.335951	hypophel protein AF301222	1.00	4.40
404877			NM_005365 Homo sapiens melanoma antigen,	1.00	4.45
443054	A745185	Hs.0939	yes-associated protein 65 kDa	1.00	4.45
403347			NM_005697 Homo sapiens transmembrane pr	1.00	4.50
406434			NM_000579 Homo sapiens cytochrome b5 ou	1.00	4.65
412530	AA766268	Hs.266273	hypophel protein FLJ13346	1.00	4.65
433365	AF026944	Hs.263797	ESTs	1.00	10.05
427686	A7791465	Hs.180142	salmodin-like tian protein (CLSP)	0.99	0.60
428504	X98133	Hs.204339	lipoic acid 24p3	0.99	1.00
431474	AL133990	Hs.190642	CEGPI protein	0.94	9.14
411880	AW872477		gbln:3003x1 NCL CGAP_Thy1 Homo sapiens	0.93	21.15
414221	AW450919		gbln:3003x1 NCL CGAP_Thy1 Homo sapiens	0.91	2.80
444649	AW207523	Hs.197626	ESTs	0.89	11.15
465034	AW450919		gbln:3003x1 NCL CGAP_Thy1 Homo sapiens	0.89	5.13
414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	0.84	0.85
439669	AW022166	Hs.222399	CEGPI protein	0.84	2.42
432222	A204995		gbln:3003x1 Stralagene schizo brain S1	0.81	6.75
407848	AA426202	Hs.40403	Chp300-interacting transactivator, wit	0.80	0.57
457292	A1921270	Hs.281462	hypophel protein FLJ14251	0.77	1.40
431089	BE041336		ESTs, Weakly similar to unknown protein	0.76	14.89
459702	A1024965		gbln:3003x1 Stralagene schizo brain S1	0.74	11.03
424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.56	0.80
406964	M21305		gbln:3003x1 Stralagene schizo brain S1	0.53	11.16
418225	AA577730	Hs.135654	ESTs, Weakly similar to PCH259 keratin	0.48	3.01
402265	X08250	Hs.149639	integrin, alpha 5 (fibronectin receptor	0.40	0.70
421218	NM_000489	Hs.729112	cytochrome P450, subfamily 1 (aromatic c	0.40	0.61

TABLE 3B

Phay: Unique Ecol probe identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

50	Phay	CAT Number	Accession
	411880	1263110_1	AW972477 BE089101 T05990
	413804	1390710_1	T04682 BE081190 BE168256
	414221	142690_1	AW450919 AA136653 AA136856 AW419381 AA94358 AA492073 BE168945 AA809054 AW208038 BE011212 BE011359 BE011367
55	415989	156454_1	BE011368 BE011362 BE011215 BE011365 BE011363
	431089	237525_1	A1287700 A1270344 AA191424 A1023543 AA06833 AA172056 AW959465 AA172236 AW963397 AA355056
	431322	331543_1	BE041396 AA491828 AA521946 AA715980 AA605102
	432222	343347_1	AW970722 AA500009 AA502096 AA502095 AA502095 T92158
	436008	42381_3	A1204565 AW527539 AW989968 AWA40776 AA528755
60	439780	47673_1	AA628890 A128603 BE0504035
	444163	893652_1	AL126390 A161746 A140521
	445192	632151_1	AW189277 A1215430 AW268489 AW205930 A1392907 BE093017 BE093019 BE093010
	451644	888230_1	T01430 A1820546 A1821336
65	456034	142696_1	AW450919 AA136653 AA136856 AW419381 AA94358 AA492073 BE168945 AA809054 AW208038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 3C

Phay: Unique number corresponding to an Ecol probe
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Danham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Danham L et al., Nature (1989) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

75	Phay	Ref	Strand	NL_position
	400773	8131629	Minus	4116-44236,46208-48321

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	400843	9188605	Plus	5853-5970,7653-7784,8892-9023,9673-9807,10534-10789,15254-15403,23827-23958
	400844	9188605	Plus	24748-24872,25035-25204
	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	35310-39474
5	401391	8516137	Minus	22335-23166
	401747	9782672	Minus	118596-118616,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131865-131932,132451-132575,133580-134011
	401750	9629699	Plus	83126-83250,83320-85540,94019-96267
10	401750	7249190	Minus	26397-26517,28958-29045,29135-29296,29411-29657,29705-29787,30224-30573
	401751	7249190	Minus	83215-83435,83531-83556,83740-83901,84237-84393,84955-85037,86290-86814
	402075	8117407	Plus	121907-122055,122804-122921,124015-124161,124455-124610,125572-126076
	402230	9696312	Minus	29782-29902
	402239	7690131	Plus	38175-38304,42133-42266
15	402250	5399865	Minus	113765-113910,115653-115765,116806-116940
	402335	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
	402777	9586235	Plus	126786-126948
	402901	8984222	Minus	175406-176567
	403547	3540153	Minus	59793-59966
20	403381	9438267	Minus	26009-26178
	403903	7710671	Minus	101165-102587
	404403	7272157	Minus	72053-72236
	404440	7538051	Plus	80430-81581
25	404875	9901324	Plus	96588-96732,97722-97831
	404877	1519284	Plus	1085-2107
	404877	3738341	Minus	43581-43229
	405233	7107731	Minus	140268-142566
	405932	7767612	Minus	123525-123713
30	406081	9123861	Minus	38115-38691
	406389	9295288	Minus	63448-63554
	406434	9339251	Minus	17803-17831
	406487	9796551	Plus	162212-162968

TABLE 4A: Preferred diagnostics for bladder cancer

	Pkey	Ex/Con	Unique D	Unique Title	R1	R2	R3
	<p>Pkey: Unique Eos probe/seq identifier number</p> <p>Ex/Con: Exemplar Accession number, Genbank accession number</p> <p>Unique D: Unique number</p> <p>Unique Title: Unique gene title</p> <p>R1: 80th percentile of muscle-invasive bladder tumor (stage T2-T4) AIs divided by the 80th percentile of anaplastic non-invasive carcinoma (stage Ta) AIs</p> <p>R2: 80th percentile of bladder tumor AIs minus background divided by 90th percentile of normal body sample AIs minus background, where background equals the 10th percentile of all sample AIs</p> <p>R3: 90th percentile of bladder tumor AIs divided by the 90th percentile of normal body sample AIs</p>						
5							
10							
15	423961	D13666	Hs.136348	porin-like (OSF-2a)	11.22	1.40	1.44
	446619	AL076643	Hs.313	secreted phosphoprotein 1 (ectopontin)	8.40	1.31	1.38
	444381	BC387335	Hs.283713	ESTs, Weakly similar to S64054 hypophell	7.88	2.06	2.44
	408243	U00787	Hs.624	interleukin 6	7.54	2.80	4.85
	413063	AL058737	Hs.76194	chitinase 3-like 1 (cartilage glycoprotein	6.14	1.19	1.18
20	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32	1.34	1.36
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	5.27	0.61	0.57
	419007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17	1.47	35.50
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30	1.75	1.54
	448921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cγ	4.29	1.35	1.80
	413324	V00571	Hs.75294	corticotropin releasing hormone	4.20	6.27	45.75
25	412429	AF050262	Hs.75765	GRO2 oncogene	4.00	0.94	0.93
	406036	L12694	Hs.750	gli-Homo sapiens (clone WR4.12V) anti-H	3.95	1.25	1.25
	429330	L23524	Hs.2295	matrix metalloproteinase 7 (matrilysin,	3.98	2.07	2.26
	408987	M31126	Hs.295049	matrix metalloproteinase 11 (stromelysin	3.41	4.37	3.37
	422500	BE297626	Hs.295049	microfibrillar-associated protein 4	3.09	0.39	0.40
30	410887	X03555	Hs.750	filipin 1 (Marfan syndrome)	2.95	0.44	0.45
	418558	U02722	Hs.79432	filipin 2 (peroneal) contractural ara	2.90	1.94	3.46
	414812	X72755	Hs.77357	monokine induced by gamma interferon	2.80	1.67	3.10
	423673	BC003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.77	5.62	26.07
35	421379	Y15221	Hs.103882	small inducible cytokine subfamily B (Cγ	2.71	2.25	2.91
	422600	X78555	Hs.169114	lecithinase (tenascin C, cytostatin)	2.40	0.47	0.27
	417849	AF291587	Hs.82733	elodigin 2	2.34	0.88	0.86
	400419	AF084545	Hs.82733	Target	2.33	1.54	2.12
	407811	AW190802	Hs.40086	cysteine knot superfamily 1, BMP antagonist	2.10	1.01	1.01
40	400289	X07630	Hs.226	matrix metalloproteinase 10 (stromelysin	1.99	3.19	17.50
	414774	X02418	Hs.77274	plasminogen activator, urokinase	1.94	24.9	1.94
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100K), lamin	1.94	2.02	5.39
	428227	AA321649	Hs.2246	small inducible cytokine subfamily B (Cγ	1.84	1.99	8.55
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	1.75	0.33	0.31
45	431639	AF000680	Hs.26175	phosphoprotein associated with GENs	1.76	1.13	1.16
	421958	AA357185	Hs.109518	ras homolog gene family, member H	1.75	1.33	1.27
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.58	2.42	1.39
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.57	2.02	8.55
	427483	BC303341	Hs.101025	ectodermal neural cortex (with G1B-like	1.55	1.57	1.55
	407539	AF05609	Hs.312579	ESTs, Weakly similar to A45019 dynein he	1.41	0.79	0.57
50	428344	B94038	Hs.199538	inhibin, beta C	1.36	1.36	1.34
	402727			NM_025065:Homo sapiens hypothetical prot	1.34	1.34	1.56
	412420	AL035688	Hs.73553	bone morphogenetic protein	1.31	1.83	2.22
	423217	NM_0010394	Hs.1940	collagen, type VII, alpha 1 (epidermis)	1.27	2.00	1.57
55	424206	NM_003734	Hs.196241	amine oxidase, copper containing 3 (vasc	1.25	0.16	0.30
	415138	C16356	Hs.255944	tissue factor pathway inhibitor 2	1.23	1.70	4.34
	424479	AF064238	Hs.148598	smoothelin	1.19	0.27	0.47
	445537	AJ249571	Hs.12844	EGF-like domain, multiple 6	1.17	1.59	2.83
	417079	BS5590	Hs.81134	interleukin 1 receptor antagonist	1.16	0.82	0.80
60	421634	AA437414	Hs.106283	hypothetical protein FLJ10282	1.16	1.05	1.05
	438569	AW02166	Hs.222399	CEGP1 protein	1.15	2.01	2.42
	431346	AA371059	Hs.251635	ubiquitin specific protease 3	1.10	1.94	1.52
	448801	AF010021	Hs.22025	hypothetical protein FLJ10159	1.10	0.31	0.31
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	1.03	1.51	1.42
65	424244	A1186431	Hs.289538	prostate differentiation factor	1.02	2.77	2.68
	426781	AA444821	Hs.63085	ESTs, Weakly similar to MPP3_HUMAN MAGUK	1.00	1.64	5.45
	445413	AA151342	Hs.10677	CSF-147 protein	1.00	1.51	5.20
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	1.00	1.55	4.30
	403106			C8000064:g11045233[emb]CAC10283.1(A	1.00	1.48	4.24
	402075			ENSP1000025166:Pleuro membrane cadum	1.00	1.67	3.95
70	403460			C1003394:g11291422[emb]CAC00691.1(A	1.00	1.40	3.90
	434337	AF116601		WW domain-containing oxidoreductase	1.00	1.58	3.70
	405738			CX000390:g16014645[emb]AA1438.1(AFA187	1.00	1.36	2.95
	427585	C31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.00	1.45	1.80
	438849	AW050614	Hs.239651	KAA1715 protein	1.00	1.28	1.59
75	452567	CSF7120	Hs.239862	predicted osteoblast protein	1.00	1.10	1.31
	401271			C8000555:g11251419[emb]CA99338.1(A	1.00	2.12	1.00
	411339	BE164688	Hs.274251	hypothetical protein FLJ20275; KAA1757	1.00	2.05	1.00

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	403005		C21000027:g[1817559]EAA13672.1 (O	1.00	1.80	1.00
	431146	Z83850	Human DNA sequence from PAC B2J11 and co	1.00	1.86	1.00
	434939	AF161422	Human sapiens HSPC304 mRNA, partial cds	1.00	1.86	1.00
	431753	Z76029	neurexine U	1.00	1.82	1.00
5	419121	AA374372	parvalyroid hormone-like hormone	1.00	1.69	1.00
	435505	AF220462	interleukin 1 homolog 1	1.00	1.67	1.00
	452401	NM_007115	tumor necrosis factor, alpha-induced pro	1.00	1.67	1.00
	404488		C16001447:g[1265370]ene[CAC20418.1 (1.00	1.66	1.00
10	441206	BE552914	NM_030658:Human sapiens organic anion tr	1.00	1.56	1.00
	407853	AA336797	ESTs, Weakly similar to TEFA HUMAN [L]sa	1.00	1.49	1.00
	486119	D29527	dcknpl (Xenopus laevis) homolog 1	1.00	1.47	1.00
	405471		ESTs	1.00	1.47	1.00
	402110		Target Exon	1.00	1.44	1.00
15	407911	AF104822	C18000173:g[1190079]em[CAC19648.1 (A	1.00	1.42	1.00
	404289		growth differentiation factor 8	1.00	1.40	1.00
	421925	S80310	C1002357:g[1490230]h[122933] hypothe	1.00	1.37	1.00
	405076	AL390179	acidic epidermal growth factor-like 1	1.00	1.26	1.00
20	468522	AA972412	Human sapiens mRNA; cDNA DKFZ647P134 (tr	1.00	1.19	1.00
	415018	AW138239	I-box and WD-40 domain protein 2	1.00	1.09	1.00
	429357	N73628	proprotein convertase subtilisin/kexin 1	1.00	1.04	1.00
	435684	AW976319	caspain, large	1.00	1.03	1.00
	435178	BE152396	ATP-binding cassette, sub-family A (ABC1	1.00	0.84	0.84
25	422522		hypothetical protein DKFZ564C00523	1.00	0.91	0.80
	425735		C1000569:g[12607905]d[BA21801.1 (A	1.00	0.80	0.67
	401905		ENSP000002221547:CAA1578 protein (Fragm	1.00	0.86	0.58
	404152		ENSP00000252237:Stenil regulatory elem	1.00	0.66	0.52
	418693	A1750878	C6000931:g[656645]d[BA613398.1 (A8	1.00	0.58	0.51
30	461375	A178006	thrombospondin 1	1.00	0.85	0.51
	439132	AF246086	Human sapiens BAC clone RP11-481J13 from	1.00	0.46	0.38
	465983	A1081687	hypothetical protein FLJ20547	1.00	0.44	0.33
	436881	AW384815	thymopoiesin	1.00	0.61	0.29
	409039	T97480	KIAA1555 protein	1.00	0.60	0.28
35	429186	NM_001874	small inducible cytokine subfamily A (Cy	1.00	0.39	0.19
	410023	AB017169	calcycalcipressin M	1.00	0.43	0.13
	420674	NM_000056	sIt (Drosophila) homolog 3	1.00	0.30	0.12
	415165	AW887604	butyrylcholinesterase	1.00	0.30	0.08
	426545	N96529	complement component 7	1.00	0.08	0.06
40	446256	BE814140	Human sapiens, clone MGC12401, mRNA, com	1.00	0.10	0.01
	417389	BE260894	CQI-27 protein	0.96	1.32	1.55
	403214		midline (neurite growth-promoting factor	0.95	3.15	2.34
	414759	A1752416	NM_016222:Human sapiens interleukin 1 re	0.94	1.63	2.61
	406665	U22961	insulin-like growth factor binding prote	0.92	1.67	1.60
45	401519		albumin	0.92	1.09	1.03
	417501	AL041219	C15000476:g[12737279]et[XP_012163.1	0.88	1.46	3.44
	409632	W74001	serma domain, immunoglobulin domain (Ig),	0.87	0.41	0.50
	425494		serine (or cysteine) protease inhibito	0.85	1.38	1.43
50	444171	AB016249	C2001837:g[12597932]d[BA21770.1 (A	0.83	1.46	4.65
	439708	AW872527	small inducible cytokine subfamily A (Cy	0.80	0.91	0.91
	436396	A1683487	ESTs, Weakly similar to DAF1_HUMAN DEATH	0.79	0.58	0.43
	428716	NM_008379	wingless-type MMTV integration site fami	0.77	1.47	2.37
	431347	A1133461	serma domain, immunoglobulin domain (Ig),	0.75	1.13	1.18
	413753	U17760	insulin-like growth factor 2 (somatomedi	0.68	2.61	1.87
55	428322	J05068	laminin, beta 3 (picotin [T25ID], kalinin	0.68	2.70	4.96
	426514	BE816833	tranocobalamin 1 (vitamin B12 binding pr	0.67	1.50	1.36
	422862	AF019025	bone morphogenetic protein 7 (osteogenc	0.56	2.05	2.46
	409757	NM_001993	apolipoprotein L	0.55	3.91	3.52
	427450	AB014526	cystatin SN	0.53	2.72	2.93
60	414655	N96569	KIAA0528 gene product	0.52	1.34	1.97
	423714	L39064	phospholipase A2, group IIA (platelets),	0.50	1.24	1.06
	404977		interleukin 3 receptor	0.49	2.91	6.46
	428336	AA531115	insulin-like growth factor 2 (somatomedi	0.28	5.78	5.17
	451668	Z43948	microsminoprotein, beta-	0.21	1.47	1.56
	428651	AF190478	cartilage acidic protein 1	0.18	4.05	3.60
65	421110	A1250717	annexin A10	0.17	5.14	27.75
			calpasein E	0.12	5.49	45.35

TABLE 4B

70	Key:	Unique Eot probest identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
75	Key:	CAT Number
	431146	283850
	431037	37918_1
		Accession
		283850 AA459717 AW966384 AA336635
		AF116601 A1110681 AF063556

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TABLE 4C

5	Key:	Unique number corresponding to an Exon probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:486-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NT_position:	Indicates nucleotide positions of predicted exons.		
10	Key	Ref	Strand	NT_position
	401271	9797373	Minus	61252-61911
15	401519	6649315	Plus	157315-157360
	401935	8671965	Plus	153365-154441,155599-155819
	402075	8117407	Plus	*12107-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402110	8131878	Minus	*73885-174062
20	402522	9798493	Plus	20605-20731
	402727	9211324	Plus	94596-94777
	403005	5791501	Minus	16945-17053,20018-20403
	403106	7331404	Plus	77162-77350,81338-81511
25	403214	7630945	Minus	76723-77027,79317-79484
	404152	5884757	Plus	41111-41281,45465-45718,47601-47910
	404488	8113285	Minus	64835-64994
	404829	6624702	Minus	4913-5063,7310-7455,9472-9621,9951-10082
30	404860	8878555	Plus	65802-66081
	404977	3738341	Minus	43081-43229
	405494	9500952	Minus	70264-70516
	405735	9931101	Minus	29864-29976
	405738	9943998	Plus	44370-45410
	406076	9123123	Plus	89972-90319
	406387	9293243	Minus	127317-127454
	406471	9795595	Plus	87383-87589

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TABLE 5A: Genes upregulated in bladder cancer

Proy:	Unique Eos. probe/seq identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als			
5				
10				
15				
20				
25				
30				
35				
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45				
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60				
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5	451541	BE279383	Hs.26557	plaiophlin 3	1.16
	406906	Z25424		gh-1Lsp/ens putelin-sensine/threonine ki	1.11
	429504	X99133	Hs.204238	lipocalin 2 (onco gene 24p3)	1.00
	444002	NM_006732	Hs.75579	FBJ murine osteosarcoma viral oncogene h	0.96
	431369	BE184455	Hs.251794	secretory leukocyte protease inhibitor (0.81

TABLE 5D

10 Play: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15	Play	CAT Number	Accession
	414221	142696_1	AW450979 AA136653 AA136655 AW419381 JA964368 AA492073 BE168945 AA809054 AW238038 BE011212 BE011369 BE011367 BE011368 BE011367 BE011215 BE011365 BE011363
20	417324	165714_1	AV255484 AA455504 AA196677 AW265432 AW991005 AA456370
	439608	42361_3	A402896 AJ129533 DE594035
	451385	86787_1	AA017656 AA017374 AA018761
	454609	1226517_1	AW810004 AW810555 AW810196 AW810618 AW810507
	459787	1366826_1	BE097833 BE091874 BE091871

TABLE 5C

25 Play: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in the column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

35	Play	Ref	Strand	NL_position
	400665	7770576	Minus	173043-173554
40	401066	8217436	Plus	71448-71574
	401335	9894961	Plus	15736-16362
	401981	4561193	Minus	124054-124209
	402226	7690131	Plus	38175-38304,42133-42266
45	402260	3399685	Minus	113765-113910,115653-115765,116908-116940
	402305	7326724	Plus	40832-41362
	402440	5369459	Minus	143456-143626,143808-143935
	402694	2996843	Minus	4727-4969
50	403383	9436287	Minus	116837-121197
	403477	9958251	Plus	111834-112008
	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404617	7341951	Plus	49330-49498
	405531	9665194	Plus	36602-36803
	406367	9296180	Plus	116228-116371,117512-117651
	406542	7711499	Plus	117335-116473

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TABLE 6A: Genes upregulated in bladder cancer

	Play	Exon	Unique Ees probe/identifier number	Exemplar Accession number, Genbank accession number		
5	Unigene ID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1	90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy AIs				
	R2	90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy and normal bladder AIs				
10	Play	Exon	Unigene ID	Unigene Title	R1	R2
	439928	AW014875	Hs.137007	ESTs	11.21	11.31
	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15	9.15
	421110	AJ25017	Hs.1335	calgaglin E	9.07	9.07
	417308	H60720	Hs.81892	KIAA0101 gene product	8.50	8.50
15	418406	X73501	Hs.84905	cytochrome 20	8.10	8.10
	446819	AU076943	Hs.313	secreted phosphoprotein 1 (pactopontin,	7.98	7.98
	433001	AF217513	Hs.273905	clone HCD310 PRO03'bp1	7.67	7.67
	408433	Y00797	Hs.524	interleukin 8	7.55	7.55
	416065	BE267931	Hs.79396	proliferating cell nuclear antigen	7.17	5.17
20	425387	J04088	Hs.155346	topoisomerase (DNA) I alpha (170kD)	7.17	8.24
	414183	AW957446	Hs.301711	ESTs	7.14	4.62
	419007	M13503	Hs.301693	matrix metalloproteinase 1 (matrilysin)	7.12	7.12
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	6.90	3.38
	427337	Z46223	Hs.170663	Fc fragment of IgG, low affinity (IgG1, r	6.85	4.98
25	441833	AW585444	Hs.112242	normie mucosa of esophagus specific 1	6.42	6.42
	436081	AK353362	Hs.159322	nuclear receptor subfamily 1, group 1, m	6.32	6.32
	415083	AL035737	Hs.75184	cytochrome 3-like 1 (carbamoyl glycine	6.09	3.67
	414219	W20010	Hs.75823	ALL-1 fused gene from chromosome 1q	5.93	4.63
30	405033	NM_000823	Hs.78209	C1002652-g[544327]p[Q04793]FMO5_RABIT	5.84	5.84
	413132	AA508115	Hs.153722	protein kinase (cAMP-dependent), catalytic	5.79	5.68
	428336	AA507115	Hs.153722	microsomal protein, beta	5.75	4.57
	449230	BE513348	Hs.211579	metastoma cell adhesion molecule	5.69	5.82
	423673	BE003054	Hs.16395	matrix metalloproteinase 12 (macrophage	5.69	7.30
35	415511	AF732617	Hs.152362	ESTs	5.65	5.65
	426028	NM_001110	Hs.172028	a delinquent and metalloproteinase domain	5.60	5.90
	421948	LA2583	Hs.334309	keratin 6A	5.59	14.20
	428651	AF198473	Hs.188401	annexin A10	5.55	5.55
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.38	5.63
	426687	M31120	Hs.153722	matrix metalloproteinase 11 (stromelysin	5.35	5.34
40	439453	BE284674	Hs.65566	thyroid hormone receptor-interactor 13	5.35	5.35
	408246	N56889	Hs.333823	mitochondrial ribosomal protein L13	5.20	3.50
	427678	BE267756	Hs.180312	mitochondrial ribosomal protein S16	5.13	4.10
	426159	NM_019382	Hs.195057	v-erb-b2 avim erythroleukemia v	4.97	3.71
	442315	AA173992	Hs.7866	ESTs, Moderately similar to ZNF1_HUMAN Z	4.90	4.90
45	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.90	4.77
	417720	AA205825	Hs.203057	ESTs	4.84	7.34
	423879	AF221981	Hs.138844	CS box-containing WD protein	4.81	4.81
	422691	LA5094	Hs.100724	peroxisome proliferative activated recep	4.81	4.43
	433470	AW950554	Hs.197298	transmembrane 4 superfamily member 1	4.72	4.72
50	429138	AB020857	Hs.197298	NS1-binding protein	4.71	4.71
	403063	BE086548	Hs.42346	calcitonin-binding protein calcarein-1	4.71	4.71
	462714	AW770594	Hs.30340	hypothetical protein KIAA1165	4.69	4.69
	424932	BE025890	Hs.381178	hypothetical protein FLJ22468	4.68	4.68
55	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 ts, clone NT	4.65	4.65
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.64	4.64
	427490	Z56152	Hs.178655	mitogen-activated protein kinase 13	4.63	4.62
	412490	AW805854	Hs.288850	Homo sapiens cDNA FLJ22528 ts, clone H	4.61	4.51
	416030	BE207573	Hs.83321	asporinomed B	4.50	4.50
	401192			Target Exon	4.60	4.29
60	426761	A1015708	Hs.172089	Homo sapiens mRNA: cDNA DKFZp58610222/	4.59	3.51
	422747	BE153855	Hs.81490	ty superfamily receptor LNR	4.58	5.33
	445818	A107463	Hs.15878	KIAA1272 protein	4.58	4.58
	423725	A1403108	Hs.132177	hypothetical protein LOC57822	4.55	4.55
	415701	NM_003873	Hs.78619	gamma-glutamyl hydrolase (conjugase, bi	4.52	4.70
65	446742	AA232119	Hs.16505	putative G-protein coupled receptor	4.49	4.11
	419433	AA814607	Hs.7205	hypothetical protein FLJ21862	4.48	4.48
	412326	R07586	Hs.73817	small inducible cytokine A3 (homo/ovine	4.47	4.47
	427528	AU077143	Hs.175585	mitochondriome maintenance deficient (S,	4.45	4.45
	444371	BE540274	Hs.239	forkhead box M1	4.44	3.87
70	444006	BE365656	Hs.102465	type 1 transmembrane protein Fe14	4.43	3.63
	424308	AW975531	Hs.154443	mitochondriome maintenance deficient (S,	4.43	4.43
	401093			C12000589-g[53015]p[3]BAA86477.1 (A	4.40	4.40
	447644	AW661622	Hs.108646	Homo sapiens cDNA FLJ14534 ts, clone PL	4.39	4.39
	417933	X02206	Hs.82982	thymidylate synthase	4.38	4.35
75	409481	AA382169	Hs.54463	N-ras (and STAT) interactor	4.36	3.68
	401451			NM_004496-Homo sapiens hepatocyte nucle	4.35	4.35
	450746	D82873	Hs.273589	general transcription factor II, i	4.35	3.38

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5	414683	S78296	Ha.76888	hypothetical protein MGC12702	4.34	4.74
	434203	BE262877	Ha.283558	hypothetical protein PRO1855	4.31	4.31
	417616	BE548641	Ha.82314	hyposanthine phosphoribosyltransferase 1	4.30	4.30
	415815	U41514	Ha.80120	UDP-N-acetyl-alpha-D-glucosaminic poly	4.30	4.30
	440266	NM_055402	Ha.288757	vesicicular stomatitis virus oncoprotein	4.29	4.29
10	417715	AW695687	Ha.86366	ESTs	4.27	7.45
	400757	NM_001898	Ha.123114	cystein SN	4.24	3.39
	417140	AA219691	Ha.73825	RAB5 interacting, kinase-like inhibitors	4.24	4.24
	435942	AW074638	Ha.334432	hypothetical protein MGC2465	4.21	4.72
	446847	T51454	Ha.82345	Homo sapiens cDNA: FLJ21930 fls, clone H	4.20	4.20
15	430856	AA469355	Ha.127310	ESTs	4.19	4.19
	428450	NM_014731	Ha.184339	KIAA0175 gene product	4.16	4.90
	425324	AW151222	Ha.155909	ESTs, Weakly similar to 130022 hyphe	4.14	4.14
	400231	AA446644	Ha.692	CA735-2 antigen; epithelial glycoprotein	4.14	5.90
	426263	NM_033837	Ha.169139	lysozyme (L-lysozyme hydrolase)	4.12	4.12
20	446849	AU076617	Ha.16261	cleavage and polyadenylation specific fa	4.12	3.43
	403643			NM_003105-Homo sapiens scotin-related	4.11	5.51
	449722	BE283074	Ha.23960	cytofl	4.09	4.09
	405056			Target Exon	4.09	3.75
	420344	BE463721	Ha.97101	putative G protein-coupled receptor	4.07	4.07
25	426997	BE620738	Ha.173125	peptide/prolyl isomerase F (cyclophilin	4.05	4.80
	455255	AW465897	Ha.100000	S100 calcium-binding protein A8 (calgran	4.00	7.64
	437150	RS1407	Ha.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.02	4.02
	413794	AF234632	Ha.61638	myosin X	4.02	4.02
	422511	AU076442	Ha.117938	collagen, type XVII, alpha 1	4.02	4.72
30	414020	NM_002994	Ha.75703	small inducible cytokine A4 (homologous	4.01	3.59
	415391	AU076527	Ha.72284	metoderm specific transcript (mouse) hom	4.01	4.01
	422609	AK001379	Ha.121028	hypothetical protein FLJ10549	4.00	4.00
	400277			Eos Clon	4.00	3.47
	415791	H03366	Ha.78853	uracil-DNA glycosylase	3.99	3.37
35	412510	X09090	Ha.74136	fatty acid binding protein 6, foal g	3.98	4.77
	427557	NM_002659	Ha.179557	plasminogen activator, urokinase recept	3.98	3.95
	413753	U17760	Ha.75517	laminin, beta 3 (lamin (125kD), lamin	3.96	6.95
	420659	AW465367	Ha.100000	S100 calcium-binding protein A8 (calgran	3.92	5.04
	420429	AF153241	Ha.72284	Homo sapiens vitreous body/acidic trans	3.91	3.68
40	409898	AL119844	Ha.49476	Homo sapiens clone TUA5 C1-ds-chut raj	3.90	3.90
	411678	AW071114	Ha.71465	squalene epoxidase	3.89	3.89
	428113	D08236	Ha.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	3.87
	428426	AL037544	Ha.164298	cyclin-dependent kinase 7 (homolog of Xe	3.87	3.87
	442932	AA457211	Ha.8689	homodimeric adjuvant to zinc finger doma	3.85	4.00
45	428063	Y06397	Ha.227817	BCL2-related protein A1	3.85	3.85
	439863	AW247528	Ha.6783	platelet-activating factor acetylhydrola	3.82	3.77
	441362	SC14410	Ha.23044	RAE51 (S. cerevisiae) homolog (E coli Re	3.82	3.82
	432659	AJ002144	Ha.245155	UDP-N-acetyl-alpha-D-glucosaminic poly	3.81	3.81
	417771	AA046968	Ha.82547	retinoic acid receptor responder (czaro	3.81	3.62
50	430259	BE550182	Ha.127626	Raf/Gef-like protein 3, mouse homolog	3.80	3.80
	447573	AB011169	Ha.20141	similar to S. cerevisiae SSM4	3.77	3.77
	404675			NM_022815-Homo sapiens phospholipase A2	3.77	3.46
	411299	BE406857	Ha.69499	hypothetical protein	3.76	3.76
	418827	BE327311	Ha.47166	HTO21	3.76	3.76
55	446839	BE091926	Ha.16244	mitotic spindle coiled-coil related prot	3.75	3.75
	407137	T97307	Ha.169159	glycylserine 51 S. cerevisiae fetal liver sp	3.73	3.73
	433315	A249361	Ha.74122	caspase 4, apoptosis-related cytokine pr	3.71	3.71
	400234	N95796	Ha.276959	Homo sapiens protein mRNA, complete cds	3.70	3.45
	400518	BE364036	Ha.3454	KIAA1821 protein	3.69	3.69
60	433024	AW078180	Ha.227730	integrin, alpha 6	3.69	3.69
	425089	AF038007	Ha.169159	ATPase, class I, type B5, member 1	3.68	3.68
	419478	U03645	Ha.1174	cyclin-dependent kinase inhibitor 2A (mo	3.68	3.66
	414761	AL077228	Ha.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.67
	413670	AB000115	Ha.75470	hypothetical protein, expressed in oesop	3.67	3.41
65	424840	C79997	Ha.153479	extra spindle poles, S. cerevisiae, homo	3.67	3.68
	434263	N34895	Ha.44648	ESTs	3.65	3.65
	438280	AW015634	Ha.217493	annexin A2	3.63	3.36
	443426	AF098158	Ha.9329	chromosome 20 open reading frame 1	3.63	3.68
	426999	AW361565	Ha.19520	KIAA0746 protein	3.61	3.65
70	416540	BE235478	Ha.79404	neuron-specific protein	3.60	4.22
	416926	H03109	Ha.108920	HTO16 protein	3.59	3.69
	414368	W70171	Ha.75939	uridine monophosphate kinase	3.59	3.53
	402727			NM_023065-Homo sapiens hypothetical prot	3.58	3.58
	415381	AB023420	Ha.90093	heat shock 70kD protein 4	3.56	3.77
75	416114	AB095649	Ha.183868	glucuronidase, beta	3.55	3.55
	424941	AA128376	Ha.153884	ATP binding protein associated with cell	3.55	3.55
	431958	BE3629	Ha.2877	cadherin 5, type 1, P-cadherin (placenta	3.54	4.83
	425236	NM_002849	Ha.195208	protein tyrosine phosphatase, receptor 1	3.53	3.52
	420759	AB274846	Ha.89105	Homo sapiens cDNA: FJ21245 fls, clone C	3.51	5.77
	400289	X07620	Ha.2258	matrix metalloproteinase 10 (stromelysin	3.50	5.70
	418203	X54942	Ha.83758	CDC28 protein kinase 2	3.50	3.50

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5	416220	AA431880	Ha.181174	ESTs, Weakly similar to T19201 hypoheii	3.50	3.50
	428371	AB012193	Ha.183874	collin 4A	3.46	3.46
	418663	AK001100	Ha.41690	desmocollin 3	3.45	4.74
	450877			insulin-like growth factor 2 (somatomedin)	3.46	3.69
	422883	AW505087	Ha.119047	zinc finger protein 175	3.44	3.44
10	434061	AW024973	Ha.283678	NF0009 protein	3.41	5.64
	418113	AI221241	Ha.83484	SPY (sex determining region Y)-box 4	3.41	4.32
	431689	AA305888	Ha.257095	URF-GaTteteGctNAc beta 1,3-galactosyltr	3.40	3.40
	411943	BE532436	Ha.79522	ESTs, Weakly similar to 644608 CD2F.5 p	3.39	4.27
	420005	AW271106	Ha.133294	ESTs	3.38	3.40
15	453450	AW797627	Ha.347459	ADP-ribosylation factor 6	3.38	3.67
	410315	AB638871	Ha.17625	Homo sapiens cDNA FLJ22524 fs, clone H	3.36	3.36
	428639	AI767756	Ha.82302	Homo sapiens cDNA FLJ14614 fs, clone NT	3.35	3.35
	437469	AW783112	Ha.15514	hypothetical protein NC032369	3.35	3.35
	407151	H25836	Ha.301527	ESTs, Moderately similar to unknown [H.s]	3.34	3.34
20	428157	AI738719	Ha.199427	hexokinase 2	3.33	3.73
	451293	H36754	Ha.171116	hypothetical protein FLJ00026	3.33	3.33
	407050			Target: exon	3.33	3.33
	450139	AK001838	Ha.293233	serum/glucocorticoid regulated kinase	3.33	3.33
	412636	NM_004415		desmoplakin (DPI, DPL)	3.30	4.81
25	447578	AA912347	Ha.136585	ESTs, Weakly similar to JCS314 CDC28cdc	3.27	3.38
	432315	NM_004293	Ha.238147	guanine dinucleoside	3.26	4.30
	421894	R45689	Ha.21889	Homo sapiens cDNA FLJ12578 fs, clone NT	3.26	3.41
	443030	R88048	Ha.9238	hypothetical protein FLJ23515	3.19	3.34
	436911	AA142984	Ha.5344	adaptor-related protein complex 1, gamma	3.17	3.40
30	443006	AF030517	Ha.5844	hypothetical protein FLJ20510	3.06	3.62
	443711	BE281128	Ha.20330	TGNDU	3.05	3.43
	425343	AK000785	Ha.199480	Homo sapiens, Similar to epain 3, clone	3.01	3.53
	408380	AF123050	Ha.44532	duizigulin	2.99	4.11
	421508	NM_004833	Ha.105115	absent in melanoma 2	2.99	3.67
35	432950	AL359053	Ha.57664	Homo sapiens mRNA full length insert cDN	2.97	4.55
	462046	AB018345	Ha.27657	KAA0802 protein	2.95	3.39
	451940	AI357559	Ha.52620	integrin, beta 8	2.93	3.58
	407722	BE252241	Ha.38041	pyridoxal (pyridoxine, vitamin B5) kinase	2.90	3.68
	422282	AF019225	Ha.114309	apoptosis protein L	2.89	3.57
40	422230			Target: Exon	2.88	5.36
	406685	M16726		gbl/human nonspecific crossreacting anti	2.80	5.80
	417880	BE241595	Ha.82848	selectin L (lymphocyte) adhesion molecule	2.73	3.69
	447957	NM_14821	Ha.20126	KIAA0371 gene product	2.75	3.45
	418004	U07519	Ha.87535	aldehyde dehydrogenase 3 family, member	2.75	3.46
45	417275	X63578	Ha.295440	parvalbumin	2.73	3.54
	431211	M88840	Ha.323733	gap junction protein, beta 2, 26kD (conn	2.72	8.39
	401781			Target: Exon	2.62	4.15
	407242			gbl/human nonspecific crossreacting anti	2.54	5.98
	428423	AU076517	Ha.184276	case/casr family 9 (sodium/hydrogen	2.52	4.27
50	430200	BE813337	Ha.234869	germinin	2.51	4.15
	451036	AU079785	Ha.430	plastin 1 (isoform)	2.51	4.15
	443912	T49351	Ha.30229	DMP2P430302 protein	2.48	3.66
	441435	AW294803	Ha.127739	ESTs	2.45	3.60
	449246	AW411239	Ha.23363	hypothetical protein FLJ10963	2.45	3.62
55	401780	U85593	Ha.81134	NM_005557-Homo sapiens keratin 16 (loca	2.22	4.49
	427168	AA506894	Ha.113406	interleukin 1 receptor antagonist	2.20	3.55
	435394	AA149250	Ha.56105	3100 calcium-binding protein A7 (psorias	2.15	6.08
	427315	AA179940	Ha.175553	ESTs	2.05	3.95
				Homo sapiens mRNA; cDNA DKG256-40753 (f	1.79	3.68

TABLE 6B

Play:	Unique Eex probedet identifier number	
	CAT number:	Gene cluster number
Accession:	Genbank accession numbers	
60	Play	Accession
	412636	NM_004415
		13165_1
70	Play	Accession
	412636	NM_004415
		13165_1
75	Play	Accession
	412636	NM_004415
		13165_1

TABLE 6C

35

Play	Ref	Strand	N. position
407050	8115067	Plus	159991-159168,193016-193548
40843	9198065	Plus	158991-7653,17784,8692-9123,8673-9807,10634-10786,15254-15403,23827-23968
410393	8616137	Minus	22335-29166
411192	1751502	Minus	69558-70101
410451	6834068	Minus	118926-121272
421918	72419180	Minus	12951-28517,28920-29046,25-35,20296-29411-29567,29905-29767,30224-30673
401781	7149180	Minus	83215-83336,83369-83740,83801,84237-84339,84950-85637,86290-88614
422230	9986312	Minus	29752-29932
420727	9211334	Plus	54598-54767
404575	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405533	7107739	Minus	142358-142546
405536	6046489	Plus	82014-82401,80580-81125

TABLE 7A: Genes downregulated in bladder cancer

	Play:	ExAcen	UnigeneID	Unigene Title	R1	R2
	Unique Eos probe set identifier number					
	Example: Unigene number, Genbank accession number					
5	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1	90th percentile of normal urothelium biopsy AIs divided by 79th percentile of bladder tumor AIs				
	R2	90th percentile of normal urothelium biopsy and normal bladder AIs divided by the 50th percentile bladder tumor AIs				
10	Play	ExAcen	UnigeneID	Unigene Title	R1	R2
	403010			C21000152:g[6226463;p]Q52118/YM03_ERWS	4.85	2.49
	426786	S76234	Hs.172405	cell division cycle 27	4.26	2.48
	416225	AA577330	Hs.198664	ESTs, Weakly similar to PC4259 Ierlin	4.04	2.07
	455006	AV226631	Hs.27721	Walt-Hirschhorn syndrome candidate 1-k	3.82	2.86
	404917			Target Exon	3.78	2.00
15	426488	X03360	Hs.4	alcohol dehydrogenase 1B (class I), beta	2.64	1.79
	419543	AA244170	Hs.172405	glucocorticoid-induced leucine aminopeptidase	2.63	3.42
	451362	NA24243	Hs.110373	ESTs, Highly similar to T42678 second	2.22	3.24
	426957	NM_003881	Hs.194676	WNT1 inducible signaling pathway protein	2.20	3.80
20	451529	AI517901	Hs.208541	ESTs	2.19	3.69
	417076	AV573454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.03	3.03
	425438	TG2216	Hs.270940	ESTs	2.00	5.17
	450515	AV304228		bitheyl hydrolase-like (serine hydrolase)	1.89	2.46
	432873	AI183728	Hs.276368	Homo sapiens mRNA; cDNA DKFZp598M2022 (1	1.70	2.75
25	452123	A267615	Hs.38022	ESTs	1.69	2.46
	424378	V28920	Hs.167588	neural cell adhesion molecule 1	1.65	4.67
	437601	AA781546	Hs.24894	ESTs, Weakly similar to ALU1_HUMAN; ALU S	1.50	3.34
	402096			ENSP00000217729:Laminin alpha-1 chain p	1.48	3.02
	439563	AI018768	Hs.12482	glycerophosphate O-acyltransferase	1.47	3.22
30	412810	M21574	Hs.74815	platelet-derived growth factor receptor, beta	1.46	2.30
	458661	AV1512481	Hs.104105	ESTs	1.36	2.86
	414033	AL070707	Hs.207443	hydropyruvate protein MGC10648	1.36	2.80
	433572	AL046855	Hs.3407	protein kinase (cAMP-dependent), catalytic	1.35	3.49
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23178 ts, clone L	1.34	2.93
35	423412	AV576974	Hs.125100	ESTs	1.32	6.13
	421406	AF176857	Hs.104105	Mus (mouse) homolog 2	1.21	4.07
	417446	AL118671	Hs.82153	monoamine oxidase B	1.27	2.86
	452886	A478250	Hs.13751	ESTs	1.26	1.95
	446806	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp596B211 (1)	1.25	3.44
40	443105	X26765	Hs.5004	chondroitin sulfate proteoglycan 4 (male)	1.24	2.07
	421348	M54048	Hs.103724	peripherin myelin protein 22	1.24	2.63
	433070	N75345	Hs.306121	CDC20 (cell division cycle 20, S. cerevisiae)	1.23	2.80
	420028	AF161486	Hs.94769	RAB23, member RAS oncogene family	1.22	3.43
	409451	A08063	Hs.7882	ESTs	1.20	6.01
45	447384	A377221	Hs.40528	ESTs	1.00	7.52
	421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	1.00	7.38
	409619	AK001015	Hs.53220	BCL2-associated athanogene 2	1.00	6.40
	444755	A153358	Hs.160316	ESTs	1.00	5.53
	402465	V68796	Hs.237731	ESTs	1.00	5.05
50	417124	BE122782	Hs.23338	ESTs	1.00	4.73
	443598	A620681	Hs.295276	ESTs	1.00	4.36
	436303			C15000322:g[7499163;p]IT20903 hypo	1.00	4.37
	422594	AV1851802	Hs.266276	ESTs	1.00	4.37
55	422195	AB007903	Hs.113062	QAA0443 gene product	1.00	4.35
	452877	A250789	Hs.32478	ESTs	1.00	3.90
	452487	AV207656	Hs.6630	Homo sapiens cDNA FLJ13325 ts, clone OV	1.00	3.30
	417159	R01761	Hs.197335	glycylserine 11 Scavenger-like liver lipase	1.00	3.82
	445607	AA468107	Hs.30159	ESTs, Weakly similar to unnamed protein	1.00	3.82
	406274			Target Exon	1.00	3.58
60	410611	AV1564134	Hs.20924	QAA1628 protein	1.00	3.06
	426456	NM_001151	Hs.2343	poliovirus capsid family 25 (mitochondrial)	1.00	2.69
	422252	AV151033	Hs.114360	transforming growth factor beta-4-stimulat	1.00	2.51
	413040	AA153338	Hs.12321	sodium/calcium exchanger	1.00	2.51
	428923	NM_005308	Hs.211589	G protein-coupled receptor kinase 5	1.00	2.05
65	456607	AB60190	Hs.108070	cyclin-dependent kinase inhibitor 1C (p5	1.00	2.01
	421413	A333327	Hs.197335	plasma glutamate endopeptidase	0.97	2.45
	400288	X02656	Hs.149690	integrin, alpha 5 (fibronectin receptor,	0.90	2.47
	424268	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kinase	0.88	5.08
	414445	AA557680	Hs.75152	desmin	0.86	3.13
70	412014	AA506560	Hs.43251	ESTs, Weakly similar to A45010 X-linked	0.76	1.88
	426100	AF051650	Hs.154557	supervillin	0.70	3.90
	432054	AV558590	Hs.61426	Homo sapiens mesenchymal stem cell prote	0.68	3.41
	427818	AV151222	Hs.133765	ESTs	0.63	3.75

TABLE 7B

Play: Unique Eos probe set identifier number

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CAT number: Gene cluster number
Accession: Genbank accession numbers

5	Key:	CAT Number	Accession
	417159	1653899_1	R01761 R01760 H49767
	418543	185746_1	AA244170 A1018087 AA244355
	450515	63710_1	AV0304228 AW0028420 AA3462212 H15015 AA317021 AJ223484 H25061 H61744 AB06147 AB837938 AW167766 AW802578 AW1842369
10			AV0304228 AW0028420 AA3462212 H15015 AA317021 AJ223484 H25061 H61744 AB06147 AB837938 AW167766 AW802578 AW1842369
			BE5439526 AA0572417 AW0234409 AAD10052 A10058319 A1280242 AWW22925 H08848 H06808 R51905 RA50223 A10675471 H28475 A1086507
			A1197815 A1825355 N69134 A1075956 A1470122 AA449986 AW662833 AA860423 AA513342 T23825 A194207 A1310319 T32467 A1689870
			A1682293 A1610533 BE222045 H14620 AA626645 AA878023 T33571 AA653982 A1136631 H15016 A1304356 AA963631 A1350090 A1143993
			A1708171 AA526961 H26247 W03486 AA847598 H61745 AW855486 BE299005 A1079409 A278050 AJ223168 A1860904 AW026415 A1330003
			A1393692 A1364302 A462638 N60104 A1015651 H04543 BE285397 A1086154 W24135
15	TABLE 7C		
	Key:	Unique number corresponding to an Eco probe set.	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA	
20		sequence of human chromosome 22." Dunham L et al., Nature (1999) 402:469-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
	NL_position:	Indicates nucleotide positions of predicted exons.	
25	Key:	Ref	Strand
	402096	8117697	Minus
	403010	3132346	Plus
	404917	7341851	Plus
	406274	7543797	Plus
30	406303	6575965	Plus
			NL_position
			24933-25196
			73305-79052
			49330-49408
			932-1123
			173622-173766

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TABLE 9A: Genes predictive of bladder cancer progression

	Play:	Unique Ecos probe/ identifier number				
	EXACON:	Exon/ Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1	80th percentile of Ta or T1 tumor AIs from patients who upstaged divided by 80th percentile of Ta or T1 tumor AIs from patients who did not upstage				
	R2	median of Ta or T1 tumor AIs from patients who upstaged divided by the median of Ta or T1 tumor AIs from patients who did not upstage				
5						
10	Play:	Unique Ecos probe/ identifier number			R1	R2
	EXACON:	Exon/ Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1	80th percentile of Ta or T1 tumor AIs from patients who upstaged divided by 80th percentile of Ta or T1 tumor AIs from patients who did not upstage				
	R2	median of Ta or T1 tumor AIs from patients who upstaged divided by the median of Ta or T1 tumor AIs from patients who did not upstage				
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75						

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432331	W37862	Hs.274368	MSTP332 protein	4.36	2.18
451736	AW080356	Hs.23885	ESTs, Weakly similar to ALU1_HUMAN ALU 5	1.51	3.45
413106	AW086945	Hs.110855	ESTs	4.34	5.58
413643	AA133587	Hs.186729	ESTs	1.30	2.42
433217	AB040814	Hs.270828	KIAA1481 protein	1.70	2.45
432322	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	1.75	1.66
438006	BE148795	Hs.127551	hypothetical protein FLJ14503	1.76	2.04
410102	AW246508	Hs.273727	ESTs, homologous of PLEM-3 [clone swainy]	2.32	2.45
432656	AW514541	Hs.252065	ESTs, Weakly similar to I78955 scfknth	1.14	1.50
415714	NM_002290	Hs.78672	laminin, alpha 4	2.52	1.13
450282	AA007655	Hs.53523	ESTs	1.40	2.58
428655	AJ074665	Hs.133405	ESTs	1.54	2.20
432917	NM_014125	Hs.241577	PRO3027 protein	2.24	3.03
425041	AJ132820	Hs.194768	a disintegrin and metalloproteinase domain	1.61	2.50
428807	AL045274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp554H203 (tr	1.73	1.19
427719	AI393122	Hs.134726	ESTs	1.46	2.00
408778	AB050519	Hs.63362	hypothetical protein PRCC2714	1.45	2.58
418870	AF147204	Hs.59114	chromatin [C-X-C motif], receptor 4 (fus	1.40	2.03
424425	AB031450	Hs.146824	SPR1 protein	1.60	1.11
445351	TS2576	Hs.191168	ESTs	1.69	2.40
448899	NM_005357	Hs.16426	pocockshy-like	1.22	2.42
420956	AF001527	Hs.100695	hypothetical protein FLJ10462	2.66	2.96
424900	ST8187	Hs.153752	cell division cycle 25B	2.16	1.33
413593	AA205248	Hs.254299	gluc276c12.r1 Straateno HNT neuron (537	1.69	2.00
406734	AW264996	Hs.118915	ESTs	2.06	2.94
413880	AB650942	Hs.118915	histone H2B receptor	1.24	2.20
437063	AA351109	Hs.5437	Tax1 Human T-cell leukemia virus type I	1.78	2.50
418044	AI640532	Hs.119830	ESTs, Weakly similar to ALU1_HUMAN III	1.54	2.53
441971	W27060	Hs.262855	ESTs	1.62	2.13
450401	AW353261	Hs.5164	ESTs	1.42	2.30
440137	AA868358	Hs.343636	ESTs	1.36	2.60
457687	AA922641	Hs.27263	KNA1458 protein	1.47	2.42
440707	BE250751	Hs.22667	Homo sapiens cDNA: FLJ22073 fs, clone H	1.16	2.10
422441			Target: Exon	2.58	2.52
413425	AA430155	Hs.151343	KNA1524 protein	1.22	2.45
418735	R11275	Hs.194465	ESTs	1.14	2.14
421582	AI910275		trifol factor 1 (breast cancer, estrogen	1.25	1.03
431031	AA830335	Hs.105273	ESTs	2.35	2.95
433336	AF017960	Hs.31365	secreted frizzled-related protein 2	3.72	1.00
420786	AW256466	Hs.43528	deleted in lymphocytic leukemia, 5	1.23	2.60
401336			Target: Exon	1.18	1.68
417670	R07785		glycylt5c0c.r1 Soares fetal liver spleen	1.55	2.00
426314			C14001020.g1 (259744) IgHAA G50049.1 (AF31	1.60	3.06
456981	AW068318	Hs.265996	hypothetical protein FLJ23375	1.70	2.50
417509	AA203414	Hs.42009	ESTs	1.82	2.05
452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	1.34	1.37
416676	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.37	1.02
457871	AI168278		ESTs	1.20	2.19
444163	AI168298		gluc276g07.x1 Soares_placenta_8to9weeks_	1.43	1.22
413276	ZN4725	Hs.75260	milogen inducible 2	1.78	2.28
421097	AJ261112	Hs.125232	Homo sapiens cDNA FLJ13206 fs, clone OV	2.65	2.60
417151	AA194055	Hs.253956	ESTs	1.68	1.57
426356	AA25414	Hs.33287	nuclear factor IIB	2.06	2.40
440959	AW070965	Hs.346390	ESTs	1.12	1.70
426629	AW204343	Hs.156823	ESTs, Weakly similar to T30958 RhoA-bleb	1.21	2.38
422363	TS5979	Hs.115474	replication factor C (p200) 1) 3 (8	1.58	2.15
434831	AA245508	Hs.272397	KNA4070 gene product	1.65	1.75
412055	AA009607	Hs.271936	ESTs, Weakly similar to ALU1_HUMAN ALU 5	1.36	2.65
445468	AW450439		ESTs	1.52	2.50
444550	BE250716	Hs.87614	ESTs	3.00	2.28
417259	AW063638	Hs.51600	chemokine st1a1a1 proteoglycan 2 (vers	1.50	3.02
430233	AW067802	Hs.236443	Homo sapiens mRNA; cDNA DKFZp554H1053 (f	1.24	2.95
413444	BE141019		gb.MR0-HT0067-201085-002-b10 HT0067	1.68	2.80
433844	AA610175	Hs.170647	Homo sapiens cDNA FLJ12165 fs, clone MA	1.45	2.01
427055	AI301740	Hs.173381	diacylglycerol-induced-like 2	1.11	2.58
454244	RS1604	Hs.302842	KNA1458 protein	1.00	2.02
425503	AA394183	Hs.76873	ESTs	2.58	4.08
422640	BE077458		gb.CR1-HT0065-090500-015-b04 B T0605 Homo	3.48	2.46
401545	W21874	Hs.247057	ESTs, Weakly similar to Z195260A B cell	3.13	1.48
437312	AA003560	Hs.245180	ESTs	1.10	2.05
454246	TZ2251	Hs.156882	ESTs	1.22	2.08
447620	AW259551	Hs.224955	ESTs	1.80	2.18
444700	NM_003645	Hs.11729	beta-galactosidase Y ligase, very long-	1.72	2.81
436238	AW057451	Hs.107125	plasma membrane vesicle associated protein	1.59	1.90
415112	AW245188	Hs.165577	Homo sapiens cDNA FLJ14743 fs, clone NT	1.65	2.98
432877	AW574111	Hs.252477	ESTs	1.63	2.75
412085	AW851667		gb.CM3-HT0089-110500-179-409 NT0089 Homo	1.40	2.08

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5	431421	AW999118	Hs.106144	ESTs, Weakly similar to unnamed protein	1.96	3.58
	429714	AW367812	Hs.199561	ESTs, Weakly similar to ALU7, HUMAN ALU S	1.24	2.10
	429713	AW875443	Hs.222269	secreted modin or calcium-binding protein	1.49	2.09
	427963	AW920067	Hs.119304	zinc-finger protein 175	1.01	2.78
	439373	AI751438	Hs.412171	Homo sapiens mRNA full length insert cDN	1.54	2.57
10	413196	AA127386	Hs.100608	gbczn00400.1 Stratagene lung carcinoma	1.04	2.18
	433340	AA900898	Hs.195602	ESTs	2.03	2.43
	443005	AJ027184	Hs.200916	ESTs	1.42	2.10
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.58	3.43
	427373	AG007972	Hs.130760	myosin phosphatase, target subunit 2	2.08	1.70
20	413916	N46813	Hs.75615	agglutinin C-II	0.70	0.42
	418332	RC4936	Hs.76253	ESTs	2.74	2.43
	429632	BE737660	Hs.170526	mossa	1.28	1.52
	456563	AF179697	Hs.104105	Male (mouse) homolog 2	1.42	2.02
	447214	AI367288	Hs.273621	Homo sapiens cDNA: FLJ21350 fls, clone C	1.14	2.10
25	443254	WV2608	Hs.172762	ESTs	2.04	2.50
	443851	WJ22162	Hs.259520	ESTs	2.04	3.08
	421021	AA608018	Hs.105302	ESTs	1.41	2.04
	418741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.61	1.21
	432027	AL596678	Hs.272363	KIAA0657 protein	1.70	2.76
30	432585	AA721140	Hs.49930	ESTs, Weakly similar to putative p150 ^{ih}	1.60	2.95
	417042	CT5553	Hs.113029	ribosomal protein S25	2.22	3.20
	443574	UB3993	Hs.321709	putative receptor P2X, ligand-gated ion	1.21	2.51
	428372	AA461659	Hs.99253	ESTs	1.29	2.43
	424290	AA338396	gb:EST43366 Fetal brain 1 Homo sapiens c	1.62	2.03	
35	428515	AV080568	gb:EST381733 MAGE sequences, MAG/K Homo	1.72	2.52	
	455649	BE065051	gb:BC1-GT03131 10500-017-004 BT0313 Homo	1.65	3.03	
	414665	AA160873	Hs.332053	serum amyloid A1	1.36	1.08
	416286	AA250114	Hs.869182	Homo sapiens cDNA: FLJ21578 fls, clone C	1.04	2.03
	428655	U46929	Hs.211592	myosin, light polypeptide kinase	4.94	4.34
40	433924	AA618304	Hs.258765	ESTs	1.44	2.40
	452683	AI089575	Hs.5071	proteoglycan membrane binding protein	1.48	2.48
	136437	AJ207768	Hs.343258	sialyltransferase 4B (beta-galactosidase	1.36	2.33
	432314	AA335447	Hs.512980	ESTs	0.96	2.78
	400681		NM_025030 Homo sapiens hypothetical prot	1.70	3.15	
45	426477	AA379464	gb:EST92365 Skin tumor 1 Homo sapiens cD	2.01	2.37	
	454741	BE154398	gb:CM6-H10342-012299-050-405 HT0342 Homo	2.12	3.44	
	423877	AA333322	gb:EST17263 Embryo, 8 week 1 Homo sapien	1.36	2.13	
	452395	AL077022	Hs.24950	regulator of G-protein signaling 5	2.13	3.26
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in calci	1.90	2.23
50	415157	CB3257	gb:HUM514B00B Clontech human placenta po	1.29	2.30	
	418226	AW994005	Hs.237534	ESTs	1.74	2.37
	454390	AB220713	Hs.555956	KIAA0098 protein	1.47	1.36
	436143	AA705245	Hs.192185	ESTs	1.46	2.45
	436261	BE515065	Hs.296585	nuclear protein (KRED repeat)	1.43	2.07
55	450735	AI732321	SRF (box determining region Y)-box 4	1.38	2.02	
	420136	AB980190	actin, alpha 2, smooth muscle, aorta	2.70	1.68	
	447100	AI381801	Hs.167130	hypothetical protein	1.66	2.03
	453577	AL043049	gb:DNF2743A1523_r1 434 (synonym: hlec3)	1.41	2.75	
	408322	AI541214	Hs.45120	Small proline-rich protein SPRK (human,	1.59	1.38
60	412632	AL120378	Hs.74294	aldehyde dehydrogenase 7 family, member	1.61	2.51
	422291	NM_004129	Hs.128590	guanylate cyclase 1, soluble, beta 2	1.64	2.83
	456172	R93050	gb:gyq5502.1 Scanes fetal liver spleen	1.46	2.68	
	452123	AI267815	Hs.36022	ESTs	1.24	1.93
	433900	AA721688	Hs.257761	ESTs	1.76	2.86
65	408436	RC1194	Hs.77885	phosphatidylinositol binding clathrin as	1.21	2.35
	417123	BE326521	Hs.159450	ESTs	1.46	2.09
	438023	T81819	Hs.302251	ESTs	2.68	2.70
	454150	AA131853	Hs.154088	hypothetical protein FLJ22755	4.40	2.50
	444094	AI565784	Hs.202394	ESTs	4.93	1.26
70	429115	AW875921	Hs.153800	ESTs	1.06	2.53
	422259	AA307564	gb:EST178458 Colon carcinoma (HCC) cell	1.80	3.03	
	451164	AA215512	ESTs, Weakly similar to T46471 hypophos	1.47	1.17	
	417950	AL041219	Hs.82222	serin domain, immunoglobulin domain (Ig)	2.52	2.70
	455542	BE083698	gb:CA141612-0206-065-001 ET0295 Homo	1.70	2.70	
75	443367	BE139135	ESTs	1.48	2.32	
	420995	AA262495	Hs.89014	ESTs	1.45	1.51
	407329	AA579061	Hs.269534	ESTs, Weakly similar to ALLD, HUMAN III	1.13	2.36
	436197	CI5161	Hs.283040	hypothetical protein FKBP25-43	0.99	2.75
	413357	AW016773	Hs.74375	low molecular mass ubiquitin-binding pr	1.60	2.06
80	412656	AF060011	Hs.74375	dishevelled 1 (homologous to Drosophila	1.32	1.13
	427377	AL077029	Hs.177543	antigen identified by monoclonal antibody	1.24	0.79
	412200	R06110	Hs.187462	ESTs, Weakly similar to 380222 hypothetical	1.54	1.35
	425266	AA368546	ESTs	1.50	2.25	
	411590	T96183	gb:gye0067.1 Stratagene lung (G37210) H	1.22	2.53	
85	422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.27	2.20
	420256	U64722	Hs.76206	cathepsin 5, type 2, VE-cathepsin (vascula	1.59	2.11

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5	419900	AI469950	Hs.170698	ESTs	1.30	2.68
	410805	AW040742	Hs.84254	acidic protein rich in leucines	1.15	2.28
	452560	BE077084	Hs.99969	ESTs	1.44	2.58
	449428	DT7406	Hs.12123	calponin 1, basic, smooth muscle	4.02	1.00
10	424336	AW1618426	Hs.6953	gelsolin/actinogen, gelsolin subfamily a, 3	1.10	2.00
	447400	AK000322	Hs.16457	hypothetical protein FLJ20315	1.45	1.28
	422522	AI023428	Hs.34549	ESTs, Highly similar to S945411 clone 4	1.82	2.10
	443696	AW607444	Hs.136322	ESTs	1.59	2.01
15	435694	AF198701	Hs.222222	ESTs	1.34	2.40
	420168	AF217508	Hs.95594	serine carboxypeptidase vitellogenic-like	1.58	2.45
	430325	AF004562	Hs.235356	synactin binding protein 1	1.34	2.43
	439022	AA339559	Hs.173504	ESTs	2.76	2.40
20	422583	AA278327	Hs.135237	ESTs, Moderately similar to Y140_HUMAN H	1.78	2.65
	429494	AA793955	Hs.126058	ESTs	1.50	2.40
	420589	H79979	Hs.68678	ESTs	1.26	2.28
	448988	Y06763	Hs.22705	gamma-aminobutyric acid (GABA) A receptor	1.72	1.23
25	439943	AW083789	Hs.124622	ESTs	1.45	2.84
	442300	AI765908	Hs.120165	ESTs	1.24	2.35
	449514	AI589490	Hs.197703	ESTs	1.12	2.22
	444363	AI142827	Hs.143595	ESTs	1.32	2.08
30	442479	AF054238	Hs.145038	smoothelin	1.59	1.19
	437321	AA768995	Hs.292605	ESTs, Weakly similar to 2109260A B cell	1.28	2.07
	431928	AW972724	Hs.240443	gb:EST384916 MAGE resequences, MAGL Homo	1.52	2.63
	433840	AW350126	Hs.240443	Homo sapiens cDNA: FLJ23538 fls, clone L	1.89	1.30
35	415901	AW8396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.71	2.19
	437189	AI110173	Hs.305337	Homo sapiens mRNA: cDNA DKFZp554H0516 (f	1.48	2.50
	457450	AW024153	Hs.146127	ESTs	1.07	2.80
	456678	AF141305	Hs.173736	ancient ubiquitously protein 1	1.44	2.35
40	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 feni	0.95	3.00
	450944			Target Exon	1.48	2.45
	408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	1.38	2.20
	446882	AW205932	Hs.211198	ESTs	1.28	3.00
45	431380	AW610282	Hs.291003	ESTs	1.43	2.84
	442027	AI652826	Hs.126395	ESTs	1.18	2.43
	422578	AW980454	Hs.222830	ESTs	1.55	1.18
	441455	AW254903	Hs.127039	ESTs	2.80	1.73
50	417900	BE250127	Hs.82906	CCD20 (cell division cycle 20, S. cerevisiae)	1.36	1.18
	439499	AW827419	Hs.235070	ESTs	1.20	2.28
	440495	AA887212	Hs.14161	hypothetical protein DKFZp434i1930	1.74	2.78
	449448	R19156	Hs.207798	ESTs	1.12	2.23
55	439564	W77911	Hs.110008	ESTs	1.34	2.85
	423225	AA852804	Hs.126359	Thy-1 cell surface antigen	1.24	1.09
	436139	AA765796	Hs.120365	ESTs	1.20	2.10
	459988	AI174881	Hs.190233	ESTs	1.14	2.15
60	437191	NM_005846	Hs.331555	serine protease inhibitor, Kazal type, 5	1.21	2.18
	411652	AW855353		gb:CM3-CT0275-191099-024-f10 CT0275 Homo	1.85	1.94
	420732	AA789135	Hs.88850	ESTs	1.65	2.71
	426281	AW373472		gb:RC3-BT0523-181299-01-412 BT0523 Homo	1.55	2.30
65	424415	NM_001575	Hs.146580	enolase 2, (gamma, neuronal)	1.56	1.39
	424927	AW973668	Hs.153850	hypothetical protein C3D122.4	1.58	1.24
	450946	AA374599	Hs.127698	ESTs, Moderately similar to 2109260A B c	1.02	2.25
	428423	AI075517	Hs.184276	salivary center family 5 (iodine/hydrogen	1.70	2.39
70	415361	F06724		gb:HS2110221 normalized infant brain cDN	1.34	2.40
	408490			C50101926(g17511572)g175115724245 probable	1.28	2.40
	410855	X87795	Hs.66718	RAD54 (S.cerevisiae)-like	1.52	2.00
	440010	AA534935	Hs.127235	hypothetical protein FLJ12879	1.12	2.20
75	422958	AW380520	Hs.33944	ESTs, Weakly similar to 138022 hypothetical	1.28	2.38
	426340	Z97989	Hs.165370	FYN oncogene related to SRC, FGR, YES	1.88	2.18
	416889	AW250318	Hs.80395	mat, T-cell differentiation protein	1.65	1.16
	451870	AI820991	Hs.8377	ESTs	1.24	2.03
80	444051	AI541928	Hs.26278	ESTs	1.05	2.13
	410753	AW881895	Hs.65352	intra-acln 1 (SH3 domain protein)	2.00	3.13
	452222	AW805287	Hs.21432	SEX gene	1.25	1.10
	433010	AW970018		gb:EST382097 MAGE resequences, MAGK Homo	1.36	2.41
85	432074	AA641092	Hs.257339	ESTs, Weakly similar to 138022 hypothetical	1.14	2.03
	438855	AW945273	Hs.5441	Homo sapiens cDNA: FLJ15394 fls, clone PL	2.24	1.77
	443719	AA222235	Hs.153595	hypothetical protein MGC15436	1.52	2.65
	402685			Target Exon	2.04	2.46
90	424528	AW073971	Hs.236564	ESTs, Weakly similar to KIAA1204 protein	1.65	2.05
	422058	H07319	Hs.104520	Homo sapiens cDNA: FLJ15394 fls, clone PL	1.85	1.58
	451225	AI433594	Hs.253608	ESTs	1.79	2.70
	441078	AI453268	Hs.323409	Homo sapiens cDNA: FLJ1411 fls, clone MA	1.44	2.58
95	409426	H83042	Hs.49605	ESTs	1.28	2.05
	422297	AW691290		p30 DBC protein	1.20	2.73
	408711	AW375661	Hs.63335	ESTs, Moderately similar to A65010 X-link	1.20	2.08
	425696	AW383332	Hs.171644	Homo sapiens cDNA: FLJ22295 fls, clone H	1.35	2.58
100	417324	AW265494		ESTs	1.68	1.25

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408283	BE141579		gbc/QV2-HT0083-071299-010-405 HT0083 Homo	1.25	2.65
415166	NM_003652	Ha.78268	carboxypeptidase Z	1.34	1.09
408300			Target Eovs	1.61	2.47
411880	AW872477		gbc-hn30X03.1 NCL_CGAP_Thyl Homo sapiens	3.60	4.03
422287	F16365	Ha.114346	cytochrome c oxidase subunit VIIa polype	2.16	1.44
422567	AF111178	Ha.118407	glycylpro	1.57	2.03
430665	AA732624	Ha.105932	ESTs	1.08	2.75
405335			Target Eovs	0.93	2.13
447733	AF157482	Ha.19400	MAC2 (mitotic arrest deficient, yeast, h	1.18	1.07
471717	NA6778		gbc/y526Z2.1 Soares_multiple_sclerosis_	1.70	2.85
411590	AA665253	Ha.136075	RNA_L2 small nuclear	2.12	2.78
442243	AA62498	Ha.132056	ESTs	1.15	1.83
442074	AL106963		FSH primary response (LRRF1, rat) homolo	1.37	1.43
408916	AW295232	Ha.429	ATP synthase, H transporing, mitochondr	1.63	2.23
447979	AI143466	Ha.125060	ESTs	1.40	2.08
415373	T19064		gbc-NB2078-SR Normalized infant brain, S	1.00	1.85
431089	BC041395		ESTs, Weakly similar to unknown protein	1.57	2.57
434969	AW974949	Ha.186594	ESTs, Weakly similar to 138022 hypoheli	1.30	2.30
416311	D60529		gbc-ILM0814068 Human fetal brain (Fujawa	1.58	4.35
444614	RA4284	Ha.2730	heterogeneous nuclear ribonucleoprotein	1.80	2.58
452208	NM_006895	Ha.81182	histamine N-methyltransferase	1.24	2.36
410583	AW770290	Ha.36259	ESTs, Moderately similar to JCE5236 galac	1.56	4.33
430410	AF091144	Ha.334456	lyptase beta 1	1.91	1.58
408139	AA451566		RA89-beta protein	1.42	2.14
432621	AI298501	Ha.12897	ESTs, Weakly similar to T45428 hypoheli	2.06	1.94
441584	AW148329	Ha.175208	ESTs	1.12	2.05
446940	D60438	Ha.34779	ESTs	1.86	2.70
453022	AA831499	Ha.118489	ESTs	2.02	1.75
444006	BE544655	Ha.236572	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.54	1.29
442294	AI620718	Ha.19564	ESTs	3.60	3.78
402065			C18000504.gp2627439gbcAA866683.1(AF	1.36	2.53
411910	AW876354		gbc-PM4-P10019-141299-009-F00 PT0019 Homo	2.00	2.63
445608	AW979165		gbc-EST386274 MAGE resequences, MAGN Homo	1.70	3.04
425105	AI078765	Ha.21812	ESTs	1.46	2.11
425131	BE282230	Ha.99163	ESTs	2.04	2.65
440326	NM_003812	Ha.7184	a disintegrin and metalloproteinase doma	1.17	2.55
420447	AA567305	Ha.88448	ESTs	1.85	2.58
420055	AA420564	Ha.101763	ESTs	1.08	2.15
427110	AI597395	Ha.111776	secreted protein, acidic, cysteine-rich	1.75	1.82
435691	AI/677766	Ha.262133	ESTs, Moderately similar to 178885 serin	1.08	2.10
403260			C10001011.gp4755212[refNP_004411.1] d	0.97	2.45
408175	W30069	Ha.19068	hypothetical protein D1K7Z657D2416	1.42	1.41
423260	AA538177	Ha.274469	effector receptor, family 5, subfamily	1.26	0.95
443441	AW321196	Ha.52195	ESTs	1.62	2.13
419826	AA159530	Ha.53765	Igkoma -IMGC fusion partner	1.72	2.80
442526	AI589836	Ha.144763	ESTs	1.97	3.33
453381	AA236908		gbc/y526Z10.1 NCL_CGAP_GCE1 Homo sapiens	1.16	1.55
429433	AA310550	Ha.163748	hypothetical protein FLJ22490	1.08	2.20
432529	AI/985607	Ha.162245	ESTs	1.36	2.25
424951	AI/954082		gbc-EST376155 MAGE resequences, MAGN Homo	2.22	2.58
420785	H59533	Ha.191346	ESTs	1.25	2.15
411347	AW688126		gbc-QV2-LT0051-240300-097-01 LT0051 Homo	1.38	2.38
438742	AW204126	Ha.196543	ESTs	1.10	2.30
414500	AW452420	Ha.248678	ESTs	2.01	3.09
443294	AI/369813	Ha.64783	ESTs, Weakly similar to T42705 hypoheli	0.65	0.43
422049			Target Eovs	2.26	2.00
428400	AW504940	Ha.201698	transcription factor 20 (AR1)	1.16	2.00
423916	AW963496	Ha.17235	Homo sapiens clone TCCCA00176 mRNA sequ	1.59	1.05
432495	AW673537	Ha.106734	ESTs, Weakly similar to B17745 phenomex	1.00	2.05
414640	R27316	Ha.128323	hillyshahoon-c-fgq1 related with YRP	1.99	2.99
426711	R69414	Ha.56928	3'-untranslated repeat containing 5	1.77	1.83
448609	AW139420	Ha.7972	IGAA071 protein	1.14	2.26
443859	NM_013409	Ha.95914	folistatin	1.17	1.05
411141	AW195581		gbc-RC5-ST0203-140200-013-G04 ST0203 Homo	1.44	2.40
440116	AI/33551	Ha.295959	immunoglobulin gamma G	1.15	2.05
417944	AI/077195	Ha.82085	collagen, type V, alpha 2	1.10	1.37
429640	UB1508	Ha.2483	angiopoietin 1	1.92	2.98
410054	X53416	Ha.195454	Itamrin A, alpha (actin-binding protein-	1.51	1.29
455216	AI/35178	Ha.128520	ESTs	1.40	1.15
443114	AI/033377	Ha.153208	ESTs	1.38	2.05
427788	AA412397	Ha.116858	ESTs	1.45	1.85
435913	W95005	Ha.269559	ESTs, Weakly similar to S55557 alpha-1C-	1.83	3.90
457549	W65171	Ha.717141	ESTs, Weakly similar to G3845 melanoma	1.01	2.90
415203	AA448718	Ha.190151	ESTs	1.94	2.45
412510	AI/050689	Ha.133538	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	2.20
413885	BE177442		gbc-RC1-IT0095-200400-012-01 IT0095 Homo	1.48	2.80
426229	AA669615	Ha.214226	ESTs	1.36	2.50

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	40866	AW22096	Hs.255036	ESTs	1.93	2.92
	412657	A170348	Hs.128052	ESTs	1.72	1.60
	427340	BE167242	Hs.47099	hypothetical protein FLJ21212	1.46	2.13
5	412602	BE098183	gb:U9-BN0147-250403-214-c01 BN0147 Homo	0.90	2.05	
	451141	AW772113	Hs.247186	ESTs	2.38	1.95
	412626	AA114945	Hs.151839	ESTs	1.75	2.15
	405667	AA623763	Hs.7055	Target Exon	2.62	3.79
	407400			Target Exon	1.24	2.08
10	426796	S78234	Hs.172405	cell division cycle 27	2.14	1.63
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.14	2.28
	446401	AA96969	Hs.346254	ESTs	2.50	2.83
	450632	AW670602	Hs.105421	ESTs	0.55	0.39
	441057	AL045897	Hs.126483	ESTs	1.68	2.13
15	438725	AA815163	Hs.127307	ESTs	1.31	2.65
	450062	AV001043	Hs.200854	ESTs	1.30	2.48
	441214	AB02646	Hs.129136	ESTs	1.43	1.71
	437173	AV085650	Hs.161762	Homo sapiens mRNA: cDNA DKFZp964B0262 (f	1.22	2.30
	414607	X90726	Hs.77757	po/p (Drosophila)-like kinase	1.35	1.49
20	423622	BE154847		gb:PM1-HIT0345-121159-001-d05 HIT0345 Homo	1.57	2.30
	450835	BE32773	Hs.25584	hypothetical protein FLJ10767	1.40	1.12
	444014	AB09718	Hs.130315	ESTs	2.30	1.78
	431603	AA807955	Hs.325984	EST	1.26	2.03
	408697	AV419069	Hs.200670	ESTs	1.35	2.80
25	444312	RA4007		ESTs	1.95	2.07
	445286			CB001909.gi704441(hi)h[BAA19903.1] (D296	2.25	2.22
	438813	M27346		gb:Homo sapiens (clone HGP09/HGP332) T ce	1.03	2.43
	445634	AL038823	Hs.12840	Homo sapiens germline mRNA sequence	1.00	2.16
	426046	AA833655	Hs.206868	Homo sapiens cDNA FLJ14055 fs, clone H-E	1.58	2.73
30	451907	AB22265	Hs.50749	ESTs, Moderately similar to ALU7_HUMAN A	1.74	2.65
	410796	AA226351	Hs.340560	ESTs	1.26	2.12
	422431	AT759410	Hs.221481	ESTs	1.80	3.58
	417557	AA225622	Hs.293589	ESTs	1.32	2.14
35	45313	AV094409	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	1.48	2.57
	415479	P10442	Hs.4540	ESTs	1.83	2.01
	450433	AV444538	Hs.231863	ESTs	1.31	2.58
	410581	AA016582	Hs.125036	tumor endothelial marker 7 precursor	1.54	1.62
	455407	AV069813		gb:PM2-DT0023-050400-003-b10 DT0023 Homo	1.32	2.15
40	417552	R0916	Hs.166510	ESTs	1.50	2.63
	429200	AB22965	Hs.163475	Homo sapiens clone Z5061 mRNA sequence	1.94	2.70
	432351	AT732734	Hs.339827	Human DNA sequence from clone RP5-68.L22	0.95	2.38
	456283	U68162	Hs.84171	myeloproliferative leukemia virus oncoge	1.22	2.13
	436535	L06076		gb:Homo sapiens mRNA fragment	2.14	1.95
45	416564	AV795793	Hs.2575	Homo sapiens cDNA FLJ12257 fs, clone MA	1.28	1.93
	435200	AA670310	Hs.145903	ESTs	1.16	2.13
	457635	AV560976	Hs.3666	hypothetical protein	1.57	3.10
	444930	BE18538	Hs.301183	molecule possessing onkyrin repeats indu	0.95	2.45
	445919	AA373630	Hs.167150	ESTs	1.56	3.26
	418552	AV074443	Hs.87134	ESTs	1.86	2.20
50	456387	AV382787		gb:PM2-HIT0339-081159-001-h05 HIT0339 Homo	1.30	2.50
	434973	AV449285	Hs.313636	EST	1.11	2.65
	456383	BE489595	Hs.144153	ESTs	1.44	3.30
	447100	BE382685	Hs.135849	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.20	2.71
	431996	AL122067	Hs.272304	Homo sapiens mRNA: cDNA DKFZp564CC371 (f	1.24	2.27
	427681	AB018263	Hs.180038	tumor necrosis factor receptor superfam	1.70	1.68
	455148			CB001690.gi76754449(hi)h[IP_03760.1] h	2.00	0.68
	451514	AA764950	Hs.119698	ESTs	1.43	3.00
	451233	AA047221	Hs.55752	ESTs	1.38	2.20
60	446556	AB14373	Hs.164175	ESTs	1.33	3.93
	446211	BE384592	Hs.6451	PRO0659 protein	1.48	2.73
	416283	Q79895	Hs.83942	cathepsin K (pyronidocytoside)	1.33	2.68
	409619	AV444670	Hs.336655	ESTs	1.27	1.51
	450414	AV07735	Hs.21446	KIAA1716 protein	1.50	1.24
	452229	AV054938	Hs.172616	neuregulin 1	2.01	3.70
65	435112	AV076145	Hs.143198	inhibitor of growth family, member 3	1.22	1.30
	458606	AA448624	Hs.189935	ESTs	0.96	2.04
	439910	H60765	Hs.333997	ESTs	1.28	2.16
	437866	BE764111	Hs.31314	retinoblastoma-binding protein 7	1.06	2.82
	441354	AA331221	Hs.128813	ESTs	1.20	2.26
	426851	AL138153	Hs.203410	ESTs, Moderately similar to AA7562 B-cl	1.50	1.83
	438272	AL167361	Hs.143700	ESTs, Weakly similar to AA6284 reverse 1	1.34	2.51
	426642	X85264	Hs.211579	melanoma cell adhesion molecule	1.18	1.18
	422121	A757949	Hs.179633	ESTs	1.18	2.26
75	411164	AV625117		gb:PM2-ST0303-170100-003-g03 ST0303 Homo	1.18	2.21
	455571	AT257077	Hs.288327	eukaryotic translation initiation factor	1.17	1.57
	430570	AL417681	Hs.292464	ESTs	1.49	3.17
	431995	AL080157	Hs.272302	hypothetical protein	1.52	2.11

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	406432	AJ289116	CD1E antigen, c polypeptide	2.31	2.63
	457766	AA682670	ESTs	0.98	2.38
	433789	AA580465	ESTs	1.46	1.07
	338982	AW018722	SH2 domain-containing phosphatase anchor	1.36	2.13
5	401473		Target Exon	1.47	2.04
	444816	Z48633	Hs.283742	1.64	2.15
	338029	H61502	chromosome 5 open reading frame 4	1.44	2.25
	431830	Y16845	small inducible cytokine subfamily A (cy	1.26	2.21
	450817	N71597	ESTs, Weakly similar to ZNF1_HUMAN Zn/C	2.20	2.90
10	404427		C80000687:g15453573refNP_006120.1.bo	0.74	0.81
	433658	AW970093	ESTs	1.45	2.55
	433723		Target Exon	1.60	2.28
	438956	AW977385	ESTs	1.17	1.64
	411974	AW880414	acidic protein rich in leucines	1.54	2.08
15	412528	AI123476	ESTs	1.72	2.85
	446425	AW293364	ESTs	1.25	1.31
	424951	AA724471	ESTs	0.62	0.37
	443100	AI033188	g100w94c08.s1 Soares_fetal_liver_splein_	1.15	2.34
	440332	AI220225	ESTs	1.07	2.00
20	414781	CS0917	KIAA0127 gene product	1.04	3.43
	421893	NM_001078	vascular cell adhesion molecule 1	1.15	2.53
	424265	AF173901	hairlyushances-of-split related with YRP	1.26	2.00
	446667	BE161878	ESTs	1.12	2.13
	423939	AA052258	Homo sapiens cDNA FLJ1271 fls, clone: OV	2.26	1.29
25	430190	AA780320	ESTs, Moderately similar to KBF3_HUMAN H	1.44	2.07
	406672	M32053	g2/Human H19 RNA gene, complete cds.	1.38	2.11
	417086	AA194446	ESTs, Weakly similar to S55025 acoulin,	2.12	3.30
	449610	AI381109	ESTs, Weakly similar to I39C22 hypobell	1.14	2.33
30	427674	NM_003528	H26 fibrose family, member Q	1.00	1.24
	422526	AA511763	ESTs	1.00	1.29
	430317	AF086127	ESTs, Weakly similar to T47156 hypobell	1.26	2.12
	409126	AA063426	g1027C008.s1 Soares_pinea_gland_M3HPG	1.28	2.20
	412093	BE242691	ESTs	0.87	2.58
	427189	AA256128	ESTs	1.38	2.07
35	426096	D87436	h1p2	2.00	2.25
	402551		NM_006012:Homo sapiens receptor tyrosin	0.80	0.82
	402760		Target Exon	1.44	2.95
	423802		NM_002206:Homo sapiens hypothetical pro	1.53	1.27
40	423802	AW014252	ESTs	1.44	2.03
	424244	AV847184	hypothetical protein hCLA4so	1.40	1.18
	430984	BE59614	hypothetical protein	1.30	2.15
	457297	AW968188	go:EST380593 IMAGE neocsequences, MAGI Homo	1.64	3.17
	415664	AT133807	g1020B008.y5 Stratagene ovarian cancer	1.00	2.20
45	426273	AI174961	ESTs	1.19	1.16
	406187		NM_014272:Homo sapiens a disintegrin-lik	1.31	1.35
	413939	AL047051	ESTs, Weakly similar to ALL7_HUMAN ALU S	2.44	1.85
	427596	AA448506	extracellular glycoprotein EMILIN-2 prec	2.06	1.50
	406049	AW076098	desmoglein (DPI, DPII)	2.01	3.90
	409002		Target Exon	1.73	2.09
50	408294	AW248254	protein kinase PKIbeta	1.28	1.31
	431377	AW178807	ESTs	1.40	2.70
	421458	AW389183	ESTs	1.44	2.08
	427530	AA405093	ESTs	1.07	1.12
	431957	AI002104	hypothetical protein FLJ11292	1.27	2.89
55	422283	AW111307	CDCA5 (cell division cycle 45, S.cerevis	1.74	2.58
	416900	AA448958	NEU1 protein	1.74	1.15
	423314	AI400661	disintegrin metalloproteinase with throm	1.44	2.53
	451690	AW451469	ESTs	1.41	2.49
	454682	AW812715	g10RC4-ST0165-271095-01-g01 ST0185 Homo	1.35	2.85
60	454413	H635972	FNAS-123	1.79	2.03
	416981	AW877206	ESTs	1.52	2.10
	415908	H06623	ESTs	1.37	2.13
	438942	AW875398	PRO0669 protein	1.80	1.55
	407616	AW054922	Homo sapiens cDNA FLJ12366 fls, clone MA	1.66	3.18
65	429177	AA441527	ESTs	1.74	1.19
	448357	NZ0169	RAE36, member RAS oncogene family	0.77	0.73
	422008	AJ000534	sarcoglycan, epsilon	1.52	4.08
	434481	AA744046	ESTs, Weakly similar to I78855 seminoh	1.66	2.16
	413489	BE144229	g101RC4-HT0165-140200-035-c04 HT0165 Homo	1.28	2.23
70	402651		Target Exon	1.11	1.19
	441183	BE562910	Homo sapiens clone CDAP614 cDNA sequen	1.20	1.20
	456034	AA505979	g10UH-H-6103-aka-a-12-AJ.s1 NCL_GCAP_Sa	1.58	2.53
	420511	AA594636	ESTs	1.46	2.15
	422981	BE178434	ESTs, Moderately similar to G92654 ribos	1.42	2.30
75	437908	AI082424	ESTs	1.38	2.21
	423052	M28214	RAE36, member RAS oncogene family	0.74	0.43
	401927		CT70C0914:g18394367refNP_058548.1) s	2.26	2.14

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	432987	AA572549	Hs.207565	ESTs	1.52	2.28
	438159	AF087972	Hs.120838	ESTs	2.03	2.08
	415357	H22757	Hs.13471	ESTs	1.62	2.07
	442327	AA91745	Hs.42522	ESTs	1.48	2.88
	430186	AB020696	Hs.234791	KIAA0885 protein	1.46	2.23
	426971	AI80986	Hs.243209	ESTs, Weakly similar to NPA1_HUMAN NEURO	1.06	2.13
	428687	AI060823	Hs.115226	insulin like growth factor binding prote	1.61	1.37
	432954	AI076345	Hs.214195	ESTs	1.19	2.84
	429540	AL335542	Hs.248169	olfactory receptor, family 2, subfamily	1.25	1.44
10	414169	AA138169	Hs.145336	ESTs	1.59	2.51
	419882	AA687313	Hs.190043	ESTs	1.20	2.50
	428930	AF161364	Hs.142375	ESTs	1.67	1.77
	416773	T35746	Hs.325474	Target CAT	1.35	2.02
	436776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	1.32	2.10
15	428712	AI006131	Hs.190452	KIAA0365 gene product	1.41	1.52
	408839	AY077384	Hs.104207	gbcxp81N05.x1 NCLCGAP_Ov09 Homo sapiens	1.14	2.03
	455492	AI025391	Hs.221615	ESTs	1.17	2.21
	434654	AB025942	Hs.135368	Homo sapiens clone L5 polyadenylated HER	1.62	2.31
20	457567	AW396074	gbcQV1-DTC009-010200-067-c12 DT0099 Homo	1.80	3.73	
	452426	AI04823	Hs.31257	diiodoanil cyclochrome b	2.15	1.84
	418559	AA225048	Hs.104207	ESTs	1.64	2.33
	435959	AB037500	Hs.5462	protein kinase C and casein kinase subel	1.07	1.15
	451984	R05571	Hs.27408	Homo sapiens mRNA; cDNA DKFZp566F1946 (f	1.16	1.22
25	420785	AI670057	Hs.155882	ESTs	2.24	2.55
	455396	AA286653	Hs.166594	ESTs, Weakly similar to APXL_HUMAN APICA	1.07	1.14
	429446		Hs.102526	Homo sapiens hypothetical protein	2.14	1.93
	429405	AW268331	Hs.263403	ESTs	1.28	1.07
	439732	AW625904	Hs.167641	hypothetical protein from EUROMAGE 1703	0.85	0.77
30	416784	AA334592	Hs.79514	laminin	1.66	1.27
	422531	AW967280	Hs.235994	ESTs, Weakly similar to HERC2 [H sapiens	1.20	1.25
	415506	F_2295	Hs.12256	ESTs, Moderately similar to ALLU1_HUMAN A	1.03	2.35
	428671	BE297851	Hs.185422	zinc finger protein 179	1.26	2.20
	420007	H13700	Hs.31235	ESTs, Weakly similar to YES4_HUMAN HYPOT	1.60	2.23
35	400650			Target Exon	1.22	1.03
	404580			isochlorophthalane synthase gene (T	1.00	1.00
	407680	AI064284	Hs.275153	ESTs	1.02	2.28
	410420	AA224053	Hs.172405	cell division cycle 27	1.64	1.00
	421234	AA307153	Hs.182000	ESTs	1.76	1.45
40	426751	AA384610	Hs.46519	ESTs	1.12	2.15
	430439	AL133560		DKFZP434B051 protein	1.00	1.00
	434308	AI659131	Hs.197733	hypothetical protein MGC2849	1.00	1.00
	438915	AA280174	Hs.265681	Williams-Beuren syndrome chromosome regi	1.40	1.00
	440304	BE159364	Hs.126335	ESTs	1.00	1.00
45	441659	AI051128	Hs.127572	ESTs	1.00	1.73
	443383	AI792453	Hs.166507	ESTs	2.04	1.00
	445580	AI702686	Hs.201955	ESTs	1.00	1.00
	453180	AI283307	Hs.235894	H2B histone family, member L	1.00	1.00
	456513	AA271743	Hs.86861	ESTs	1.00	1.40
50	457231	AI427202	Hs.301659	proline synthetase co-transcribed (bacte	0.98	0.63
	459585	W27088	Hs.209694	ESTs	1.00	1.00
	425317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ12143 fs, clone C	1.00	1.00
	430371	MC2610	Hs.245177	H2 histone family, member L	1.14	1.40
	406378	AI0571303	Hs.252001	ESTs	1.06	1.60
55	411920	AI0878263		gb-PM4-PT0015-131299-006-E09 PT0019 Homo	0.82	0.45
	457369	AI070369		gb-EST383074 MAGE sequences, MAGK Homo	0.92	0.71
	408655	BE302544	Hs.262244	ESTs, Weakly similar to prelipidglycan re	1.00	2.10
	430866	AA336519	Hs.158064	nuclear receptor subfamily 1, group I, m	1.00	1.00
	446279	AI341135	Hs.158064	ESTs	1.06	2.02
	441851	AI015418	Hs.127556	ESTs	1.13	2.03
60	402039			Target Exon	0.44	6.36
	437133	AB016319	Hs.45480	KIAA0775 protein	0.95	0.63
	438069	W05391		nuclear receptor subfamily 1, group L m	3.12	1.00
	405842	R27430	Hs.271565	ESTs	1.00	1.00
65	428769	AI020715	Hs.106771	ESTs	1.00	1.49
	442668	AI022701	Hs.339584	ESTs	1.62	1.27
	439559	AI0364615	Hs.773921	ESTs, Weakly similar to 2105260A B cell	1.00	1.33
	428658	R10845	Hs.72579	zinc finger protein 177	1.24	2.25
	419015	T75262	Hs.14483	ESTs	1.16	2.03
70	415806	AA183950		gbcz080306.r1 Stratagene ovation cancer	1.00	1.33
	436110	AA704969	Hs.291651	ESTs, Weakly similar to 156222 hypothetical	1.60	2.21
	428760	AI08631	Hs.111334	feritin, light polypeptide	1.10	1.43
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.28	1.00
	438182	AI0142140	Hs.182545	ESTs, Weakly similar to ALLU1_HUMAN ALL S	0.90	2.31
	436091	AI073062		nuclear receptor subfamily 1, group I, m	1.70	1.00
75	441633	AW598644		normal mucosa of esophagus specific I	2.48	1.00
	432222	AI04995	Hs.112242	gbcad0303.x1 Stratagene cdh26 brain S1	1.96	2.84
	416055	Z45423	Hs.13349	Homo sapiens cDNA FLJ14647 fs, clone NT	1.52	1.46

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5	417865	AA836392	Hs.56237	hypothetical protein FLJ20405	1.05	1.18
	422659	AV647015		paired keratinoglobulin-like receptor beta	1.33	1.25
	408669	AV259299	Hs.328317	EST	1.08	2.07
	405826	HS6024	Hs.144545	Homo sapiens cDNA: FLJ23226 fs, clone A	1.18	2.38
	447446	AV1737091	Hs.18624	KIAA1052 protein	1.07	1.13
10	437315	AW976247	Hs.153248	ESTs	1.16	2.53
	458317	BRCA1b		Eos Control	1.36	1.32
	405137			Target Exon	1.11	1.18
	401366			Target	1.55	1.42
	423413	AA328560	Hs.346401	ESTs	1.78	1.57
15	433872	A1878010	Hs.278670	disiplin resistance-associated overexpr	1.62	2.98
	440146	AA451780	Hs.130353	ESTs	1.42	2.14
	422637	AA399324	Hs.118835	myoglobin	1.46	2.38
	432342	AL036128	Hs.274404	plasminogen activator, tissue	1.67	1.10
	442820	AW253459	Hs.172681	ESTs	1.02	1.13
20	436573	AA723297	Hs.127138	ESTs	1.18	1.15
	433778			Target Exon	1.13	1.15
	447686	A1939440	Hs.345192	ESTs	1.66	2.78
	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fs, clone C	1.44	2.48
	425853	BC348404	Hs.24740	ESTs	1.40	2.75
25	464487	AW763456		gltcV2-CT0261-261099-011-411 CT0261 Homo	1.52	2.00
	424132	AA333715	Hs.202299	ESTs	1.34	1.32
	421767	NM_014921	Hs.107054	lectomedin-2	1.09	1.14
	442871	A1290091	Hs.131393	ESTs	1.40	2.50
	444849	A1523975		gltcV7D04.x1 NCL_CGAP_CLL1 Homo sapiens	1.31	2.20
30	433365	AW444548	Hs.163118	ESTs	1.07	1.12
	416733	A152028	Hs.271670	ESTs, Weakly similar to 2109250A B cell	1.91	2.01
	413888	AA580289		gltcVn2d01.x1 NCL_CGAP_Co12 Homo sapiens	1.76	1.93
	408063	BE085548	Hs.42346	calcineurin-binding protein calcicarin-1	1.92	1.73
	442569	A126248	Hs.0927	ESTs	1.05	1.12
35	406110	AW444735	Hs.27894	ESTs	1.62	2.45
	424793	A1550066	Hs.259885	ESTs	1.37	2.78
	446977	CT16939	Hs.257848	ESTs	1.52	4.57
	414051	BE244127		gltcTCBAP1E0661 Pediatric pre-B cell acut	1.68	2.84
	422400	A4674434	Hs.128363	ESTs	1.04	2.20
40	443909	AW255791	Hs.13040	G protein-coupled receptor 80	1.47	2.10
	436316	AF066126	Hs.118208	Homo sapiens cDNA: FLJ11727 fs, clone HE	2.08	0.59
	438505	AA308948	Hs.173776	ESTs, Moderately similar to ALU1_HUMAN A	1.44	2.73
	439195	AC001084	Hs.333498	Homo sapiens cDNA: FLJ11222 fs, clone HE	2.17	1.00
	453740	AL121295	Hs.311820	ESTs, Moderately similar to P41225 (art)	1.88	2.58
45	431766	BE6465	Hs.269889	ESTs	1.12	1.30
	424487	T08754	Hs.0259	KIAA1636 protein	1.16	1.15
	435392	R07195	Hs.19918	ESTs	1.35	2.64
	433058	AA644684		gltcVd010.x1 Soares ovary tumor NBH07 H	1.92	2.12
	418741	H83205	Hs.8881	ESTs, Weakly similar to S41044 chromosom	1.44	2.51
50	411654	BE055059	Hs.270833	amphiregulin (schwannoma-derived growth	1.94	2.33
	416589	D44543	Hs.14144	secreted modular calcium-binding protein	1.72	2.58
	419812	A1498267	Hs.110513	KIAA0421 protein	2.28	2.45
	435940	A1462265	Hs.118348	ESTs	1.42	2.45
	433363	AA584826	Hs.276163	non-metastatic cells 2, protein (NM23)	2.07	2.53
55	422936	AA318278		gltcEST21478 Adrenal gland tumor Homo sap	1.46	1.22
	413358	BE389160	Hs.75313	alko-1-like reductase family 1, member B1	1.43	1.43
	435387	NT1630	Hs.118173	ESTs	1.44	2.93
	441083	AA913619	Hs.189025	ESTs	1.20	2.80
	450724	RS6428		gltcVJ9505.r1 Soares breast 2NBH01 Homo	1.44	4.18
60	432446	AF131782	Hs.241438	Homo sapiens clone 24911 mRNA sequence	1.93	2.34
	421577			NM_000703 Homo sapiens cytochrome P450,	1.13	1.22
	439778			C50C001C1-gltcV44644jtgB6A515755.1(A	1.22	1.66
	456702	A1204955		gltcVn003.x1 Stratagene schizo brain S1	2.72	4.60
	418708	H70838	Hs.181900	Homo sapiens clone 24911 mRNA sequence	1.30	2.03
65	451410	AL110235		DNF276881154 protein	1.51	2.78
	451159	AW258621	Hs.27721	Wied-Richthorn syndrome candidate 1-lik	1.33	1.05
	448455	A1252625	Hs.269960	ESTs, Moderately similar to S66557 alpha	0.83	4.40
	444020	RS2862	Hs.35052	ESTs	1.66	2.50
	414623	DE191030		gltcV125574F1 NIH_MGC_44 Homo sapiens c	1.84	3.86
70	450915	AW841619		gltcRCH1-CH0017-120200-012-049 CN0017 Homo	1.14	2.10
	444064	W85970	Hs.16292	ESTs	0.90	0.63
	454353	AW389583	Hs.300700	hypothetical protein FLJ20727	1.30	2.10
	447794	AA124399	Hs.161445	EST	1.26	2.05
	425696	A162832	Hs.171894	parathyroid	1.16	1.11
75	458815	AA700482	Hs.113157	ESTs	1.56	2.73
	432482	L15267	Hs.275924	dystrophin myofibrin-containing WD repea	1.10	1.15
	431062	AA491270	Hs.187945	ESTs	1.44	2.60
	428191	AF063221	Hs.198161	phospholipase A2, group I/IV (lysosomal)	1.35	1.06
	424455	AA341917	Hs.25249	hypothetical protein FLJ20696	1.21	3.45
	451124	A1186203	Hs.31432	cardiac ankyrin repeat protein	1.23	2.10
	432828	AB042326	Hs.287402	chondroin 4-sulfotransferase	1.11	2.71

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5	431668	B226400	Ha.285176	acetyl-Coenzyme A transporter	1.03	3.10
	428321	AA449521		gbrzx37g07.r1 Soares, total_fetus_Nb2HFR	1.68	2.93
	417890	R9348		gbrx87g07.r1 Soares plicofens Nb2HP Homo	1.32	1.80
	435980	AF596410		gbrx87g07.r1 Soares plicofens Nb2HP Homo	1.32	2.43
10	420332	AW450051	Ha.258295	gbrx87g07.r1 Soares plicofens full length insert cDNA	1.26	2.25
	418627	GE349315	Ha.190294	ESTs	1.46	1.23
	441940	A/298115	Ha.128152	ESTs	1.34	1.34
	471050			C9000193.g11g330729g01BAA85547.1 (AB	1.50	1.40
15	439116	AW206670	Ha.50748	chromosome 21 open reading frame 18	1.02	2.38
	438267	A/205708	Ha.292725	ESTs, Weakly similar to 118818 hypothetical	1.28	2.25
	422482	A/439305	Ha.344476	gbrx87g08.x1 NCL_GCAP_Lym112 Homo sapiens	1.05	2.81
	420067	T52431	Ha.54795	Homo sapiens mRNA; cDNA DKFZp564O222 (f	1.77	2.40
20	442180	AA583813	Ha.128529	ESTs	1.76	2.38
	424256	A/378817	Ha.161847	ESTs	1.05	2.06
	444519	A/160304	Ha.26313	ESTs	0.55	0.53
	454498	A/655738	Ha.17767	KIAA1554 protein	1.10	2.05
25	455988	BE177563		gbrx87g09-230300-021-g10 HT0590 Homo	1.70	2.64
	444510	A/367823	Ha.146872	ESTs	1.44	1.08
	456210	N45729	Ha.156875	ESTs	1.64	2.65
	450589	AW192334	Ha.38218	ESTs	1.78	2.71
30	414821	BE305551	Ha.77628	steroidogenic acute regulatory protein f	1.05	1.12
	401581			C14000165.g112590089g01BAA21853.1 (A	0.63	0.65
	439988	BE559554	Ha.61790	hypothetical protein FLJ23338	1.06	1.14
	453762	A/977286	Ha.17428	RBP1-like protein	1.42	2.68
35	419403	AA744520	Ha.87774	ESTs, Weakly similar to nonsynthetic hea	0.99	2.17
	423736	AW338874		gbrx87g10-225-120160-011-07 HT0292 Homo	2.05	1.96
	421186	A/798039	Ha.275653	ESTs, Moderately similar to T15212 hypot	1.29	1.31
	426435	AB27946	Ha.124654	hypothetical brain protein my040	1.36	1.59
40	436312	AA833602	Ha.270745	ESTs	1.60	2.50
	407924	BE537128	Ha.299797	ESTs	1.51	1.15
	409652	AE90074		KIAA1550 protein	1.72	2.21
	415449	HI5034	Ha.100526	gbrx206c03.s1 Soares infant brain 1N18 H	1.50	2.13
45	420436	R21176	Ha.100526	ESTs	1.16	2.50
	458857	A/707713	Ha.158471	ESTs	1.54	2.20
	415770	MT5207		gbrx87g11-235 Substituted Hspcosomes, Str	1.49	1.55
	448279	AW62312	Ha.224676	ESTs, Weakly similar to CRX_HUMAN+ CONE-R	2.50	3.60
50	428735	AA58759	Ha.168794	ESTs	1.84	2.31
	442124	R66412	Ha.126013	Homo sapiens cDNA FL14309 fs, clone PL	1.10	1.19
	412557	AA761612	Ha.291557	ESTs	1.10	1.18
	406335	WU_001502	Ha.53865	glycoprotein 2 (zymogen granule membrane	1.18	1.12
55	436526	AF181862	Ha.242407	G protein-coupled receptor, family C, gr	1.35	2.39
	420855	AA281092	Ha.33417	Homo sapiens cDNA; FLJ22806 fs, clone K	1.22	2.09
	458967	AA303594	Ha.265238	ESTs	1.60	2.20
	414157	Y44877	Ha.55501	ESTs	1.06	2.08
60	448800	A/571294	Ha.298889	ESTs, Moderately similar to ALU1_HUMAN A	1.65	2.79
	421338	AA287443		gbrx252c10.r1 NCL_GCAP_GCB1 Homo sapiens	1.47	2.90
	412679	BE144762		gbrx87g12-041099-065-004 HT0160 Homo	1.32	2.53
	417682	R2311		gbrx252c10.r1 Soares placenta Nb2HP Homo	1.58	2.43
65	425112	AW953291	Ha.64211	hypothetical protein MSC5061	0.70	0.63
	401688			C16000210g112855421g01A7712213_HUM	1.68	2.04
	408325	AW377549	Ha.17965	ESTs	1.68	2.21
	437402	AIS53976	Ha.121191	ESTs	1.20	2.35
70	432455	AA320436	Ha.68919	ESTs	0.98	2.53
	457329	AB54960	Ha.247043	type 1 tumor necrosis factor receptor sh	0.59	0.43
	434800	AW862235		gbrx87g13-0225-230300-189-e11 CT0225 Homo	1.24	1.12
	456936	AK54223	Ha.10026	hypothetical protein FLJ23191	1.44	2.53
75	445698	AW072215	Ha.208670	ESTs	1.38	2.53
	443310	BE552018	Ha.133152	ESTs	0.85	0.83
	424015	N56596	Ha.166361	Homo sapiens mRNA; cDNA DKFZp564H112 (f	1.42	2.25
	422229	AA258675	Ha.194558	ESTs, Weakly similar to AF295263 1 PAR3	1.70	2.39
80	406371			Target Ecan	1.50	3.43
	416744	H86002		gbrx252c10.r1 Soares retina Nb254R Homo	1.32	2.13
	424100	T74082		gbrx252c10.r1 Soares infant brain 1N18 H	1.30	2.17
	438818	AW979008	Ha.222487	ESTs	1.58	2.43
85	438751	AA625750	Ha.125863	ESTs	1.12	1.15
	411206	AW827293	Ha.18889	ESTs	1.17	2.58
	432211	BE274530	Ha.273333	hypothetical protein FLJ10086	0.42	0.30
	448918	AB011152	Ha.22572	KIAA0580 protein	1.54	2.63
90	424495	A/733451	Ha.167165	hypothetical protein FLJ12875	1.39	2.25
	410720	AW388669		Ons1 (Hsp60) homolog, subfamily B, membe	1.84	3.23
	407591	AA578512		gbrx252c10.r1 NCL_GCAP_P1 Homo sapiens	1.21	1.09
	435353	AW243082	Ha.193348	ESTs	1.90	2.98
95	417029	AW962192	Ha.273385	guanine nucleotide binding protein (G pr	1.21	1.24
	425952	AA642418	Ha.173261	ESTs	1.18	2.23
	426135	R42755	Ha.23306	ESTs	1.60	2.73
	424201	AW518704	Ha.208726	ESTs	1.74	3.20
100	429111	AB70811	Ha.7579	KIAA1151 protein	1.27	1.40

5	440357	AA379353	Hs.20950	phosphotyrosine phosphatidylserine inorganic	0.83	0.68
	440867	AA117027	Hs.166338	ESTs	1.45	1.50
	440868	AW532522	Hs.166338	gbPMH-D10054-231259-002-002 D10054 Homo sapiens	1.45	1.50
	440874	AU310135	Hs.335933	ESTs	1.54	2.45
	440812	AW576549	Hs.166728	ESTs, Weakly similar to I38022 hypotheti	1.22	2.07
10	457741	BE044740	Hs.166339	glbAm55g10x1 NCL_GGAP_RDF1 Homo sapiens	1.89	2.08
	457762	AA732484	Hs.166339	ESTs	1.24	2.58
	4118155	W17056	Hs.630623	nuclear receptor subfamily 1, group I, m	1.31	1.38
	403922	AW966480	Hs.128514	gb:EST378594 MAGE csubsequences, MAGE Homo	1.70	1.70
	425168	AW226500	Hs.128514	ESTs	1.13	1.12
15	454937	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145KD	1.26	2.28
	403673	AI161428	Hs.75916	NM_022775Homo sapiens hypothetical prot	2.00	1.00
	424091	AW341438	Hs.278036	ESTs	1.38	2.28
	424316	AA676403	Hs.145078	regulator of differentiation (in S. pom	1.06	2.10
	444608	A174683	Hs.323863	ESTs	1.55	1.82
20	447345	BE247767	Hs.16166	KIAA0670 protein	1.26	2.10
	435846	AW575249	Hs.16166	gb:EST378359 MAGE csubsequences, MAGE Homo	1.68	2.63
	428546	D42046	Hs.194665	DNA2 (DNA replication helicase, yeast, h	1.32	2.33
	403214			NM_016232?Homo sapiens Interleukin 1 re	1.02	2.15
	404485			CB011441?gll8523061yrolpNP_060114.1) hy	2.20	2.49
25	443471	AW286536	Hs.172154	Homo sapiens clone FLE3-442 PR00672 m-RNA,	1.58	1.74
	437116	ALC45253	Hs.195162	ESTs	1.22	2.53
	451557	A3020640	Hs.26315	Human DNA sequence from clone RP3-46/L1	0.94	2.35
	406255	AW807321	Hs.152671	gbMIM-517002-240300-003-005 ST0052 Homo	1.12	1.36
	448331	AI597806	Hs.346823	ESTs	1.30	2.29
30	422343	AI598533	Hs.346823	ghly77405.x1 NCL_GGAP_Gld11 Homo sapien	1.86	2.32
	407140	AA059106	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	1.37	1.01
	428187	AA447648	Hs.163872	ESTs, Weakly similar to S65657 alpha-1C-	1.74	1.55
	423814	A457940	Hs.205532	ESTs	1.48	2.63
	429373	AA448187	Hs.47395	ESTs	1.24	2.00
35	415732	AA167566	Hs.271570	ESTs, Weakly similar to 210526DA B cell	1.31	2.34
	412634	U55984	Hs.285088	heat shock 50KD protein, 1, alpha	0.42	0.22
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.54	1.27
	415307	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	0.78	0.71
	402654			Target Exon	0.50	0.65
40	457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	0.86	0.50
	405340			C2002662p11346564pP10079PBP1_S TRPU	1.46	2.33
	422028	BE365776	Hs.186400	analysis, progressive (widespread) homolog	1.53	2.75
	442237	AW905607	Hs.24587	ESTs, Weakly similar to K5F3_HUMAN NUCLE	1.08	3.38
	456370	AA234598	Hs.87384	ESTs	0.77	2.83
45	407041	X15673	Hs.274281	gdchuman pT702 mRNA for repetitive sequen	2.00	1.84
	452021	AI827675	Hs.274281	fdgulin	1.38	2.03
	445137	AT733837	Hs.145661	ESTs	1.60	3.00
	440808	AK001335	Hs.7432	hypothetical protein FLJ10477	1.17	2.10
	404418			Target Exon	1.50	3.36
50	447698	AI916872	Hs.213424	ESTs	1.90	2.21
	434414	AI758375	Hs.213424	gb:U9407.x1 NCL_GGAP_Ov23 Homo sapiens	1.58	1.54
	400834			NM_022240?Homo sapiens potassium inward	1.25	2.33
	445542	AW857362	Hs.268855	ESTs, Weakly similar to I38022 hypotheti	1.46	1.28
	441043	AA513422	Hs.152104	ESTs	1.26	1.05
55	403391			C3001164?gll1730199gP50573GAR3_RAT	1.46	2.55
	445129	AI631602	Hs.258499	ESTs	1.27	2.48
	418321	DE3477	Hs.84087	KIAA0143 protein	0.56	0.52
	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fs, clone HE	1.31	2.06
	443676	AK001810	Hs.9670	hypothetical protein FLJ10598	1.34	1.22
65	422554	RA6070	Hs.5407	ESTs	1.04	2.08
	401890			Target Exon	1.24	1.14
	415501	AW843822	Hs.208343	gb:CM4-CN0045-010200-514-008 CN0045 Homo	1.74	1.38
	457095	A1805202	Hs.208343	ESTs, Weakly similar to cerebroside sulf	0.82	0.87
	426123	AA370362	Hs.232157	gb:EST27246 Prostate gland 1 Homo sapien	1.26	2.36
70	445445	AW197349	Hs.232157	ESTs	1.24	2.13
	430683	AC004862	Hs.247768	Homo sapiens PAC clone RP4-92TH17 from 7	1.30	2.00
	440642	AI744995	Hs.247768	ESTs, Moderately similar to ALU4_HUMAN A	1.29	2.44
	452385	AW875572	Hs.247768	gb:CM5-PT0014-071289-G51-b05 P10014 Homo	1.78	2.55
	446822	AW013815	Hs.196578	ESTs	1.45	2.20
75	415116	AA160363	Hs.269956	ESTs	2.02	1.03
	457269	AI339953	Hs.134536	ESTs	1.53	1.35
	427677	AW138725	Hs.178067	ESTs	1.91	2.42
	454631	AW811524	Hs.178067	gb:U3-ST0141-131059-017-402 ST0141 Homo	1.00	3.13
	456330	AI752985	Hs.132372	ESTs, Weakly similar to ALUC_HUMAN III	1.02	2.21
	435844	AA700856	Hs.59661	ESTs, Weakly similar to T68685 serineth	0.85	0.81
	427237	AA305964	Hs.57763	ESTs	1.57	1.44
	426855	TE3061	Hs.131946	Homo sapiens mRNA for KIAA1727 protein,	1.20	2.13
	442151	AI733404	Hs.128865	ESTs	1.50	2.13
	412708	R26630	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	1.16	3.00
	417262	AA195276	Hs.263858	ESTs, Moderately similar to B3-067 hypot	1.25	2.40
	413632	N64116	Hs.24624	hypothetical protein FLJ21945	1.38	2.48

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447248	AW255831	Hs.6496	ESTs	1.56	2.03
415622	F13010	Hs.12400	ESTs	1.48	2.30
414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ135801b, clone PL	1.26	2.88
414585	W49354	Hs.334716	hypothetical protein MGC15291	1.24	2.05
443197	Z43613		gb-HSC1GD051 normalized infant brain cDN	1.11	2.04
428266	A1382001	Hs.43590	ESTs	1.09	2.03
447083	AW72124	Hs.157757	ESTs	1.66	3.53
412302	AW533334		gb-QV4-DT0021-261259-670-g05 DT0021 Homo	1.74	3.00
445555	AW674013		ESTs	1.32	1.25
453117	AW162044	Hs.104203	hypothetical protein MGC12981	0.73	0.81
436757	AW575663	Hs.234004	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	1.88
431976	AA719001	Hs.291065	ESTs	1.23	2.01
430557	AA402510	Hs.275654	ESTs	1.64	2.65
438744	BE314727	Hs.75721	protein 1	0.85	0.85
438325	AF068130	Hs.150423	cyclic-dependent kinase 9 (CDC2-related	1.16	2.05
438117	AA328041	Hs.194329	hypothetical protein FLJ21174	0.79	0.76
441686			NM_0145877 Homo sapiens SRY (sex determi	1.32	2.31
442059	U72537	Hs.96264	alpha-haemerescentin-related syn	0.78	0.53
434288	AW109076	Hs.116265	tubulin3	2.42	4.23
433215	AB040812	Hs.191098	hypothetical protein FLJ11558	1.36	1.36
419429	BE133117	Hs.278881	ESTs	1.30	2.58
426417	AA377908	Hs.132554	ESTs	1.06	1.77
413882	AA132973	Hs.184492	ESTs	1.55	2.10
413346	AA126586		gc24H06.1 Scarus_pregnant_uterus_NBH	1.29	1.77
445020	A1206855	Hs.147221	ESTs	1.90	2.00
416175	AW987054	Hs.205312	ESTs, Weakly similar to 139022 hypotell	1.06	3.70
429582	A1680468	Hs.222477	ESTs	1.06	2.38
405134	AW340389	Hs.250585	ESTs	1.64	2.57
415642	U19878	Hs.336224	transmembrane protein with EGF-like and	0.73	2.33
435657	F10625	Hs.124163	ESTs	1.10	2.33
440513	BE407108	Hs.65957	Homo sapiens, clone IMAGE3059816, mRNA,	0.85	2.03
419711	Q52621	Hs.155282	ESTs	1.22	2.00
434249	AA687537	Hs.129575	ESTs	1.29	2.48
437355	AL359557	Hs.306508	Homo sapiens mRNA; cDNA DKFZ67201415 (f	1.85	2.08
426360	H10291	Hs.30574	ESTs	1.40	2.05
435339	AI358300	Hs.129627	ESTs	1.38	2.18
435345	AW360966	Hs.6653	ESTs	1.49	2.27
436105	AA78982	Hs.131859	Homo sapiens F-box protein FEX11 mRNA, p	1.78	2.33
458645	AA74546	Hs.250715	ESTs	1.50	2.40
446801	AA021453	Hs.21413	schile carrier family 12, (potassium-chl	0.74	0.69
426955	T96509	Hs.248549	ESTs, Moderately similar to S55557 alpha	1.42	2.75
437272	AW705957		gb-EST350066 MAGE resequences, MAGN Homo	1.00	2.16
458935	NM_009525	Hs.168975	splicing factor, arginine/serine-rich 5	0.84	0.81
421382	AF000501	Hs.103853	hypothetical protein FLJ20043	1.30	2.21
457926	AA452378	Hs.11637	Homo sapiens mRNA; cDNA DKFZp584A216 (f	1.27	2.12
446557	A1167637	Hs.146924	ESTs	1.83	2.35
434476	AW688520	Hs.84264	acidic protein rich in leucines	1.43	3.90
458055	AW015588	Hs.137232	ESTs, Weakly similar to S55557 alpha-1C-	1.30	2.23
419355	AW235215	Hs.16145	ESTs	2.10	2.43
417281	R68773	Hs.268883	ESTs	1.26	2.10
446689	BE158609		gb-QVQ-HT0395-210100-066-006 HT0395 Homo	1.15	2.15
423249	AA325802	Hs.125374	ESTs, Weakly similar to S75655 hypotell	1.75	1.50
406866	AW511265	Hs.246442	ESTs	1.74	2.91
441359	AA435179	Hs.126820	ESTs	2.43	1.59
413068	BE063792		gb-QV3-BT0295-260100-066-006 BT0295 Homo	1.52	2.09
441322	AW071851	Hs.130628	ESTs	1.42	2.10
405124	AW202029	Hs.50777	N-acetylglucosaminidase, alpha- (Sanfil	1.11	2.20
432413	AF000257	Hs.274505	Homo sapiens mRNA; cDNA DKFZp584A216 (f	1.10	2.25
425391	AQ48252	Hs.160672	ESTs	1.17	2.38
443861	AW448402	Hs.134743	ESTs	1.44	2.30
454609	AW810204		gb-HR4-ST0125-021159-017-008 ST0125 Homo	2.30	1.33
423603	AA429805		gc24H307.11 Stratagene lung carcinoma	1.76	2.51
443611	NM_014397	Hs.9525	NIMA (never in mitosis gene a)-related k	1.61	2.90
410359	R38624	Hs.106313	ESTs	1.78	2.05
424716	TS1344	Hs.326263	NM_025192 Homo sapiens hypothetical prot	1.52	2.24
435073	AA664078		ESTs	1.40	2.45
420681	AA278459	Hs.151540	gb-ac0A05.11 Stratagene lung (S37210) H	1.06	2.26
435579	AF332973	Hs.150524	ESTs	1.48	2.58
429533	AF060484	Hs.86248	ESTs	1.46	2.08
430551	AA481150	Hs.138343	ESTs	1.40	2.28
450555	T97988	Hs.255605	mannosidase, alpha, class 2A, member 2	1.48	2.40
444326	AB393557	Hs.270710	ESTs	0.88	2.28
412149	R63355	Hs.273824	ESTs	1.58	2.19
455116	AW857271		gb-QM2-CT0307-210100-158-g09 CT0307 Homo	1.56	2.50
446926	AA771247	Hs.301637	zinc finger protein 258	0.60	0.53
410047	A1167810	Hs.132350	zinc finger protein 36 (KCOX 18)	0.66	0.58

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	418865	AW117500	Hs.104241	ESTs	1.58	2.83
	402752			ENSP00000235171-GAP junction beta-4 pro	0.81	0.82
	436449	AH18027	Hs.123951	ESTs	1.46	1.46
5	403488			ENSP000000215948-KARYOPHERIN BETA2B HOMOL	1.98	2.23
	431235	AA318271	Hs.250905	hypothetical protein	1.14	2.55
	448576	AB026730	Hs.21495	UDP-Galactose 4-epimerase 1,3-galactosyltr	0.70	0.78
	402800	AW205382	HA42676	RNA/DNA protein	1.36	2.86
	433335	AW162404		Smoo (Smoothened) like 6, RNA binding	0.90	2.15
	427337	R26572		glycyltyr^{11,11} Sarcosine intake brzin 1N1B H	2.23	1.71
10	426150	AA205020	Hs.167460	splicing factor, arginine/serine-rich 3	1.08	2.05
	447708	BE310189		nuclear receptor subfamily 1, group 1, m	1.26	1.27
	420141	AA470261	Hs.124103	ESTs, Weakly similar to ES594A like, ca	1.46	2.50
	423940	AA32434	Hs.72465	ESTs, Weakly similar to non-lens beta ga	1.26	2.47
	447793	AI424924	Hs.211203	ESTs	2.38	1.83
15	407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.11	2.54
	432451	AW672771	Hs.253471	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.03	2.05
	421311	WT1846	Hs.263609	hypothetical protein PRO2202	0.51	0.40
	444649	AW207523	Hs.197528	ESTs	1.21	2.24
20	448588	RS4570	Hs.265889	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	3.25
	428547	AB644833	Hs.98881	ESTs	1.48	2.65
	413750	8E161453		gblp2-HT0437-292200-045-A06 HT0437 Homo	1.22	1.00
	423555	AW973253	Hs.292689	ESTs	1.86	2.35
	427798	AA412499	Hs.104779	ESTs	1.82	2.33
25	431178	A.338644	Hs.195432	aldehyde dehydrogenase 2 family (mitoch	0.80	2.00
	451715	AS373532	Hs.197910	ESTs	1.26	3.85
	438094	AB821755	Hs.181835	ESTs, Weakly similar to A56194 thromboxa	1.74	2.54
	418504	BE159718	Hs.85335	Homo sapiens mRNA: cDNA DKFZP564D1462 (f	0.52	0.45
	407414	AF072164		glt-Homo sapiens HSF-1 mRNA, partial cds	1.67	2.28
30	416410	H53777	Hs.36822	ESTs	1.65	2.28
	430141	AI241470	Hs.269922	ESTs	1.08	2.28
	441181	AF418925	Hs.121076	peptidylprolyl isomerase (cyclophilin)-4	1.81	2.02
	434482	AF143331	Hs.16073	ESTs	1.22	2.00
35	455757	B5578531	Hs.155029	gblp2-HT0437-292200-045-A06 HT0437 Homo	1.53	2.21
	425727	AA363987		ESTs	0.76	1.13
	441846	AW850980		CX001244(git1142042)refl(git_004811) be	1.70	2.21
	451945	BE504055	Hs.211420	gltc-L3-CT0220-150200-068-B03 CT0220 Homo	1.16	2.14
	439432	AW444990	Hs.238800	ESTs	0.84	2.73
40	451140	AW411354	Hs.25902	ESTs, Weakly similar to 136022 hypothei	1.60	2.43
	407341	AA918886	Hs.204918	LIM domain binding 1	1.14	1.20
	436041	AI880737	Hs.280068	ESTs, Weakly similar to ALU6_HUMAN ALU S	1.03	2.42
	437613	R15952	Hs.10657	Homo sapiens cDNA FLJ11918 fs, clone HE	1.60	3.43
	451507	AW227109	Hs.200787	ML1 protein	1.16	2.11
45	430259	8E551182	Hs.127636	ESTs, Weakly similar to T31511 hypothei	1.22	0.65
	453669	AL049029	Hs.7258	Ra/GEF-like protein 3, mouse homolog	2.85	1.00
	455065	AW854352		hypothetical protein FLJ22021	0.75	0.64
	442220	AL337800	Hs.8148	gblp2-HT0437-292200-045-A06 HT0437 Homo	1.49	2.20
	437036	AW758475	Hs.268549	selenoprotein T	0.50	0.18
50	442556	AL137781	Hs.8379	hypothetical protein FLJ14710	1.50	2.44
	402223			Homo sapiens mRNA: cDNA DKFZp596L2424 (f	0.54	0.37
	437225	AW975982	Hs.292635	Target Exon	1.09	2.80
	421101	AF015446	Hs.101840	ESTs	1.03	2.47
	438200	RS1386	Hs.124881	major histocompatibility complex, class	0.72	0.57
	402025			ESTs	1.64	2.93
55	407619	UA0973		NM_021624-homo sapiens histamine H4 rece	1.52	2.28
	451385	AW005671	Hs.211191	glt-Human Tigger 1 Transposable element, c	2.40	2.12
	423450	AJ290445	Hs.128759	ESTs, Weakly similar to A46010 X-linked	1.24	3.25
	423139	AAW02725	Hs.288500	KIAA0524 protein	1.64	2.13
60	451763	AW254647	Hs.233034	hypothetical protein FLJ21106	1.61	2.28
	458115	AB155889	Hs.210781	hypothetical protein FLJ14220	2.39	2.08
	452829	AW655570	Hs.633368	NM_021932-homo sapiens glutamate recept	1.62	0.92
	446383	T05816	Hs.92011	ESTs, Weakly similar to TRHY_HUMAN TRICH	0.60	0.41
	432676	AW157424	Hs.165954	ESTs	2.08	1.48
	433820	AI401627	Hs.174067	ESTs, Weakly similar to 136022 hypothei	1.88	2.49
65	415719	AA844700	Hs.352927	ESTs	1.30	2.90
	416988	H06728	Hs.210107	ESTs, Moderately similar to ALU1_HUMAN A	1.33	2.00
	420738	NM_004185	Hs.258575	ESTs	1.42	2.29
	446514	AF007133	Hs.15552	wingless-type MMTV integration site fami	0.79	0.78
	404167			hypothetical protein FLJ10671	1.47	2.06
70	417074	Z49878	Hs.81131	NM_021932-homo sapiens glutamate recept	1.62	0.92
	401215			guaridinacetic acid N-methyltransferase	0.72	0.75
	421600	AW953889	Hs.323321	C12000457(git7512178)prj130337 polypr	1.14	2.08
	426248	T16986	Hs.293693	Homo sapiens cDNA FLJ115146 fs, clone HE	1.88	2.56
	454323	AW653880		ESTs	1.17	3.44
75	420956	AA270098	Hs.187636	gblp2-HT0437-292200-045-A06 HT0437 Homo	1.34	2.40
	402833			ESTs	1.22	2.43
	439910	AA827521	Hs.291658	C100250e(git691937)omb(CAG65737.1) (ALU	1.31	2.00
				ESTs, Weakly similar to ALUC_HUMAN (H	1.39	3.13

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416170	H42654	Ha.220645	ESTs	0.99	2.18
433988	AI762836	Ha.271433	ESTs, Moderately similar to ALL2_HUMAN A	2.04	1.28
476699	T91491	Ha.119670	ESTs	1.36	2.50
489925	AL045773		gbcDKFZp334F246_r1 43k (synonym: hba3)	2.21	2.13
453204	R10799	Ha.191990	ESTs	3.12	2.96
468971	AL119206	Ha.126257	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.34	2.05
457040	N77624	Ha.173717	phosphatidic acid phosphatase type 2b	1.68	2.00
404914	AF063716	Ha.263966	Homo sapiens CAT-2 mRNA, complete cds	1.70	2.54
426263	AB06774	Ha.259765	canine pancreatic trypsin, liver	0.96	2.14
438334	AI148976	Ha.112062	ESTs	1.50	2.45
455527	AV084479		gbcPM1-HN0012-22030-001-b12 HN0012 Homo	1.46	2.28
406064	AL040832	Ha.160422	Homo sapiens clone PP502 unknown mRNA	1.61	2.23
432859	AF227151	Ha.272387	heste receptor, type 2, member 4	1.06	2.15
426791	AW015667	Ha.119427	ESTs	1.51	2.83
438695	AI661190	Ha.156089	ESTs, Weakly similar to repressor protein	1.19	2.03
458136	AB267111	Ha.253147	ESTs	1.42	2.10
413035	BE155563		gbcPM4-H10052-171199-001-C06 V10352 Homo	1.62	2.30
429444	AA310688		gbcEST161501 Jurkat T-cells V Homo sapie	1.38	2.05
405546	AW410190	Ha.250624	hypothetical protein MGCA473	1.87	2.18
411432	AW846272		gbcCVO-C01079-30099-024-d12 C01075 Homo	1.04	2.03
445327	AQ200682	Ha.147722	ESTs	1.16	2.10
424629	AB011138	Ha.151385	KMA0664 protein	0.61	0.63
440197	AW340708	Ha.317714	palid (mouse) homolog, palidin	0.56	0.35
406864	BE081731		gbcV2-BT0635-220400-158-40/ BT0635 Homo	1.50	2.45
422776	AA316887	Ha.125846	ESTs	1.38	2.20
426255	AB27478	Ha.187670	ESTs	1.34	2.40
414844	AA112050	Ha.265561	ESTs	0.97	2.00
432789	D26361	Ha.3104	KMA00042 gene product	1.44	2.73
430100	AA766178	Ha.291601	ESTs, Highly similar to T00350 hypobell	1.06	2.02
415628	AA244000	Ha.222385	ESTs	1.54	2.06
417930	AA684549	Ha.158785	ESTs	1.80	2.70
426468	AF033579		T-box 10	0.71	0.61
410248	AA166653	Ha.268171	ESTs	2.55	2.10
401818			NM_006644 Homo sapiens acetyl-Coenzyme	1.75	2.58
451724	AB063765		gbcU8-1007-301258-102 BT037 Homo sapien	1.64	2.28
431866	NM_012058	Ha.8025	angiotensin-II-re 2	1.56	2.36
432719	AV035411	Ha.314460	ESTs	1.36	2.25
418977	AA233064	Ha.191517	ESTs	2.06	3.00
404220			C0000669 gbj573285 (amb) C007544.1 [AL	1.54	2.23
446708	BE549905	Ha.231754	ESTs	1.35	2.16
453823	AL137567		gbcDKFZp761D2315_r1 761 (synonym: hary2)	1.42	2.38
422050	AA302741	Ha.257586	ESTs, Moderately similar to J05228 galac	1.40	2.50
404704			Target Exon	1.46	1.80
409104			Target Exon	1.22	2.03
411008	AW813238		gbcMR3-ST0161-020200-207-404 ST0191 Homo	1.00	2.13
426582	AA381797	Ha.281121	ESTs	1.35	2.45
430853	AI74175	Ha.105676	ESTs	1.43	2.23
432420	AL044658	Ha.43761	ESTs	1.15	2.03
403157			C2002793 gbj1353148 (gpc00958) YR86_CAE	0.52	0.47
432407	AA221036		gbcz0312.1 Stratagene NF2 neuronal pr	1.93	2.23
414596	AW747800	Ha.55016	hypothetical protein FLJ21635	1.56	2.72
407016			ENSP00000227125:NAALADASE II PROTEIN.	2.45	2.45
453335	AA584134	Ha.269454	ESTs	1.31	2.24
459888	BE244127		gbcTCBAP1E0661 Pediatric pre-B cell acul	1.16	2.03
437722	AV020947	Ha.122872	ESTs, Weakly similar to J00033 hypobell	3.75	2.72
452277	AL045013	Ha.26783	KMA1223 protein	0.33	0.26
425712	AA115548	Ha.21423	ESTs, Moderately similar to ALU1_HUMAN A	1.34	2.21
475758	AA408057	Ha.57998	ESTs	1.06	2.05
412585	M8575	Ha.344089	gbcEST02500 Fetal brain, Stratagene (cat	1.24	2.59
420243	AL133645	Ha.110533	retinoic acid induced 1	0.48	0.41
421814	L12350	Ha.108623	thrombospondin 2	1.46	2.45
413645	AA130692		gbczot1502.1 Stratagene colon (937204)	1.32	2.45
435663	AF210317	Ha.95457	solute carrier family 2 (facilitated glu	0.30	0.28
452396	H10302	Ha.112577	ESTs	1.00	2.45
406112	BE581384		gbcB0134969F.1 NH_MGC_8 Homo sapiens cD	1.08	2.50
454721	AW615558		gbcCVO-ST0216-061259-966-a09 ST0216 Homo	1.44	1.65
417796	AA206141	Ha.6786	ESTs	1.68	3.85
432664	D16217	Ha.279607	calpain-like	0.43	0.35
454480	AA088375	Ha.22612	hypothetical protein DKFZp566D1346	2.19	1.91
434460	AF143870	Ha.15246	ESTs	2.26	2.07
418797	AA615814		gbczot4003.1 N1_Q2_CGAP_Lip2 Homo sapiens	1.42	2.55
403871			C5001783 gbj780367gbcNAVD05844.1 (L416	1.60	2.63
441283	AA927670	Ha.191704	ESTs	1.31	3.63
442250	AV282871	Ha.129121	ESTs	1.14	2.38
466747	AL037587	Ha.125864	Inorgmodulin 2 (neuronal)	1.61	1.26
425757	AA363171		gbcEST12986 Ovary II Homo sapiens cDNA 5	1.29	2.95
405494			C2001837 gbj12697903gbcBAE21770.1 [A	2.09	1.00

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5	432250	AA652088	Hs.274170	Opo-interacting protein 2	1.26	2.71
	431911	AK000156	Hs.272153	Homo sapiens cDNA FLJ20149 lis, clone CO	1.46	2.60
	413923	AF733852	Hs.198959	ESTs	1.62	2.10
	446590	AA694070	Hs.263836	ESTs	1.20	2.63
	438467	AA809027	Hs.123277	ESTs	1.46	2.10
10	432121	AB248979	Hs.211286	ESTs, Weakly similar to 1207285A reverse	1.27	3.13
	412298	AW953300		gb:QV4-TT0021-261259-070-a04 D10021 Homo	1.42	2.68
	408519	AF673082	Hs.43481	hypothetical protein DKFZp564K152	1.64	3.70
	416807	TT97132	Hs.14633	ESTs	1.11	3.03
	420497	AW206286	Hs.263548	ESTs	1.90	2.48
15	405704			NM_001544*:Homo sapiens collagen, type I	1.42	2.90
	423443	AK32601	Hs.168812	Homo sapiens cDNA FLJ141132 lis, clone MA	1.42	2.03
	415904	Z44679	Hs.330391	ESTs	1.62	2.94
	413786	AW613780	Hs.135500	ESTs	0.33	0.17
	404031			C5001700*:gB256616[ref][NP_061761.1] pr	1.54	2.29
20	457412	N40711	Hs.333300	hypothetical protein FLJ14026	1.52	3.20
	438719	AF068554	Hs.268168	Homo sapiens mRNA; cDNA DKFZp434M040 (f	1.61	2.42
	418181	AF050754	Hs.61716	ESTs	0.21	0.21
	425984	AW954011	Hs.160711	ESTs	0.52	2.20
	419988	W35388	Hs.55336	Homo sapiens, clone M/GC-17421, mRNA, com	1.34	2.57
25	439608	A1091277	Hs.302634	frizzled (Drosophila) homolog 8	1.67	2.66
	450177	AW680951	Hs.107845	ESTs	1.50	2.35
	455704	AA719572	Hs.274441	Homo sapiens mRNA: cDNA DKFZp434N011 (fr	1.27	3.35
	410357	AW63814		gb:U22604x1 NCL_CGAP_U8 Homo sapiens	0.66	0.59
	455234	AF040426		gb:CMO-CT0062-150795-024-004 CT0062 Homo	0.67	2.08
30	421313	NM_1148123	Hs.103329	KIAA0070 protein	0.57	0.26
	431322	AW570622		gb:EST382704 MAGE sequences, MAGK Homo	1.60	2.73
	423086	AB028984	Hs.123420	KIAA1061 protein	0.40	0.56
	427580	AA360551		gb:EST17963 Pancreas tumor III Homo sapi	1.33	2.50
	423185	BE296950	Hs.125078	ornithine decarboxylase antizyme 1	0.60	0.56
35	410840	AW808924		gb:QV4-TT0023-165405-172-x10 ST0023 Homo	1.50	2.88
	437384	AB747710		Target Exon	1.82	2.02
	444369	AW435340	Hs.174397	ESTs	1.26	2.05
	443318	AB051680	Hs.189720	ESTs	1.35	2.13
	441053	AB068138	Hs.131341	ESTs	1.46	2.20
40	439432	A1584203	Hs.126919	ESTs	1.40	2.35
	454629	AW811114		ESTs	0.86	2.18
	402307			gb:VR2-ST01231-111155-016-a04 ST0131 Homo	1.96	2.31
	444872	A1532624		Target Exon	2.77	2.55
	401906			p30 DBC protein	1.46	2.45
45	404730			C17000154:gB12003560[gb]AA6438.30.1AF21	1.15	2.28
	457458	AF732230	Hs.191737	Target Exon	1.84	2.78
	448471	A1158617	Hs.21276	ESTs	1.45	2.55
	438978	A1095207	Hs.307972	collagen, type IV, alpha 3 (Goodpasture	0.37	0.36
	418786	A7795317	Hs.203594	ESTs	1.57	2.39
50	400416	AF083130		Homo sapiens uncharacterized gastric pro	2.95	3.34
	450446	AW96334	Hs.14460	Homo sapiens CATX-14 mRNA, partial cds	2.03	1.55
	419751	A1575908	Hs.105104	ESTs	1.32	2.38
	449436	AA860329	Hs.273307	ESTs	0.41	0.27
	439080	L08063	Hs.247960	hypothetical protein DKFZp4342117	2.01	1.50
55	443316	A1033387	Hs.132225	meanoorlin 4 receptor	1.09	2.18
	427923	BE088433	Hs.334695	ESTs	1.30	2.25
	403294			hypothetical protein KIAA1335	1.40	2.50
	436007	A1247716	Hs.232168	Target Exon	0.98	2.16
	439549	AB040541	Hs.247713	ESTs	1.38	1.90
60	427271	AL137445	Hs.28849	KIAA1506 protein	1.52	2.85
	444500	AW651273	Hs.282966	Homo sapiens mRNA: cDNA DKFZp566G134 (fr	1.29	2.56
	447434	R16890	Hs.137135	ESTs, Moderately similar to 2105260A B c	1.22	2.05
	400830			ESTs	1.72	2.85
	426114	AB211548	Hs.38363	NM_020063:Homo sapiens hypothetical prot	2.04	2.88
65	409608	A1150485	Hs.38363	ESTs, Weakly similar to 138022 hypotell	1.09	2.74
	440781	BE561823	Hs.281434	gb:U36a10.x1 Scores_Jesús_NHT Homo sap	1.67	1.38
	442662	U78168	Hs.85578	Homo sapiens cDNA FLJ14026 lis, clone HE	1.28	2.50
	443078	N78726	Hs.135594	Rap1 guanine-nucleotide-exchange factor	1.52	2.26
	440175	A1890151	Hs.122504	Homo sapiens cDNA: FLJ23149 lis, clone L	1.42	2.01
70	446780	R31107		ESTs	1.46	2.63
	444173	A126452	Hs.149493	gb:hy1Ig01.L1 Scores_placenta Nb2HP Homo	1.96	2.78
	417939	R53683	Hs.337612	ESTs	1.50	2.10
	426490	BE301728	Hs.45906	ESTs, Weakly similar to ALUC_HUMAN III	1.60	2.03
	443859	A141520	Hs.151464	ESTs, Weakly similar to A46010 X-linked	0.47	0.44
75	426322	J05068	Hs.2012	ESTs, Weakly similar to ALUC_HUMAN III	1.26	2.68
	411630	U42345	Hs.71119	transcobalamin I (vitamin B12 binding pr	2.12	1.15
	455701	AW854930		Pulvate prostate cancer tumor suppresso	0.64	0.48
	438795	N77294	Hs.194294	gb:PMO-CT0263-261059-063-05 CT0263 Homo	1.30	2.33
	425546	BE409762	Hs.26118	ESTs	1.17	2.33
	411245	AW833441		hypothetical protein MGCI3033	1.17	2.85
				gb:QV4-TT0008-271059-020-g01 TT0008 Homo	1.90	3.98

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	402294		Target Exon	1.80	3.08	
	417789	R13567	Hs.12548	ESTs	1.63	2.58
	417827	AA203524		gb:z55610.r1 Soares_fetal_liver_spleen...	1.52	2.02
	427526	AA165082	Hs.345930	gb:ca12601.r1 Soares_Jettie_MH Homo sap	2.03	1.90
5	455300	AW091707		gb:CM3-NT0090-040550-171-a02 NT0090 Homo	1.12	2.20
	448121	AL045714	Hs.128653	hypothetical protein DKF2564F013	0.93	2.28
	412855	AB21875		glcwp076Hx1 NCQ_CGAP_Kic12 Homo sapien	1.43	2.08
	425702	NS5555		gb:py7605.s1 Soares fetal liver spleen	1.61	2.26
10	441656	H37950	Hs.125720	ESTs	1.11	2.10
	400311	AF072164	Hs.137570	Homo sapiens HSFE-1 mRNA, partial cds	2.04	2.95
	451478	NM_012331	Hs.26459	methionine sulfoxide reductase A	0.50	0.20
	425288	AA354502		gb:E576279 Jurlkat T-cells V Homo sapien	0.99	2.08
	456397	W83339	Hs.150590	PTD010 protein	1.11	2.29
	405654			C12001521.g17513934(p17)T31081 cca3 pr	2.30	1.90
15	450151	AI088196	Hs.22968	Homo sapiens clone IMAG-451939, mRNA se	1.21	2.60
	419851	AA287987	Hs.13477	ESTs, Weakly similar to 1207285A reverse	1.26	2.60
	408016			Target Exon	0.57	0.48
	440903	AA68079	Hs.126823	ESTs	2.02	1.61
	445026	W90337	Hs.282966	ESTs, Moderately similar to 2105263A B c	1.56	2.23
20	414182	AA193301	Hs.344442	KIAA1105 protein	1.32	2.55
	457048	AA600382	Hs.112891	ESTs	1.54	2.05
	440542	AA89143	Hs.295605	ESTs, Weakly similar to PC4259 fertilin	1.48	2.15
	422857	R71461		gb:cy51507.r1 Soares placenta Nb2HP Homo	1.42	2.78
	445548	AW444952	Hs.202247	ESTs	1.50	2.48
25	454002	8E298567	Hs.271749	ESTs, Moderately similar to ALU8_HUMAN A	1.31	2.25
	413565	TY1703		glycylglycyl-S1 Stralagene lmg (307210) H	2.10	1.69
	420441	AA988160	Hs.103833	dual specificity phosphatase 6	0.99	2.33
	412682	H09124	Hs.202341	Homo sapiens cDNA: FLJ23573 Bc, clone L	2.14	1.61
	408991	8E501816	Hs.281527	ESTs	1.76	2.83
30	432534	AV361625	Hs.335833	hypothetical protein FLJ11240	0.41	0.28
	435136	R27299	Hs.101772	ESTs	0.76	3.40
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 Bc, clone H	2.16	1.85
	413528	AA242498	Hs.6700	ESTs, Moderately similar to Z155_HUMAN Z	1.30	2.00
	439448	AA507078	Hs.257598	NM_003343 Homo sapiens soluble carrier fa	1.67	2.22
	432344			NM_003343 Homo sapiens soluble carrier fa	1.36	2.22
	418056	AA524886		gb:ca34002.s1 NCQ_CGAP_P3 Homo sapiens	1.42	2.85
	435428	AI791746	Hs.130293	ESTs	2.44	1.32
	419964	AA811657	Hs.226133	ESTs	1.32	2.08
	440926	AV198572	Hs.131323	ESTs	1.80	2.65
40	450925	AA747771	Hs.314525	ESTs	1.64	2.18
	452757	AI369787	Hs.7145	ESTs	1.47	3.16
	436120	AI248193	Hs.119860	ESTs	1.41	2.83
	448567	AI901750	Hs.193514	ESTs	1.48	2.45
	409829	A302165	Hs.55378	potassium voltage-gated channel, Shal-e	1.70	2.23
45	416617	H85311	Hs.205980	ESTs	1.83	2.04
	462286	AI767250	Hs.165240	ESTs	0.58	0.43
	404606			Target Exon	1.47	3.78
	401614			Target Exon	2.00	1.91
	428403	AI393408	Hs.225159	Insulin rich repeat (in FLJ) Interactin	0.33	0.21
50	433390	AA598950	Hs.260180	Homo sapiens mRNA; cDNA DKF2p761G18121 (2.00	4.90
	451443	AV256327	Hs.210303	ESTs	1.87	2.25
	411188	8E161168		gb:P40-HT0425-170100-002-a11-T0425 Homo	1.15	1.59
	452704	AA127233	Hs.149424	Homo sapiens PNAS-130 mRNA, complete cds	2.64	1.65
	424080	X92108		H.sapiens mRNA for subtelomeric repeat s	2.40	2.58
	433331	AI738815	Hs.117323	ESTs	1.46	2.10
55	428620	AA331901	Hs.134738	hypothetical protein FLJ10067	0.44	0.19
	439432	AF882010	Hs.103169	ESTs	0.42	0.26
	426736	AA431615	Hs.130722	ESTs	1.90	2.45
	416225	AA577730	Hs.189594	ESTs, Weakly similar to PC4259 fertilin	2.72	6.25
	404817			Target Exon	1.60	2.15
	448955	AW207597	Hs.29102	ESTs	2.08	1.75
	402797			Target Exon	2.12	1.37
	457951	U23660		gb:Human clone mcag19 chromosome 16 CTG	1.72	2.00
	426982	AA145707	Hs.173991	ubiquitin-like 3	0.36	0.17

TABLE B6

Play: Unique Eos probe/identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Play	CAT Number	Accession
	408139	10421_1	AA451566 NM_016370 AB036683 AL129228 RS8124 AK34847 AL119333 W07265 AI334284 H20505 AI152885 AA652438 AW172843 W19794 N21450 AI743862 AW330522 AG61348 AD24553 AA092684 NB0848 AA699329 AB24676 R26624 R49663 AW807321 AW807262 AW17704 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140542 AW807178 AW807167 AW807398 AW807320 AW807305 AW845866

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408283	1050275_1	BE141579 AW807555 AW807502 BE141596 AW845845 AW807500 AW845854 AW807480 AW807486 AW807478 AW178109 AW807228 AW807374 AW807129 AW846124 AW807470 AW807477 AW807510 AW807208 BE141573 AW807455
408839	1065657_1	AW273084 R27662 R26190 D78194
409128	110156_1	AK263436 AW832323 AW180863 A083503 AA72927 AW763492 BE175371 AA311147
409282	111512_1	AW866480 AW866640 AA354646
409291	1115745_1	AW733472 AW373484 BE071899 BE071898
409367	1123651_1	AW382767 BE153835 BE153702 BE153572
409688	114831_3	A150485 AW839352 AW076894 AW834222
409692	114881_1	AW80724 AA396661 AA395981 AWT1084 AA423611 T07531 AID94335
409894	1157906_1	BE021731 AW817738 AW503629 BE081969
410154	117860_1	F06959 Z43559 AA082002
410357	1197159_1	AW863814 BE046540 AW457600 AW627443 BE046544
410542	1213736_1	AW730274 Z44444 X06393
410725	1218207_1	AW795275 AW795395 AW799392 AW799276 AW799479 H57895
410730	121847_1	AW366850 AA457091 AID90341 AA088523 W88852 AW979154 AA826016 R54779
410744	1219465_1	H88002 V92289 AW801558 AW801324 AW801270 AW801307 AW801357 AW801299 AW801609 AW81356 AW601420 AW801425 AW81355 AW801429 AW801428 AW801427 AW801424 AW8001305
410840	1223800_1	AW986624 AW866537 AW866473 AW866256 AW866390 AW866475 AW866454 AW866309 AW865539 AW355521 AW868547 AW866517 AW869453 AW866569
410966	1227882_1	AW936322 AW938307 AW538320 AW538323 AW811840
411008	1229027_1	AW813238 AW813474 AW813334 AW816061 AW813296 AW813363 AW813397 AW813327 AW813328 AW815903 AW816140
411020	1229372_1	AW813765
411141	1233793_1	AW819581 AW819682 AW819583 AW819588 AW819489 AW819458 AW819090 BE065061
411184	1234977_1	AW821117 AW855541 AW855505 AW855374
411188	1235093_1	BE161198 BE162486 AW621260
411245	1236412_1	AW333441 AW533552 AW533700 AW833610 AW833873 AW833675
411347	1238924_1	AW838126 AW838294 AW838247 AW838251 AW538292 AW538299 AW838374
411432	1245630_1	AW846272 AW846264 AW846545 AW846265 AW846135 AW846317 AW846200 AW846265 AW846326 AW846199 AW846357 AW846153 AW846286 AW846319 AW846277 AW846381 AW846438 AW846481 AW846352
411495	1248073_1	AW849241 AW849359 AW849243
411507	1248774_1	AW851650 AW851703 AW851735 AW851723 AW851708 AW851712
411590	125064_1	T98183 T64070 AA094314
411808	1251259_1	AW853441 BE145228 BE145421 BE145162 BE145283
411652	1252638_1	AW855593 AW855550 AW854524
411680	1263110_1	AW873477 BE089101 T05999
411918	1265907_1	AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198
411920	1266512_1	AW876293 AW876257 AW876261 AW876273 AW876231 AW876358 AW876334 AW876134 AW876371 AW876308 AW876314 AW876328 AW876199 AW876331 AW876426 AW876427 AW876322 AW876323 AW876240 AW876141 AW876131 AW876129 AW876168 AW876376 AW876269 AW876415 AW876329 AW876388 AW876343
412085	1278467_1	AW891967 H53998
412252	1285293_1	AW903782 AW903688 AW903672 AW903763 AW903784
412274	128647_1	AA101443 R20532 F07484
412298	1288095_1	AW938300 AW938336 AW938386
412302	1288128_1	AW938334 AW938371 AW938474
412579	1321220_1	BE144782 AW975091
412902	1335168_1	BE080818 BE080825 BE080828 BE007569 BE007594 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020 BE008015 BE008021 BE008028 BE008023 BE008030 BE008014
413035	1345295_1	BE155583 BE155574 BE155556 BE061294
413068	1348104_1	BE063792 BE063803 BE063775 BE063901 BE063806 BE063777 BE063794 BE063806 BE066125 BE063782 BE063805 BE063812
413196	1353222_1	AA127385 R15644 AA127404
413340	136323_1	AA127656 AA455087 AA252503
413444	1370831_1	BE141019 BE141473 BE141529
413489	1373392_1	BE144228 BE144291
413593	137691_1	AA205248 AA130656 AA204737
413645	1381441_1	AA130692 AA593635 AW986537
413650	1381628_1	T97703 BE155222 BE155240 BE155274 BE155275 T92469
413750	1385590_1	BE161453 W28203
413855	1397268_1	BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177443
413898	139750_1	AA580288 AA315856 AA133031 AA377478
414051	1413105_1	BE244127 BE246216
414623	1458592_1	BE391650 BE389191 BE389697
415054	151827_1	AT733067 AA159708 AT732614
415110	1522905_1	H04043 D80988 D80337
415157	1526616_1	D62557 D78198 D63214
415291	1534070_1	F08724 Z43620 R21681
415378	1535274_1	T16954 F07075 H10236
415449	1537026_1	H15034 T17195 F00069
415770	155437_1	AT92327 AD39728 AA169206
415808	155896_1	AA169580 AA169840
415850	156990_1	AID21875 AA170935 AA866613
416269	156454_1	AID26700 AA720344 AA191420 AID23543 AA168633 AA172056 AW958465 AA172236 AW959397 AA355066
416311	158797_1	D60529 D87178 H48333 AA175446 AA357794
416463	1595998_1	H55241 H57540 R00735
417089	154830_1	AA194446 AA194460 AA193162 AA196396 Z24810
417117	1551230_1	NA6778 W88339 N75221
417324	166714_1	AW265494 AA455904 AA156677 AW265432 AW991605 AA455370

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		A1608126 AW000569 AW053317 AL115781 T61046 A1063563 H51956 AF114144 AA306739 AW059034 AW75928 AW793510 ALD47737 AV055047 AV0550632 AD750389 AA020063 AA052978 H85367 T61597 R23745 Z20418 T58445 AT751528 AW008121 AA853188 AT752459 AA053711 AW059663 R7894 R3035 R21026 R21522 AV056568 AA504121 AW061186 AA425703 A3145158 AA445521 AA445522 C75005 AF033579 NM_009555 AA454584 N85405 AA547586 AL133561 AL106100 AL117481 AL122069 AW435252 A1568626 BE041295 AA445162 AA521546 AA715590 AA689102 AW070522 AA563005 AA020598 AA502585 AA502805 T52 188 AW572724 AA522631 AA877958 A1034565 AW027539 AW056996 AW400775 AA528756 AA221058 R07170 DES07038 DES4757 C18536 AW012068 T52565 AA227415 AA233942 AA223237 AA68403 AA801627 AW069639 BE061833 BE000320 AW061170 AW047519 AA308542 AW021833 AW945688 CD4699 AA205504 AA372741 AW021687 AA025720 AW017581 AW056468 AA155715 AA117928 T03007 AW754296 AA227407 AA113928 AA307504 C16859 AA568548 AE000306 AA554053 AB11555 AB26259 AW070318 AA1573619 AW573602 R08736 AW162474 AA58442 AW02040 A1798376 546400 AW061161 AW081161 W00557 BE142245 AW068222 AW061851 AW068362 AA232351 AA218567 AA005556 AW088231 AW057541 AW041472 H06214 AW014358 AF134164 AA243083 AA117345 AA199942 AA223384 AA227092 AA227080 T12379 AA062174 T61139 AA149776 AA059520 AW079188 AW013367 AW013538 A0207168 AA157718 AA157715 AA103472 AA100774 AA130056 AA157706 AA157730 AA157715 AA053238 AW04581 AW054566 C05254 AW062338 T02637 AW011621 AA205593 AA220204 BE159625 AA228624 A1823309 AW0591567 H06951 AA027374 H06215 AA045564 A694260 H0608 AB145726 AW155620 BE081333 BE075424 AW017662 AW0817705 AW0817703 AW0817659 BE081531 H05570 AW082235 AF156166 R07008 AA654078 AW063313 A1850909 AA628601 AL129633 BE050435 BE146154 BE146151 X00138 AW057957 AA479543 AA811289 A082428 AD740585 AA717764 AA771806 A033876 BE000596 AW0204531 C08676 W00581 Y56157 H05313 AW070708 AA281642 AW04440 A334464 R0024 T83378 AW073562 T55662 A1299190 BE174210 AW579001 HC1811 W40186 R67100 AB220386 AW052164 AA628440 AW058607 AW058616 AA709126 AW098628 AW059544 AA047932 AW059825 AW058622 A176125 AL185720 AW051069 AA567330 T52532 BE487706 AW243400 AW043842 A1828245 A1185532 DE2654 DE0217 D52715 D53477 D53933 D54679 A028739 AF145864 A1622204 N58343 BE174213 AA045571 AB13854 A1214515 AB35252 A133455 AF107007 A185085 AW064520 A024766 A004722 AW008740 A165513 N54664 A102835 AW512380 A061126 A338138 AB051066 A1636506 A1024765 AA513015 AA573598 X55196 AA502595 A1334784 A1869754 AA010207 AW090091 AW513771 A1851381 A1337571 T52459 AA050205 A1640608 H75566 AA63487 AA35868 AB01767 A1866255 AA780964 A1658715 BE174156 AD028094 AW052155 T55581 H76072 A1611201 AA510812 A1220713 AW145305 A1758412 AA045713 R79750 W0608 L06708 L0345 L09094 L09096 L03165 L09102 M27346 AF086410 Y94386 W74609 AW0578245 DE3277 AA840568 BE351384 AW732707 A1245665 A1973095 R16291 AA532515 AA057534 A1690070 BE175102 A1694512 AW050890 AA069613 AW067693 A1033188 BE004743 AW064704 BE004795 BE178660 BE089438 BE089378 DE089433 DE089437 BE089423 DE089426 DE089424 BE089426 Z43813 AA320151 AW054563 H15886 R03872 AW016773 A0522778 AA02357 AW005239 A1126068 A184746 A1148521 T17870 AL103987 A1139527 RA4007 N54421 A140476 AW018548 T53038 A105354 A1145229 A102007 A10300771 A1635739 A1606226 AW044010 R09042 R40388 AW150439 AW297340 A1238945 A131119 AW074013 AA557267 N3812 A187998 A873565 A185869 A1248241 BE158865 BE158868 R131107 A041136 A185193 H01953 BE101805 AW079041 A0030038 AW000325 AA343675 AW044205 AL038020 BE001013 BE010033 AW053901 BE174377 A1309717 A1345651 A15033726 BE176651 AW050394 A1233875 R45082 R45781 T44706 A1820675 A1732253 R53428 A1820074 A172293 R54983 A1733221 R55640 R55639 A1820744 A1503765 A1811154 BE0007147 AW130760 DE069552 BE066341 A1507683 AL0434915 T515976 AL137967 DE054160 BE064186 AL138129 AL138175 BE064231 AW1753456 AW753036 AW051868 AW054862 AW030580 AW030574 AW010024 AW010555 AW0810196 AW010615 AW010507 AW0811114 AW0811095 AW0811087 AW0811124 AW0811054 AW0811054 AW0811157 AW0811324 AW0811325 AW0811326 AW0811333 AW0811329 AW0811328 AW0811332 AW0811335 AW0811335 AW0811633 AW0811652 AW0811698 AW081275 AW0812846 AW081274 AW0854530 AW081431 AW0814190 AW0814115 AW0854541 AW081558 AW081571 AW0815453 AW0815856 AW0815613 AW0815450 AW0815808 AW0815426
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5	454741	1232559	DE154336 AWB17058 DE154393
	454826	1236377	AWB33376 AWB33379 AWB33677 AWB33449 AWB33630 AWB33626 AWB33444 AWB33395 AWB33791 AWB33959 AWB33432
	454815	1242343	AWB33634 AWB33659 AWB33853
	454866	1251800	AWB61610 AWB1958 AWB33501 AWB51985
	455087	1252832	AWB53522 AWB54311 AWB54340 AWB54461
	455116	1254206	AWB53539 AWB55559 AWB55420
	455236	1259642	AWB57271 AWB57308 AWB57296 AWB57528
	455500	1276462	AWB57167 AWB575983 AWB76974 AWB76000 AWB75966 AWB76050
10	455560	1289442	AWB76192 AWB76559 AWB81917 AWB76119 AWB76112 AWB76580 AWB76189 AWB76182 AWB76188 AWB76169 AWB76185 AWB76186
	455547	1289347	AWB33815 AWB35351 AWB35728 AWB36360 AWB339581 AWB339551
	455508	1318907	AWB76165 C04000
	455527	1322125	AWB84478 AWB84468 AWB84495 AWB84477 AWB84480 AWB845404
	455942	1348153	AWB76192 AWB76368 DE004334 DE046428 DE063874 DE063895 DE064033 DE064043 DE064043 DE064043 DE064043 DE064043 DE064043
15	455743	1349789	AWB568261 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181 AWB56181
	455755	1350570	BE075124 BE075124 BE075278
	455753	1356657	BE075931 BE079371 BE079372 BE079373 BE079496 BE073604 BE075950
	455906	1382301	BE159305 BE159188 BE159238 BE159377 BE159374
	455979	1382794	BE159770 BE159770 BE159770 BE159770 BE159770 BE159770 BE159770 BE159770 BE159770 BE159770 BE159770 BE159770
	455988	1392794	BE159729 BE159815 BE159844 BE159831 BE159849 BE159797 BE159764 BE159801 BE159603 BE159763 BE159652
20	455988	1392794	BE179983 BE178322
	455988	1425951	AWB50979 AWB135603 AA136556 AWB14381 AA364358 AA62073 BE160845 AA09054 AW238038 AW102112 DE046105 AW1011367
	456172	1630643	DE11938 BE0111932 BE011215 DE011365 DE011363
	456332	1719014	795950 R05007 H5742
25	456381	1841231	AA226357 AWB41786 AWB41716
	457297	1317374	AA236005 AA459341 AA237099
	457395	1331064	AWB90981 AA46168 AA465268 AA466298
	457581	1357446	AWB57689 AA522167 AA507545
	457581	1359836	AWB57689 AA522167 AA507545
	457581	1359836	AA578512 AWB55535 BE177533
30	457671	1365757	BE04740 AWB42730 AWB27623 BE114139 BE044716 BE046237 BE046551 AA653908 BE166581
	457671	1426379	AA102724 AA66236 BE550796 AA521204 AA197307 AA375358 AW990086 AB28424 AA95270 AA91608 AA370741
	457851	144517	U28500 U0739
	457851	144517	AB04205

TABLE 8C

Key: Unique number corresponding to an Eos probe set
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham I. et al., Nature (1999) 402:489-495.
Strand: indicates DNA strand from which exons were predicted.
Nt position: indicates nucleotide positions of predicted exons.

	Filey	Ref	Stand	NI_positon
45	406704	8118864	Minus	83110-83201
	406800	8570385	Plus	157683-158036
	406834	8705192	Plus	121853-122086
	406840	8118868	Plus	113882-114121
	406850	1927150	Minus	4506-4691
50	406881	2824777	Minus	91446-91503 9213-92266
	401016	8117441	Plus	128234-128339, 128503-128236
	401080	8492074	Plus	118236-119146, 119392-119657
	401215	9659408	Plus	103739-103919
	401241	8827300	Minus	35053-30404 31056-31248
	401335	8848481	Plus	16736-16035
55	401381	8570225	Minus	118236-119146, 119392-119657
	401400	7705276	Minus	33028-33585
	401459	8862292	Minus	125251-126239
	401473	7349301	Plus	115142-117005
60	401577	6280197	Minus	115142-117005
	401588	5100594	Plus	89638-89024 14115-141281, 142217-142240
	401595	7688975	Minus	182379-183621
	401589	8468551	Plus	5006-5425, 5810-7042
	401713	7656694	Plus	106934-107403
	401814	7409552	Plus	136003-136726
	401828	7476933	Minus	169604-11674, 11671-1817
	401850	8516144	Plus	148955-153904, 149559-150002
	401860	8968070	Plus	126688-127024
	401913	8395020	Minus	33753-33801
70	401927	3873185	Plus	112000-112137
	402025	7547159	Plus	172835-173690
	402036	7774532	Plus	590-1294
	402049	8072515	Plus	100555-100411
	402098	7245164	Plus	308397-308749, 849-85158
75	402241	7690313	Minus	129073-122026, 130996-131158
	402284	7226012	Plus	2575-3030
	402305	7332195	Plus	42203-41262

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	402368	9454515	Plus	159906-156863
	402551	9855793	Minus	37346-37633
	402654	8076979	Plus	44029-44003
5	402665	8318556	Plus	59692-55294
	402762	9230904	Minus	123298-124005
	402787	3421043	Minus	12769-15930
	402833	8918545	Plus	26967-27778
	402901	8894222	Minus	175408-125667
10	402948	9358458	Minus	143436-143026,143806-143935
	403068	8654202	Plus	138189-158433
	403072	8654241	Plus	141879-152206
	403146	9798812	Plus	162877-163118
	403197	9630749	Plus	79990-80237
	403214	7630945	Minus	76723-77027,79317-79484
15	403217	7630969	Plus	54089-54163,55427-55523
	403290	8083176	Plus	16294-20076
	403291	7230870	Plus	95177-95435
	403294	8096496	Plus	41555-41681
20	403315	8247953	Minus	125117-125287
	403332	8568139	Minus	31409-31674
	403344	8569725	Plus	70823-70900
	403362	8571772	Plus	64099-64260
	403371	9087276	Plus	105555-105690
25	403391	9438337	Plus	42410-42544,83317-83540,85640-86922,87970-88110
	403488	9866515	Minus	12459-12753
	403536	8076924	Plus	34772-35182
	403779	8018040	Minus	95902-95959
	403859	7708954	Plus	143736-113858
30	403971	7716262	Plus	124545-104737
	403983	7711671	Minus	101185-102597
	403917	7711849	Plus	109718-109847,109927-110202
	403878	8576014	Plus	97326-97308
	404031	7671252	Plus	17477-172316
35	404157	9625594	Minus	77330-77280
	404220	6706820	Plus	45107-45439
	404286	2326514	Plus	51086-51301
	404418	7382420	Minus	153339-153481,155099-155294
	404427	7407959	Plus	127179-127358
40	404428	7407979	Plus	31352-31488
	404440	7528051	Plus	80430-81581
	404495	8151634	Minus	59449-60477
	404560	8539738	Minus	245386-241599
	404605	9212938	Minus	22390-23259
45	404730	8389582	Plus	119832-120016,124110-124275
	404917	7341851	Plus	48330-49488
	405033	7107731	Minus	142358-142546
	405137	8576507	Plus	159889-159423
	405146	9438278	Minus	102529-102633
50	405158	9966252	Plus	42873-43056,43815-43949
	405187	7229825	Plus	117025-117170,118657-118736
	405223	7239814	Plus	161814-160313
	405340	6084835	Plus	46944-40760
	405494	8050982	Minus	70284-70518
55	405551	1552506	Plus	12825-12997
	405654	4895155	Minus	53624-53759
	405657	4726099	Plus	5798-5814
	405673	4589984	Plus	50700-50942
	405704	4204244	Plus	138842-139051
60	405723	9801868	Plus	114895-115351
	405727	9538331	Minus	78865-78954
	405760	8069938	Minus	37424-33045
	405779	7280331	Minus	33048-33355
	405944	7837302	Minus	5143-5934
	406002	8547797	Minus	154007-154579
65	406106	8272661	Plus	41341-41940
	406097	7107918	Minus	36898-37269
	406104	9124028	Plus	35309-35977
	406155	7144867	Plus	378-587
	406207	5923650	Minus	163607-162800
70	406300	6479046	Minus	15234-19401
	406308	9211532	Plus	358406-358651
	406314	9211609	Minus	12399-13011,18022-18135
	406317	9211852	Plus	138618-139410
	406432	9256504	Plus	3904-3903,4029-4120,4928-5109
75	406490	7711309	Minus	80295-80480
	406584	3983530	Minus	3938-4497

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TABLE 9A: Genes predictive of no/border cancer progression

	Exon:	Unique Ecos probe(s) identifier number	Unigene Title	R1	R2
	Exon:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	RT	80th percentile of Ta or T1 tumor AIs from patients who did not upstage divided by the 80th percentile of Ta or T1 tumor AIs from patients who did upstage			
	R2	median of Ta or T1 tumor AIs from patients who did not upstage divided by the median of Ta or T1 tumor AIs from patients who upstaged			
5					
10					
15					
20					
25					
30					
35					
40					
45					
50					
55					
60					
65					
70					
75					

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	424637	NM_015057	Hs.151411	KIAA0916 protein	2.32	2.55
	413804	T64682		cbyce/EBG2.L1 Stratagene liver (537224)	2.32	1.46
	411069	NM_000074	Hs.318501	Homo sapiens mRNA full length insert cDN	2.32	2.90
	430028	BE564110	Hs.227750	Target CAT	2.32	2.26
5	417720	AA205625	Hs.208067	ESTs	2.32	2.09
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.31	1.13
	454219	X75042	Hs.44313	v-sil avian reticuloendotheliosis viral	2.30	4.38
	447445	AF117754	Hs.11881	tryptid hominase receptor-associated prot	2.30	1.06
	401879	AL024244	Hs.40445	poly(A)-specific ribonuclease (deadenyla	2.29	2.15
10	424679	RS3718	Hs.107682	hypothetical protein FLJ10369	2.29	2.79
	458949	AW291777	Hs.346137	ESTs, Weakly similar to T08590, probable	2.28	1.85
	407191	AA608751		gbac56067.s1 Stratagene lung carcinoma	2.27	2.42
	446387	AI955411	Hs.94109	Homo sapiens cDNA FLJ13534 f5, clone PL	2.27	1.18
	405155			Target Exon	2.26	1.94
15	445594	AW056463	Hs.12940	zinc-fingers and homeoboxes 1	2.26	1.55
	417458	NM_003695	Hs.82173	TGFb Inducible early growth response	2.25	1.95
	430315	NM_001295	Hs.235147	guanine dinucleoside	2.24	1.84
	411945	AL033527	Hs.52137	w-myc avian myelocytomatosis viral oncog	2.24	2.73
	408937	AA210734	Hs.291386	ESTs	2.24	3.18
20	414174	AL133990	Hs.190542	CEGP1 protein	2.23	1.00
	434094	AA050599	Hs.236205	hypothetical protein PRC2013	2.22	4.08
	426097	AK001214	Hs.103914	hypothetical protein FLJ10362	2.22	2.15
	420164	AW039037	Hs.24908	ESTs	2.22	2.16
	414099	U11313	Hs.75760	sterol carrier protein 2	2.21	4.05
25	424800	AL035568	Hs.152303	MyoD family inhibitor	2.21	3.53
	459055	AA447478	Hs.144538	ESTs, Weakly similar to ALU1, HUMAN ALU S	2.21	2.90
	416290	NM_000016	Hs.75158	acyl-Coenzyme A dehydrogenase, C-4 to C-	2.20	4.00
	439206	AK000299	Hs.180552	dyncortin 4 (p62)	2.20	1.88
	401563			C10061262.g17049811r0[NP_038526.1] ca	2.20	1.77
30	424867			C90002715.g111994817f0[AB062754.1] JA	2.19	2.80
	443203			compar 7, opothic-related cysteine pr	2.19	2.08
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	2.19	2.21
	403835	AW853954		chromosome 2 open reading frame 2	2.18	3.00
35	458585	APC35526	Hs.153963	MAD mothers against decapentaplegic, D	2.18	2.45
	431899	AA305688	Hs.287695	UDP-Galactose-4-epimerase 1,3-pyridoxyl	2.17	1.85
	418026	BE179727	Hs.83213	fatty acid binding protein 4, adipocyte	2.17	2.87
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.17	1.71
	499038	Y14443		zinc finger protein 200	2.17	1.71
40	434278	AW880709	Hs.283863	chromosome 8 open reading frame 4	2.17	1.00
	441623	AA515805		desmoglein 2	2.17	1.81
	459244	AW053990	Hs.142442	HPI-BP74	2.17	4.03
	424720	MB9907	Hs.152292	SWI/SNF related, matrix associated, acti	2.17	2.92
	404204			ENSG0000G252204.2 Zinc finger protein 165	2.17	1.62
45	433987	AA323750	Hs.236026	Homo sapiens, clone MA06-024732, mRNA,	2.16	2.85
	411400	AA311919	Hs.658851	nucleolar protein family A, member 1 (pV	2.16	3.60
	454849	AW847310	Hs.290131	KIAA1819 protein	2.16	1.96
	492923	AA312572	Hs.8241	phosphoinositide-3-kinase, regulatory su	2.16	1.48
	418030	BE202573	Hs.83321	neurexin 5	2.16	2.57
50	435984	AI075407	Hs.296083	ESTs, Moderately similar to IS4374 gene	2.16	2.32
	459611	AI142379		gbac35401.s1 Soares_testis_NH1 Homo sap	2.16	1.85
	437559	AI878033	Hs.121476	ESTs	2.15	1.43
	418827	BE327511	Hs.47168	HT2121	2.15	3.94
	417470	AF112219	Hs.82193	esterase D/ormylglutathione hydrolase	2.15	1.74
55	421012	XS3281	Hs.101025	basic transcription factor 3	2.15	1.26
	448772	AW390822	Hs.301528	L-lysine/epsilon-amino acidipic acid amino	2.15	4.95
	439601	AB025032	Hs.8608	KIAA1109 protein	2.15	2.15
	434471	AL110125	Hs.38443	Homo sapiens mRNA: cDNA DXF2p58F2224 (f	2.15	1.45
	424965	AF011533	Hs.153663	lymphocyte antigen T5	2.15	2.63
60	400752			NM_003100.1 Homo sapiens scf-like-related	2.14	2.67
	438516	AW188484	Hs.101515	ESTs	2.14	2.38
	430024	AB087870	Hs.227730	integrin, alpha 6	2.14	2.00
	402345	AI849109		hypothetical protein FLJ20783	2.14	1.40
	421939	BE168531	Hs.109727	TAK1-binding protein 2, KIAA0733 protein	2.13	1.58
	442315	AA173992	Hs.73956	ESTs, Moderately similar to ZN61, HUMAN Z	2.13	2.67
65	419591	AF060900	Hs.91353	Homo sapiens cDNA: FLJ21687 f5, clone H	2.13	2.00
	458025	AI275408	Hs.329450	ghn155-10.s1 Soares_NH1MP1_s1 Homo sap	2.12	0.89
	428582	BE306699	Hs.185055	GENE protein	2.12	2.65
	422749	W01076	Hs.278573	CDS9 antigen p18-20 (antigen identified	2.12	2.73
	433931	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.11	0.91
70	454421	AL130436	Hs.31973	hypothetical protein	2.11	2.61
	421508	NM_004533	Hs.156115	absent in melanoma 2	2.11	3.13
	422760			NM_021757.1 Homo sapiens eosinophil chemo	2.09	1.79
	406274			Target Exon	2.09	1.60
	408837	MS7417		g3-homo sapiens muslin (musn) mRNA, par	2.09	1.00
75	439632	W74031	Hs.55279	serine (or cysteine) proteinase inhibitor	2.09	2.92
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 f5, clone C	2.09	3.20
	442271	AF000852	Hs.8180	syndecan binding protein (syndecan)	2.09	1.90

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	128336	AA031115	Hs.183752	microsomino protein, beta-	2.08	1.15
	405165			ENSP0000228074? Homeobox protein NKX2-3	2.07	2.83
	416099	AW192747	Hs.21122	hypothetical protein FLJ11835 similar to	2.07	3.71
5	436865	AA307279	Hs.35947	methyl-CpG binding domain protein 4	2.07	1.71
	439924	AS85897	Hs.125283	ESTs	2.07	1.00
	439004	AW570652		glcES1391172 MAGE resequences, MAGP Homo	2.07	2.13
	407855	BE538759	Hs.10909	ESTs	2.06	1.91
	412986	BE045264		glcHS3608x2 NCL_GCAP_RDF2 Homo sapiens	2.06	2.58
10	414013	AA766605	Hs.47059	hypothetical protein FLJ21212	2.06	5.00
	415249	RA0516	Hs.21248	ESTs	2.05	2.18
	427352	RG5418	Hs.261161	ESTs, Weakly similar to I38022 hypothetical	2.05	3.35
	426521	AF161445	Hs.170219	ESTs, Weakly similar to T50606 hypothetical	2.06	1.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 25kD (conn	2.06	6.03
	423851	R33605	Hs.133342	Homo sapiens clone 24566 mRNA sequence	2.05	1.88
15	410028	AW576154	Hs.346502	ESTs	2.04	1.95
	405575			Target Exon	2.04	1.55
	467148	AF091035	Hs.184627	KIA04118 protein	2.04	3.11
	449524	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fs, clone H	2.04	2.42
20	429837	NM_003895	Hs.225930	sialyltransferase 9 (CMP-NeuAc:GlcA2) alpha	2.04	1.57
	440875	AW055054	Hs.47885	ESTs, Weakly similar to HCC1_HUMAN CALCI	2.04	2.08
	411588	AA455459	Hs.164460	ESTs, Weakly similar to T50606 hypothetical	2.04	2.85
	433203	AF007835	Hs.32417	hypothetical protein MGC4309	2.04	2.35
	446187	AK001241	Hs.14220	hypothetical protein FLJ10370	2.04	2.03
25	420838	AW118210	Hs.42321	ESTs	2.03	1.00
	445481	AW051845	Hs.346330	ESTs	2.03	2.49
	448175	BE298174	Hs.225190	hypothetical protein FLJ13102	2.03	2.25
	410500	AW575742		ESTs, Moderately similar to S55557 alpha	2.02	2.10
	401177			Target Exon	2.02	2.59
30	448474	A792014	Hs.13803	hypothetical protein FLJ10548	2.02	4.23
	434782	NM_006032	Hs.4114	platelet 3 (T) alpha	2.02	1.48
	424125	M31569	Hs.1735	inhibin, beta B (activin AB beta polypep	2.02	2.93
	424241	AW595848	Hs.182330	Homo sapiens pyruvate dehydrogenase kina	2.02	2.63
	424573	AA345551	Hs.264052	ESTs, Weakly similar to I38022 hypothetical	2.02	3.43
35	414721	J90302	Hs.77051	ribosomal protein L10	2.02	1.60
	429869	AIDC7018	Hs.15977	Target CAT	2.02	1.47
	439177	AW820275	Hs.76811	ESTs, Weakly similar to I38022 hypothetical	2.01	1.94
	437175	AW598678	Hs.87772	protein kinase, cAMP-dependent, catalyti	2.01	1.84
	452046	AB018345	Hs.27657	KIA04032 protein	2.01	4.31
40	417515	BE548541	Hs.82034	hypoxanthine phosphoribosyltransferase 1	2.01	6.75
	420337	AW205840	Hs.14555	Homo sapiens cDNA: FLJ21513 fs, clone C	2.00	2.75
	408232	AL137289	Hs.43859	Homo sapiens mRNA; cDNA DKFZp434C1714 J	2.00	2.02
	408409	AW838191	Hs.276337	Homo sapiens cDNA FLJ11537 fs, clone HE	2.00	1.95
45	433258	AW694447	Hs.329408	ESTs, Weakly similar to S25595 hypothetical	2.00	0.91
	429959	A1836504	Hs.2093	CDC-like kinase 1	2.00	3.60
	420553	R35343	Hs.20958	Human DNA sequence from clone RP1-233G16	2.00	1.95
	444918	AB028958	Hs.12144	KIA1003 protein	2.00	1.23
	452286	AJ358070	Hs.12935	ESTs, Weakly similar to ZNF1_HUMAN ZINC	2.00	5.30
50	414006	AA157911	Hs.72200	ESTs	1.99	1.22
	414178	BE140538	Hs.76794	endothelial differentiation, lysophospha	1.99	3.63
	414557	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	1.99	2.31
	428448	AA062160	Hs.63359	ESTs, Weakly similar to TRIM_HUMAN TRICH	1.99	3.43
	408437	AW937744	Hs.27849	lactoferrin-rich protein	1.98	2.15
	435205	AF087990	Hs.42758	Homo sapiens, clone IMAGE3354845, mRNA,	1.98	2.28
	442505	BE865411		ESTs	1.98	3.95
55	447731	AA373527	Hs.15985	OG-59 protein	1.98	2.87
	410579	AK001678	Hs.54951	KIA04043 protein	1.97	1.43
	426716	NM_006379	Hs.171922	semA domain, immunoglobulin domain (Ig)	1.97	2.50
	458141	AT751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fs, clone H	1.97	3.03
60	419576	AK002060	Hs.91251	hypothetical protein FLJ11158	1.96	2.85
	407241	MA5416		glutathione conjugate light chain protein 14.1	1.96	1.99
	420564	A1881270	Hs.59824	BCE-1 protein	1.96	1.75
	448586	AF285120	Hs.283734	OSL-204 protein	1.96	3.23
	409089	HE5799	Hs.42644	Nicotinamide-like	1.96	4.00
65	421100	AW351630	Hs.124650	Homo sapiens cDNA: FLJ21763 fs, clone C	1.95	2.12
	452518	AA298722	Hs.14758	ESTs, Weakly similar to I38022 hypothetical	1.95	3.45
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA UICP-59500724 f	1.94	2.89
	434263	N34895	Hs.44648	ESTs	1.94	4.50
	409829	M33352	Hs.56729	lymphocyte-specific protein 1	1.94	1.73
70	425593	AA278921	Hs.1958	proteoglycan 1, secretory granule	1.94	2.39
	461835			Target Exon	1.94	2.27
	409557			C5000893.7[622685]pp[38526]EFG_THEMEA	1.94	2.29
	440052	A1350518	Hs.126952	ESTs	1.94	3.15
	410442	BE24024	Hs.93788	oxopropyl Coenzyme A carboxylase, beta 2	1.94	2.70
75	437891	BE255012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.94	2.60
	420230	AL034344	Hs.284186	protein bound box C1	1.93	2.28
	452970	NM_012238	Hs.31176	sirtuin (silent mating type information	1.93	4.35
	403728			Target Exon	1.92	1.70

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5	415789	H01581	(b3)3308r1 Scores pazonia Nb2HP Homo	1.92	2.16
	405759	AA654582	ATP synthase, H transporing, mitochondr	1.92	2.10
	442073	AW973443	RNA (guanine-7) methyltransferase	1.92	4.45
	438023	AF204883	FEM-1 (C. elegans) homolog b	1.92	4.00
	445502	AW379160	DKFZP454J214 protein	1.92	2.13
10	405474	NM_014892	NM_001033+Homo sapiens acetyl-Coenzyme	1.92	2.58
	430007	AF151196	KIAA1116 protein	1.92	3.78
	418066	AW971155	CG1, Weakly similar to ISHUSJ protein d	1.91	1.88
	744440	AF153230	hypothetical protein DKFZp656K142	1.91	1.61
	451154	T07643	transcription factor F-like 2 [T-coff.sp	1.90	3.35
15	414716	AA587891	amyl-1.6-glucosidase, 4-alpha-glucanotr	1.90	3.55
	445841	AL080115	DKFZP66G0222 protein	1.90	1.46
	425294	AF155560	NS1-associated protein 1	1.90	3.65
	437549	NM_016353	rec	1.89	1.73
	445426	AI373652	hypothetical protein MGCS370	1.89	2.75
20	400111		Eos Cortisol	1.89	3.84
	437762	T76028	Hs.154567s	1.89	1.00
	404069		synaptotagmin I	1.89	1.00
	434502	AW974687	Target Exon	1.90	2.61
	414220	BE259094	glsE31305776 MAGE resequences, MAGM Homo	1.89	3.35
25	422506	R20505	glsE3110231F1 NH_MGC_17 Homo sapiens c	1.89	1.00
	417439	AW602154	socle	1.87	1.13
	404561		E74-like factor 2 (zeta domain transcript)	1.87	1.13
	420187	AK001714	Target Exon	1.87	1.00
	445950	AA305800	hypothetical protein similar to aakrin	1.86	2.93
30	400834		hypothetical protein AF140225	1.86	1.90
	404455	C19034	C10000818+gi7681882[enNP_055697.1] K	1.86	2.80
	422562	TE3882	Homo sapiens cDNA FLJ114175 fs, clone NT	1.86	1.32
	452170	AF064801	ESTs	1.86	3.44
	436004	AV650537	palchid related protein translocated in	1.86	2.64
35	425484	AA379558	succinate-CoA ligase, GDP-forming, beta	1.85	1.81
	411609	AV653580	KIAA1457 protein	1.85	2.60
	411293	AL137751	gRRC3-2N1033-4250209-013-003 EN0343 Homo	1.85	1.10
	412643	AF007555	Homo sapiens mRNA cDNA DKFZp434A0912 f	1.84	3.70
	401512		protein tyrosine phosphatase, receptor I	1.84	2.58
40	415969	H11294	NM_014083Homo sapiens dual oxidase-like	1.84	1.52
	444736	AA333491	ESTs	1.84	3.08
	426418	M90464	ESTs	1.84	1.22
	415968	AA412686	collagen, type IV, alpha 5 [Alport syndr	1.84	2.35
	442561	BE814474	ESTs	1.84	2.18
45	418650	BE386750	F-box only protein 22	1.84	2.18
	420523	AF057021	polyl endopeptidase	1.84	1.58
	432834	F08459	diffusely expressed in hematopoiet	1.84	1.00
	424885	BE092285	cytochrome b5 reductase 1 (B5R-1)	1.83	3.93
	427659	AW963076	hypothetical protein FLJ13187	1.83	3.10
50	447387	A128331	hypothetical protein 659	1.83	3.03
	418663	AK001100	lybly-type-family protein	1.83	1.78
	419733	AW362955	desmocollin 3	1.82	1.53
	405287	NM_012453	Homo sapiens cDNA FLJ114415 fs, clone HE	1.82	1.00
	413341	H78472	transducin (beta)-like 2	1.81	1.57
55	423910	AL132655	ESTs, Weakly similar to T18067 hypothet	1.81	2.05
	416274	AW160404	BCL2/adrenocortical E10-190-interacting pr	1.81	1.99
	400843	N23532	guanine nucleotide binding protein 10	1.80	1.91
	408285	AW295684	NM_003105+Homo sapiens sortilin-related	1.80	4.88
	413753	U17760	Homo sapiens cDNA FLJ23034 fs, clone L	1.80	2.61
60	428004	AA449653	ESTs, Weakly similar to A48303 P18-associ	1.80	2.33
	401613		laminin, beta 3 (cysteine 125K0), kalfalin	1.80	3.17
	407173	T64349	glutamate-cysteine ligase, catalytic sub	1.80	1.00
	413145	AA049671	Target Exon	1.79	2.66
	418698	AW976721	glycylaldehyde 1 Stragone ne lmg (3772'g) H	1.79	2.39
65	437374	AL350571	EST, Weakly similar to B38022 hypothetic	1.79	2.00
	439680	AW602165	ESTs	1.79	3.52
	410577	Z25317	nirxin (ESK3E interacting protein)	1.79	1.24
	436749	AA584690	CSRP1 protein	1.79	2.39
	453016	AW254546	desmoglein 2	1.78	2.02
70	426595	AA355130	acta3, galactoside-binding, soluble, 4	1.78	0.96
	452946	AA171153	ESTs, Weakly similar to d4MGA15.3 [Hsa	1.78	2.60
	412560	R24601	ESTs, Weakly similar to AF15582 B-cell g	1.78	2.47
	411821	BE295339	hypothetical protein FLJ22804	1.78	2.17
	426768	AF062283	COR4-NOT transcription complex, subunit	1.78	3.13
75	443953	AA478160	three-POZ containing protein similar to	1.78	1.55
	435479	AF197133	B-cell CLL/lymphoma 10	1.78	2.36
	413073	AL038165	Homo sapiens cDNA FLJ13616 fs, clone PL	1.78	2.20
	424273	W27982	ATP synthase, H transporing, mitochondr	1.77	2.03
	419560	AA211505	translocase of outer mitochondrial membr	1.77	2.25
			gb-4349 Human retina cDNA randomly prime	1.77	2.93
			ESTs	1.77	4.19

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	400773		NM_003105 Homo sapiens soritin-related	1.77	1.76
	400176		Eos Control	1.77	2.04
	421351	M29971	Hs.1394	1.77	2.32
	451234	A1814901	Hs.24622	1.77	2.43
5	423332	A1091466	Hs.172741	1.76	1.82
	423960	AA164516	Hs.136309	1.76	2.00
	455469	A067190	Hs.346002	1.76	1.31
	457065	A0202212	Hs.259867	1.76	2.37
	413076	U10564	Hs.75188	1.76	2.18
10	421948	L42583	Hs.334309	1.76	1.00
	463578	R06875	Hs.81810	1.75	3.10
	411430	AW670684	Hs.73875	1.75	2.14
	433995	BE546268	Hs.74346	1.75	1.76
	431448	AL137517	Hs.3306201	1.75	2.36
15	448538	A1559444	Hs.104679	1.75	3.07
	453146	AL358652	Hs.32194	1.74	2.82
	426122	NM_006925	Hs.168075	1.74	2.68
	408969	AW061666	Hs.439500	1.74	2.07
	441715	A1929453	Hs.342655	1.74	2.06
20	412718	X79204	Hs.74520	1.74	2.46
	450789	AW167789	Hs.59438	1.74	2.02
	445537	AJ245671	Hs.3884	1.73	2.59
	400190		Eos Control	1.73	2.40
	416309	R84854	Hs.791914	1.73	1.48
25	410219	T96226	Hs.711552	1.73	2.75
	419814	AW042478	Hs.92215	1.73	2.70
	448625	AW670786	Hs.178470	1.73	2.07
	423287	AA309956	Hs.148566	1.73	2.02
30	417386	AL037228	Hs.82043	1.73	2.44
	459112		D123 gene product	1.73	2.62
	436270	C03769	Hs.339869	1.72	2.54
	405855	AW052461	Hs.101810	1.72	1.88
	411442	N25958	Hs.101810	1.72	1.63
35	402866		Target Exon	1.72	2.63
	401080		Target Exon	1.72	2.63
	402190		C19000335.g10946730y01IP_067362.1	1.72	3.33
	439191	AA281177	Hs.41182	1.71	2.17
	410444	W73454	Hs.132554	1.71	2.70
40	433093	BE185030	Hs.241305	1.71	1.33
	446066	A1343531	Hs.145383	1.71	2.25
	411299	BE409857	Hs.69499	1.71	2.92
	406246	N5569	Hs.333623	1.71	2.00
	454654	A1363529	Hs.331519	1.71	1.53
45	417381	AF164142	Hs.52042	1.70	3.70
	427820	BE222494	Hs.180919	1.70	1.60
	400750		Target Exon	1.70	2.82
	459842	BE143837	Hs.283037	1.70	2.17
	429966	BE981342	Hs.283037	1.70	1.18
50	418444	A180289	Hs.81515	1.70	2.47
	437450	AL390154	Hs.26954	1.70	3.03
	415738	BE539367	Hs.259563	1.70	2.34
	452454		Target Exon	1.70	1.99
55	454843	AA464836	Hs.251079	1.70	2.05
	413611	BE153275	Hs.251079	1.70	2.05
	410190	AW072328	Hs.55728	1.69	2.20
	434813	AA055443	Hs.179509	1.69	2.36
	432170	T58887	Hs.16262	1.69	1.83
	448182	AF244137	Hs.20557	1.69	2.11
60	436293	A1801188	Hs.120910	1.69	2.37
	448524	A1803748	Hs.21366	1.68	2.48
	454221		Target Exon	1.68	2.58
	435906	AW444652	Hs.267054	1.68	2.45
	437987	BE277414	Hs.5547	1.68	1.00
	426125	X87241	Hs.166994	1.68	3.51
65	448813	AF193902	Hs.22142	1.68	1.69
	425192	AK001390	Hs.197842	1.68	1.13
	425558	H27225	Hs.9444	1.67	2.02
	405630		Target Exon	1.67	3.00
70	421010	AA251844	Hs.104058	1.67	3.25
	422940	M37884	Hs.118845	1.67	1.23
	450857	AA529075	Hs.150090	1.67	2.48
	451688	Z43948	Hs.326444	1.66	2.55
	438281	AW182615	Hs.104058	1.66	2.65
	425595		NM_002721 Homo sapiens calcium channel,	1.66	2.23
75	433892	A1829357	Hs.323966	1.66	1.97
	443558	AA376798	Hs.286122	1.66	2.00
	412141	A1183838	Hs.48538	1.66	2.65

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	424685	W21223	Hs.151734	nuclear transport factor 2 (placental pr	1.66	2.88
	400845			NM_003105*Homo sapiens sorcilla-related	1.66	1.61
	447816	NM_007233	Hs.274329	Tp53 target gene 1	1.66	2.63
	404438			Target Exon	1.66	2.34
5	451543	AA397651	Hs.301959	proline synthetase co-transcribed (boole	1.65	2.08
	433233	AB047027	Hs.301804	QAA1494 protein	1.65	3.13
	429538	AL049998	Hs.130409	myeloidlymphoid or mixed-lineage leukemia	1.65	1.37
	435438	H81421	Hs.4890	ubiquitin-conjugating enzyme E2c (homo	1.65	2.35
	431130	NM_006103	Hs.2719	HE4, epidermis-specific, whey-acidic pr	1.65	1.00
10	433235	AB040929	Hs.35089	catenin 3 (pleomorphic tumor associated)	1.65	1.44
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	1.65	2.35
	405324	W76202	Hs.343812	ipic acid synthetase	1.65	2.00
	452207	NM_014517	Hs.26423	upstream binding protein 1 (LBP-1a)	1.65	2.35
15	423630	AB071132	Hs.125952	KJA-0560 gene product	1.65	2.13
	443368	H66417	Hs.17757	pleckstrin homology domain-containing, f	1.65	1.63
	427417	AA341561	Hs.177661	CG-110 protein	1.64	1.28
	450353	A204861	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	1.64	1.60
20	445677	H96577	Hs.6838	ras homolog gene family, member 5	1.64	1.91
	447503	AA115496	Hs.336986	Homo sapiens, Similar to RIKEN cDNA 1810	1.64	2.04
	431234	AL399985	Hs.301637	zinc finger protein 258	1.64	1.53
	418032	AW964955	Hs.5438	Homo sapiens, clone MGC-15763, mRNA, com	1.64	2.05
	407796	AA195509	Hs.39733	postsynaptic protein C9orf1	1.64	2.30
	446298	AF187813	Hs.14837	kidney- and liver-specific gene	1.64	2.05
25	439578	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	1.64	2.26
	429113	D28235	Hs.196384	proteoglycan-endothelium synthase 2 (p	1.64	2.10
	433846	AA460319	Hs.151595	ESTs	1.64	2.05
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	1.64	1.00
	419982	AA252544	Hs.55610	solute carrier family 30 (zinc transport	1.64	2.16
30	401603			NM_022041*Homo sapiens giant axonal neu	1.64	2.73
	431804	AF175265	Hs.264190	nuclear protein sorting 35 (yeast homol	1.64	2.75
	400788			C2030984*gc[10435784:4463614]6688.1[1]	1.63	2.04
	416221	BE513171	Hs.73086	mitochondrial ribosomal protein L3	1.63	2.64
	422491	AA338458	Hs.117546	neuronal	1.63	0.96
35	424737	BE391883	Hs.152107	glioblastoma amplified sequence	1.63	3.45
	416078	AL034349	Hs.7905	protein tyrosine phosphatase, receptor 1	1.62	1.39
	403988			C5001631.g[11056014]ref[HP_067651.1] ac	1.62	2.11
	411486	H88785	Hs.181165	eukaryotic translation elongation factor 1	1.62	2.63
	407874	AU765311	Hs.285047	Homo sapiens cDNA FLJ14059 fs, clone HE	1.62	2.19
	445700	AW206267	Hs.155326	human DNA sequence from clone RP11-145L2	1.62	3.03
40	438184	AA775697	Hs.122125	ESTs	1.62	2.79
	405502			C7000609*gc[280122]p[AC59333 myosin I	1.62	2.55
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	1.62	2.48
	457961	AA772119	Hs.270721	ESTs, Weakly similar to 136522 hypoph	1.62	2.30
45	435774	AW975819	Hs.152654	hypothetical protein FLJ13224	1.62	2.17
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	1.62	2.03
	458660	AU269739	Hs.99601	hypothetical protein FLJ12553	1.62	2.25
	408806			Target Exon	1.62	2.15
	421205	AL137460	Hs.102541	nefrin 4	1.62	1.00
50	424012	AW368377	Hs.137589	tumor protein 63 kDa with strong homolog	1.62	1.74
	427016	AA397525	Hs.191579	ESTs	1.61	2.16
	458182	AW447996	Hs.155933	ESTs, Weakly similar to spliceosomal pro	1.61	2.74
	4511109	F11875	Hs.5534	Homo sapiens cDNA FLJ122951 fs, clone AT	1.61	5.59
	414807	AU738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-N	1.61	1.78
55	465058	AA502764	Hs.123469	ESTs, Weakly similar to AF208555 1-BM-01	1.61	2.10
	447532	AK000614	Hs.18791	hypothetical protein FLJ210607	1.61	1.75
	439544	AA858767	Hs.124623	ESTs	1.61	2.41
	414602	H98931	Hs.166557	ESTs, Moderately similar to ALUC_HUMAN.1	1.60	1.05
	433187	RS3995	Hs.293381	ESTs, Moderately similar to ALU7_HUMAN A	1.60	2.63
	448425	BE268922	Hs.344057	Igfbn A, alpha (actin-binding protein-	1.60	2.43
60	441196	AA921738	Hs.132473	ESTs	1.60	2.69
	425871	AL007089-2	Hs.153336	spnbn-A2	1.60	1.40
	406836	AW514501	Hs.155110	immunoglobulin kappa constant	1.60	1.08
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11345 fs, clone PL	1.60	1.47
	445268	AW365278	Hs.23412	hypothetical protein FLJ20160	1.60	2.89
65	403772			NM_003105*Homo sapiens sorcilla-related	1.60	1.57
	445733	BE295568	Hs.13225	UDP-Gal:betaGalNAc-beta 1,4-galactosyl	1.60	2.03
	429172	U09367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	1.60	2.69
	421887	AW161450	Hs.109207	CGI-86 protein	1.59	1.39
	419127	BE243692	Hs.93552	membrane cofactor protein (CD46, lympho	1.59	1.67
70	402267	AU127035	Hs.308261	hypothetical protein DKFZp454O1279	1.59	2.19
	434538	AW502718	Hs.8115	Homo sapiens, clone MGC-16169, mRNA, com	1.59	2.26
	417924	AU077237	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	1.59	1.76
	418067	AU127958	Hs.83393	crystallin EM	1.59	1.26
	421727	AW602982	Hs.22265	pyruvate dehydrogenase phosphatase	1.59	2.25
75	451938	AU354355	Hs.16697	down-regulator of transcription 1, TBP-5	1.59	2.10
	407325	AA291190	Hs.328476	ESTs, Weakly similar to alternatively sp	1.58	2.43
	410796	Z44547	Hs.3731	ESTs, Moderately similar to 138022 hypot	1.58	1.26

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5	417343	AA197132	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.58	2.84
	416643	U62531	Hs.79410	solute carrier family 4, anion exchanger	1.58	1.26
	408447			NM_001677 homo sapiens scrlin-related	1.58	1.48
	436760	AW069927	Hs.5305	hypothetical protein DKFZ565F122 siml	1.57	1.57
	434327	A1816448	Hs.171889	cholinephosphotransferase 1	1.57	1.64
	451886	BE246998	Hs.184801	hypothetical protein DKFZ564D1378	1.57	1.83
	426901	A192958	Hs.149558	KIAA1263 protein	1.57	2.23
	456028	NM_001110	Hs.173228	a disintegrin and metalloproteinase doma	1.57	3.07
10	444504	AW327895	Hs.11441	chromosome 1 open reading frame 8	1.57	1.85
	436885	W40445	Hs.235857	ESTs, Weakly similar to 138022 hypotheti	1.57	3.07
	426996	AW965634	Hs.173108	Homo sapiens cDNA: FLJ21897 fls, clone H	1.57	2.01
	447343	AA265841	Hs.238594	ESTs, Highly similar to 502392 alpha-2-m	1.57	2.83
	418942	A1955004	Hs.141259	Homo sapiens cDNA: FLJ21550 fls, clone C	1.57	1.21
	418555	A1417215	Hs.87169	hypothetical protein FLJ12577	1.58	3.08
15	402388			NM_021155 Homo sapiens CO205 antigen (C	1.58	2.05
	415749	X73608	Hs.93029	sparsely-repeated, coar and kazal-like d	1.58	2.08
	404977			insulin-like growth factor 2 (somatomedin	1.58	5.50
	441872	BE657100	Hs.154938	hypothetical protein MDC825	1.58	2.30
	415503	U36601	Hs.78473	N-deacetylase/sulfotransferase (hepara	1.58	2.56
20	451743	AW074286	Hs.23071	ESTs	1.58	1.86
	423134	NM_004428	Hs.1624	aphid-A1	1.58	1.41
	488041	AW138782	Hs.243607	ESTs	1.58	2.21
	416777	AF146760	Hs.79844	DKFZP556M1416 protein	1.58	2.00
	428013	AF161020	Hs.181444	hypothetical protein	1.53	1.53
	410072	BE334447	Hs.16034	hypothetical protein MGC15186	1.55	1.82
	411495	AF000893	Hs.70369	KIAA0136 protein	1.56	2.88
25	408182	AA993833	Hs.118527	ESTs	1.55	2.70
	413350	U02558	Hs.75307	t-complex-associated-testis-expressed 1-	1.55	1.99
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fls, clone C	1.55	1.80
	425229	AL078861	Hs.15521	methylalanyl Coenzyme A mutase	1.55	2.57
30	425184	BE278288	Hs.155045	Lutheran blood group (Lutherberg's antigen	1.55	1.65
	419011	H66244	Hs.339522	glutathione S-transferase A2	1.55	2.77
	417538	AW050885	Hs.275711	hypothetical protein MGC2452	1.55	2.78
35	493508	AW050960		gpiIU-HF-6P36-aly-b-01-O-UL1 NIH_MGC_5	1.55	2.45
	422737			Target Exon	1.54	2.58
	419825	A1754011	Hs.73326	ESTs	1.54	1.00
	410001	AB041038	Hs.57771	kallikrein 11	1.54	0.82
	407813	AL120247	Hs.40109	KIAA0072 protein	1.54	2.33
40	415996	A1751367	Hs.230741	Homo sapiens cDNA: FLJ22256 fls, clone H	1.54	2.77
	427886	AA417083	Hs.104789	ESTs	1.54	2.60
	437018	AA890978	Hs.137033	ESTs	1.54	2.48
	415049	N67334	Hs.50158	ESTs	1.54	2.57
	422315	U16286	Hs.115176	T-cell lymphoma invasion and metastasis	1.54	2.57
45	413716	AW061121	Hs.75497	Homo sapiens cDNA: FLJ22139 fls, clone H	1.54	1.98
	447144	AJ630758	Hs.17481	Homo sapiens clone 24605 mRNA sequence	1.54	2.48
	438924	BE638611		transmembrane trafficking protein	1.53	3.08
	445186	AB681116	Hs.147451	ESTs	1.53	2.08
	414073	AF088293	Hs.75737	perlecan/tolar material 1	1.53	1.70
50	402378			Target Exon	1.53	2.83
	452316	AA296848	Hs.81265	ESTs, Moderately similar to G735_HUMAN P	1.53	1.60
	450374	AA307540	Hs.50293	Homo sapiens clone 122482 unknown mRNA	1.53	3.59
	426817			C100351:1g9187638[Spw]W. 033547.1[win	1.53	2.76
	469837	R70292	Hs.166110	immunoglobulin kappa constant	1.53	1.01
55	410673	AF151057	Hs.54555	aminoadipate-semialdehyde dehydrogenase	1.53	1.23
	426359	AA376409	Hs.10382	Homo sapiens cDNA: FLJ23313 fls, clone H	1.53	0.67
	434445	A1349305	Hs.11732	ESTs	1.53	2.90
	422717	AW180369	Hs.35376	hypothetical protein	1.53	2.01
	402485	AL080276	Hs.70453	similar to prokaryotic-type class I pept	1.53	2.25
60	437404	AA868974	Hs.130992	ESTs	1.53	2.00
	458152	AW171610		gbrCR2-BT0214010599-00-E07 BT0214 Homo	1.52	3.20
	446457	AJ030490	Hs.345281	ESTs, Moderately similar to ALJ1_HUMANNA	1.52	2.35
	441465	AW673081	Hs.54828	ESTs	1.52	1.99
	421810	AK001718	Hs.108530	hypothetical protein FLJ10853	1.52	2.98
	447769	AW873704	Hs.230231	Homo sapiens cDNA: FLJ14197 fls, clone NT	1.52	2.47
65	414892	D79594	Hs.77545	Homo sapiens cDNA: FLJ21983 fls, clone H	1.52	2.55
	442165	W21813	Hs.81825	Homo sapiens mRNA: cDNA DKFZ558E1521 (f	1.52	1.31
	404348			Target Exon	1.52	2.74
	416278	AA365366	Hs.79137	protein-L-leucosparagin (D-asparagin) O-m	1.52	2.93
70	431846	BE019924	Hs.271590	unipolatin 1b	1.52	1.01
	431958	X53626	Hs.2877	collagen 3, type 1, P-orthonin (glabenta	1.52	0.93
	442670	BE410050	Hs.11859	hypothetical protein FLJ13183	1.52	2.70
	441617	AA581853	Hs.178485	Homo sapiens cDNA: FLJ13819 fls, clone Y7	1.52	1.86
	440279	A1557284	Hs.85003	ring finger protein 13	1.52	1.76
	432831	AB211702	Hs.115569	ESTs, Weakly similar to 138022 hypotheti	1.52	2.13
75	414320	U13616	Hs.175893	ankyrin 3, node of Ranvier (ankyrin G)	1.52	2.13
	442149	AB014550	Hs.8118	KIAA0850 protein	1.52	1.00
	457147	AW975000		gbcEST387105 MAGE resequences, MAGN Homo	1.51	2.38

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5	419433	AAG14807	Hs.7395	hypothetical protein FLJ23182	1.51	2.50
	431812	AA815902	Hs.130590	ESTs	1.51	1.84
	415477	NM_022228	Hs.78455	v-jen avian sarcoma virus 17 oncogene ho	1.51	2.82
	447680	A1863590	Hs.133457	ESTs	1.51	2.02
	415926	H03109	Hs.108920	HT016 protein	1.51	2.22
10	442755	W57655	Hs.109701	ubiquitin-like 5	1.51	1.34
	446594	AA478795	Hs.194477	E3 ubiquitin ligase SAMURF2	1.51	2.24
	422675	BE018617	Hs.119140	eukaryotic translation initiation factor	1.51	1.49
	404397			ENSP00000251678 KIAA1571 protein (Fragm	1.51	2.18
	412927	AA284018	Hs.75053	human immunodeficiency virus type 1 onsa	1.51	1.33
15	402371			Target Exon	1.51	3.22
	431730	AF208856	Hs.288122	hypothetical protein	1.51	1.57
	417716	AW695887	Hs.88338	ESTs	1.51	1.59
	451117	AA015752	Hs.205173	ESTs	1.50	2.70
	434727	H43374	Hs.7690	Homo sapiens mRNA for KIAA1571 protein,	1.50	3.83
20	442297	NM_035022	Hs.65901	phosphodiesterase 4A, cAMP-specific (dta	1.50	2.24
	428883	AL137709	Hs.181031	Homo sapiens mRNA, cDNA DKFZp454K0322 (f	1.50	1.13
	452558	N88904	Hs.301212	thyroid receptor interacting protein 15	1.50	1.82
	428895	A355647	Hs.185999	paralogic receptor (family A group 5)	1.50	1.00
	438567	H30340	Hs.173705	Homo sapiens cDNA: FLJ22650 fs, clone H	1.50	1.05
25	419847	AW692021	Hs.134544	Homo sapiens, clone IMAGE355365, mRNA,	1.50	2.53
	431389	BE184455	Hs.251754	secretory leucocyte protease inhibitor (L	1.49	0.57
	432655	AB040871	Hs.35098	KIAA1538 protein	1.49	1.44
	408136	AL041135	Hs.42959	KIAA1012 protein	1.49	2.24
	455465	AA102267	Hs.25795	hypothetical protein FLJ20895	1.48	2.40
30	418653	AL135743	Hs.25598	ESTs, Weakly similar to 20043994 chromos	1.48	2.84
	405193			C7007789.g11943947(gsjAAC48718.1) [U901	1.48	2.20
	408948	AW298713	Hs.221441	ESTs	1.48	2.20
	425088	AF038007	Hs.189186	ATPase, Class I, type IB, member 1	1.48	2.24
	405552			C1503035.g11906122(gsjAAC26158.1) [AF0	1.48	1.48
35	454034	NM_000891	Hs.575	aldehyde dehydrogenase 3 family, member	1.48	1.16
	422355	AW403724	Hs.300597	coagulation factor VII (serum prothrombi	1.48	1.20
	428044	AA053322	Hs.301404	RNA binding motif protein 3	1.48	2.38
	416188	AW501507	Hs.251734	Homo sapiens cDNA: FLJ22807 fs, clone K	1.48	1.28
	430453	BE387020	Hs.3393	Cox-2 effector protein 4, binder of Rho	1.48	2.73
40	401800	BE247275		US snRNP-specific protein, 115 KD	1.48	2.53
	428238	AD17717		chromosome 21 open reading frame 15	1.48	2.03
	405194			C7007789.g11943947(gsjAAC48718.1) [U901	1.48	2.00
	416179	R19015	Hs.79087	MAD (proteins against decapentaplegic, Dr	1.48	1.25
	450272	AD075170	Hs.200110	ESTs	1.48	2.35
45	413709	BE158587		gbCMD-HT0395-200100-159-009 HT0395 Homo	1.48	2.08
	442907	AA507578	Hs.288381	Homo sapiens cDNA: FLJ22996 fs, clone H	1.48	1.00
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.47	1.91
	436989	BE345585	Hs.278712	Homo sapiens cDNA FLJ11074 fs, clone PL	1.47	2.25
	404795			NM_007037-Homo sapiens, a disintegrin-li	1.47	1.24
50	420132	BE079847	Hs.301914	glcRCS-B10527-220300-012-D06 B10527 Homo	1.47	2.00
	448355	AL120337	Hs.206953	high-glucose-regulated protein 8	1.47	2.90
	421298	AL121217	Hs.109210	hypothetical protein FL110913	1.47	4.08
	449059	AK001595	Hs.38135	hypothetical protein FLJ20659	1.47	3.13
	449029	N28989	Hs.22891	solute carrier family 7 (calcium amino	1.47	1.08
55	422119	A2777825	Hs.111882	KIAA0090 gene product	1.47	1.51
	438713	H15902		ESTs	1.47	2.35
	418248	NM_005000	Hs.833915	NM_005000-Homo sapiens NADH dehydroge	1.47	1.00
	419125	AA62452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pr	1.46	2.20
	420548	AA278216	Hs.920	ESTs	1.46	2.13
60	424258	AA433848	Hs.107882	hypothetical protein FLJ10669	1.46	1.98
	414883	ST6298	Hs.76888	hypothetical protein MGC12702	1.46	1.45
	427045	HB5504	Hs.173328	protein phosphatase 2, regulatory subun	1.46	2.31
	448845	BE552004	Hs.25192	ESTs, Weakly similar to A1_U1_HUMAN ALU S	1.46	1.30
	427257	AJC28805	Hs.97726	ESTs	1.46	2.48
65	422871	A279225	Hs.145409	RAS, member of RAS oncogene family-like	1.46	0.05
	451334	AI122551	Hs.13268	ESTs	1.46	2.12
	403328			C2000428.g117705333(gjuet)NP_057536.1 GC	1.45	2.40
	453827	AF201948	Hs.35660	BUP protein	1.46	1.85
	423589	AJC62551	Hs.51703	peroxiredoxin 5	1.46	1.58
70	410891	AW252525	Hs.85450	reticulon 4	1.46	1.49
	430688	AL022101	Hs.104951	hypothetical protein similar to proferon	1.46	2.45
	438083	A1949940	Hs.121924	ESTs	1.46	2.10
	430713	AAS19547	Hs.2642	eukaryotic translation elongation factor	1.45	1.50
	427025	AF142481	Hs.5548	Clon and leucine-rich repeat protein 5	1.45	1.25
75	403342			Target: Exon	1.45	2.21
	438808	M73890	Hs.129553	Homo sapiens NOTCH 1 (N1) mRNA, complete	1.45	2.40
	444853	AK001385	Hs.15144	hypothetical protein DKFZp6540043	1.45	3.85
	414856	AW884858	Hs.118278	Homo sapiens cDNA FLJ13571 fs, clone PL	1.44	2.71
	425072	AI140832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	1.44	1.08
	426723	NM_014420	Hs.195311	diskdog1 (Xenopus laevis) homolog 4	1.44	2.24
	432901	AJ564829	Hs.281895	ATPase, H transporting, lysosomal (vacuo	1.44	1.83

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4	12210	AW01462		g1:RC0-NN1012-270300-031-h10 NN1012 Homo	1.44	2.15
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	1.44	1.83
	428115	AB022154	Hs.505855	RII-00777 protein	1.44	1.31
5	44258	BE567985	Hs.18535	ESTs, Moderately similar to ALU4_HUMAN A	1.44	2.47
	414685	139874	Hs.76894	dCMP deaminase	1.44	1.25
	413158	AA336708	Hs.75546	capping protein (actin filament) muscle	1.44	1.26
	410837	AA215594	Hs.87052	vacuolar protein sorting 26 (yeast homol	1.44	1.41
	400307	AL270770		transcription factor 7-like 2 (T-cell sp	1.44	3.43
10	49502			Target Exon	1.44	2.86
	433976	AA820807	Hs.190258	ESTs	1.44	2.46
	405376			Target Exon	1.44	2.28
	436386	Z43133	Hs.5991	Homo sapiens cDNA: FLJ21654 fs, clone H	1.44	1.34
	418182	AW018405	Hs.16648	ESTs	1.44	2.36
	430307	BE513442	Hs.235944	hypothetical protein FLJ10631	1.43	1.55
15	434024	AA443164	Hs.23259	hypothetical protein FLJ13453	1.43	2.05
	417521	BE245149	Hs.82543	protein tyrosine kinase 9	1.43	2.15
	405744			Target Exon	1.43	1.59
	405418			Target Exon	1.43	2.83
	402869			Target Exon	1.43	2.40
20	451908	AA384525	Hs.25745	hypothetical protein	1.43	1.22
	434099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.43	2.45
	401041			C11000425:c146507721refNP_003310.111	1.43	2.89
	417839	A1815732	Hs.82712	fragile X mental retardation, autosomal	1.43	2.84
	409245	AA361037	Hs.288036	tRNA inosine(ly)triphosphatase transferas	1.43	2.65
25	447808	NM_007255	Hs.13973	suppressor of 5, cerevisiae gcr2	1.43	2.03
	455402	AA530547	Hs.191167	ESTs	1.43	2.72
	449244	AW059979	Hs.32204	ESTs	1.42	1.57
	413094	H24184	Hs.25413	TOLLIP protein	1.42	1.33
30	452407	AA062909	Hs.29353	brain-specific protein p25 alpha	1.42	2.50
	407874	AW084061	Hs.293145	ESTs	1.42	2.35
	441297	AW040304	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	1.42	2.20
	421532	W51778	Hs.323940	hangel 1 (uppression of tumorigenicity	1.42	1.48
	426548	BE466566	Hs.17433	hypothetical protein FLJ20967	1.42	1.93
35	432554	AA79813	Hs.278411	NCR-associated protein 1	1.42	2.46
	431735	AW077224	Hs.75698	lymocyte, beta 4, X chromosome	1.42	1.30
	426563	NM_004376	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	1.42	1.50
	444637	AV647656	Hs.42733	CHMP1.5 protein	1.42	1.38
	402144			Target Exon	1.42	2.38
40	456789	AA325170	Hs.224627	NM_002280?Homo sapiens keratin, hair, a	1.42	2.23
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	1.42	2.18
	426663	AL137657	Hs.172803	hypothetical protein MGC10327	1.41	1.39
	410984	AA085500	Hs.170298	ESTs	1.41	1.29
	401754			upregulated by 1,25-dihydroxyvitamin D-3	1.41	1.32
45	427523	BE242779	Hs.175526	ESTs	1.41	1.37
	445289	AL584882	Hs.175870	ESTs	1.41	1.92
	409467			Target Exon	1.41	1.80
	444330	T96555	Hs.31562	ESTs	1.41	2.04
	431593	AB027643	Hs.120612	ESTs	1.41	1.41
50	413343	BE392026	Hs.334346	hypothetical protein MGC13045	1.41	1.21
	447537	AW295072	Hs.346408	ESTs, Weakly similar to AF193556 1 sacal	1.41	2.07
	428211	AA424211	Hs.183176	ESTs	1.41	1.25
	409248			Target Exon	1.41	2.40
	437412	BE089289	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (r	1.41	1.39
55	414853	M24488	Hs.79788	procollagen-proline, 2-oxoglutarate 4-di	1.41	1.33
	403885			Target Exon	1.41	2.58
	439459	AF086279	Hs.58013	ESTs	1.40	2.05
	419075	T84266	Hs.123927	ESTs	1.41	2.84
	495022			Target Exon	1.40	2.55
	401346	BE041451		hypothetical protein	1.40	2.38
60	419850	AF090907	Hs.75553	ubiquitin-conjugating enzyme E2G 1 (homo	1.40	2.38
	448023	AB932399	Hs.170308	ESTs	1.40	2.38
	439692	AA702620	Hs.251294	ESTs	1.40	2.10
	432480	AA205475	Hs.279865	ribosomal protein S19	1.40	1.37
	414309	AF000639	Hs.75584	DKFZp568A011 protein	1.40	1.18
65	440256	U25841	Hs.16851	hypothetical protein FLJ10875	1.40	1.91
	413909	T25851	Hs.851	integrin, alpha-E (antigen CD103, human	1.40	2.80
	408176	AK001553	Hs.43436	adenylate kinase 3 alpha like	1.40	2.73
	433980	AW629188	Hs.188929	ESTs	1.40	1.99
	404178			CS001439?y14503521refNP_001559.11 mu	1.40	2.83
70	402445			Target Exon	1.40	1.51
	455604	BE011183		gb:PM3-EN0218-100500-003-d09 EN0218 Homo	1.40	2.30
	426221	AB21060	Hs.158271	Target CAT	1.40	1.22
	421212	AA333642	Hs.111894	lysosomal-associated protein transmembr	1.40	1.42
	406221			Target Exon	1.40	2.60
	405879			Target Exon	1.40	2.73
75	450536	A1033745		gb:ow23a10.x1 Soares_papillarythyroid_tumor_M	1.40	1.13
	403381			ENSP00000231844?Ecoltop; virus Integra	1.39	6.03

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5	435268	AW203134	Hs.32597	ring finger protein (C3H-GC type 6	1.38	3.20
	448261	BE244072	Hs.23815	microphage erythroblast attach	1.39	1.33
	427266	AT191486	Hs.180142	calmodulin-like-skin protein (CLSP)	1.39	2.30
	413659	AW992366	Hs.8364	Homo sapiens pycnate dehydrogenase kinase	1.39	1.33
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene1	1.39	1.34
	430738	AA863296	Hs.234266	DKFZ-556G011 protein	1.39	2.38
	433941	ME3425	Hs.62	protein tyrosine phosphatase, non-recept	1.39	2.08
	444591	N46373	Hs.10247	activated leukocyte cell adhesion molecu	1.39	1.34
	440704	M69241	Hs.162	isoflavone growth factor binding prote	1.39	1.61
10	450592	AW138806	Hs.221057	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.39	2.78
	400375			NM_005137:Homo sapiens seryl-RNA synth	1.39	2.03
	403725			Target Exon	1.39	2.03
	443211	AI126368	Hs.143665	ESTs	1.39	1.83
	421510	AK000919	Hs.105191	hypothetical protein FLJ10057	1.39	2.89
15	430071	AA355966	Hs.232058	transcription factor 8 (represses inter	1.38	3.54
	451545	AB02128	Hs.208647	ESTs	1.38	2.21
	438697	NM_015310	Hs.6763	KIAA0042 protein	1.38	3.65
	428072	AB020316	Hs.134015	uronyl-2-sulfotransferase	1.38	1.00
20	410344	AW978436	Hs.62516	KIAA0494 gene product	1.38	2.22
	454539			ENSG00000087222:Mitochondrial 28S ribos	1.38	2.25
	448581	NM_002709	Hs.21537	protein phosphatase 1, catalytic subunit	1.38	1.47
	408969	BE066047	Hs.86412	chromosome 9 open reading frame 5	1.38	1.27
	447543	H10767	Hs.238465	nGAP-like protein	1.38	1.22
25	401593			Target Exon	1.38	1.68
	430007			NM_021889:Homo sapiens enamelin (ENAM),	1.38	2.39
	406396	N47812		CGI-35 protein	1.38	2.25
	401898			NM_021783:Homo sapiens XEDAR (XEDAR), mR	1.38	2.00
	421110	AJ260717	Hs.1365	cathepsin E	1.38	8.83
30	427449	AW945304	Hs.175112	DNA segment, single copy probe LINS-CAIL	1.38	1.44
	427451	AI080518	Hs.178137	transducer of ERBB2, 1	1.38	2.81
	440681	AW449656	Hs.106547	ESTs	1.38	2.95
	419990	AF005043	Hs.61390	poly (ADP-ribose) glycohydrolase	1.38	2.10
	446014	H67567	Hs.13672	calcium modulating ligand	1.37	2.62
35	400007			Target Exon	1.37	3.12
	414506	AF75337	Hs.76293	thymosin, beta 10	1.37	1.18
	402999			NM_021186:Homo sapiens zona peltoida g	1.37	2.68
	422832	AI191813	Hs.305220	ESTs	1.37	2.38
	413819	AK022682	Hs.30523	hypothetical protein FLJ11220	1.37	2.23
40	429902	H05646	Hs.5367	ESTs, Weakly similar to 138022 hypotheti	1.37	2.25
	443895	AK000574	Hs.9908	nitrogen fixation cluster-like	1.37	1.28
	453499	AA300067	Hs.33032	hypothetical protein DKFZp434N185	1.37	2.15
	424870	W51215	Hs.116551	epithelial V-like antigen 1	1.37	1.66
	426296	AW004675	Hs.194716	MAD proteins against decapentaplegic, Dr	1.37	1.33
45	411551	AA318224	Hs.296141	ESTs	1.37	2.96
	450528	NM_014072	Hs.25063	PRO0461 protein	1.37	1.19
	427605	NM_001997	Hs.337445	ribosomal protein L27	1.37	1.31
	459237	AA031975	Hs.31911	Homo sapiens, clone MGC-9653, mRNA, comp	1.37	2.90
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11b	1.37	1.31
50	404905			NM_025213:Homo sapiens spectrin, beta, n	1.36	3.08
	436246	AW450563	Hs.119991	ESTs	1.36	1.00
	441478	AA350018	Hs.307342	hypothetical protein MGC4342	1.36	1.43
	418715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.36	1.28
	426251	M24283	Hs.183883	intercellular adhesion molecule 1 (CD54)	1.36	2.16
	400129			Eos Control	1.36	2.03
55	430197	AF212223	Hs.25010	hypothetical protein P15-2	1.36	2.13
	430208	BE540385	Hs.238950	KIAA1025 protein	1.36	2.01
	434767	AF153201	Hs.238950	cyclin-dependent kinase inhibitor 1B (p2	1.36	2.03
	459729	AL037265	Hs.269848	C2H-2 (Kruppel-type) zinc finger protein	1.36	2.87
60	428653	AA538692	Hs.171695	EST, Weakly similar to ALU4_HUMAN ALU SU	1.36	1.27
	450512	AE011684	Hs.48924	dual specificity phosphatase 1	1.36	2.90
	409844	AW502336		KIAA0512 gene product, ALEX2	1.35	2.68
	402817			gb.U1-HF-BR0p-aka-b-05-0-U1.r1 NIH_MGC_5	1.35	2.29
65	447042	AB035863	Hs.182217	Target Exon	1.35	2.10
	405000			succinate-CoA ligase, ADP-forming, beta	1.35	1.25
	452065	AK000690	Hs.27721	Target Exon	1.35	2.32
	404686			Wol-1-hirschhorn syndrome candidate 1-lik	1.35	2.36
	451081	AW078645	Hs.431	C5000743:gR32:c209gpVAG34364.2 (S775	1.35	2.55
70	427979	BE331778	Hs.181309	murine herpesvirus virid (hm-1) oncogene h	1.35	1.70
	436525	R15702	Hs.31147	proliferone (procaine, meprobamate) subunit,	1.35	2.23
	426469	BE297686	Hs.209370	ESTs	1.35	2.39
	447002	BE242666	Hs.16933	methylmalonate-semialdehyde dehydrogenas	1.35	1.40
	410846	AW011502	Hs.16933	Hep-1 related protein	1.34	2.88
75	451083	AW503322	Hs.11114	gb.CN2-57015-06:289-015464 ST0145 Homo	1.34	2.13
	440512	AA827645	Hs.11973	hypothetical protein DJ1181N3.1	1.34	2.13
	409865	AW502208		suppressor of S. cerevisiae ser2	1.34	2.05
	447390	X95364	Hs.18426	gb.U1-HF-BR0p-aka-b-05-0-U1.r1 NIH_MGC_5	1.34	2.63
				translational inhibitor protein p14.5	1.34	1.00

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5	460293	X56754	Hs.171118	hypothetical protein FLJ00026	1.34	2.45
	445831	NM_006065	Hs.12361	Zn/C bacterial lysozyme synthetase c	1.34	1.60
	418610	AW245993	Hs.223394	hypothetical protein MGC27142	1.34	1.36
	441946	AW298716	Hs.120775	ESTs	1.34	2.30
	446192	H49944	Hs.14231	selenoprotein W, 1	1.34	1.17
10	416265	BC537933	Hs.46617	Homo sapiens cDNA FLJ12540 fls, clone NT	1.34	2.22
	425690	H5544908	Hs.195321	headful filament structural protein 2, ph	1.34	2.50
	407498	U28131		gch human HMGC C chromic transcript mRNA	1.34	1.13
	441331	A1216764	Hs.149971	ESTs, Moderately similar to ALUB_HUMAN f	1.34	2.06
	411789	AF245305	Hs.72157	Adiccan	1.34	1.27
15	420542	NM_005056	Hs.1521	coagulation factor VII (Hageman factor)	1.33	1.25
	413892	A187821	Hs.75807	myristoylated alanine-rich protein kinase	1.33	1.41
	439750	AL359053	Hs.576954	Homo sapiens mRNA, full length insert cDN	1.33	1.99
	414861	AL118366	Hs.77508	glutamate dehydrogenase 1	1.33	1.66
	421507	AL305308	Hs.106923	hypothetical protein MGC14797	1.33	2.18
20	410846	AW901057		gh-NR4-ST0052-031199-016-363 ST0052 Homo	1.33	2.07
	443637	R60571	Hs.24501	ESTs	1.33	2.02
	432380	BE045243	Hs.274416	Target CAT	1.33	1.12
	443119	AA312204	Hs.7980	hypothetical protein MGC12968	1.33	2.68
	439484	AA595735	Hs.324743	protein phosphatase 4 regulatory subunit	1.33	1.89
25	401371			ENSP00000193152-BM453P3.1 (novel) protei	1.33	1.10
	405643			Target Exon	1.33	2.11
	463764	BE008190	Hs.282946	Homo sapiens cDNA FLJ14353 fls, clone Y7	1.33	2.88
	424924	AL391103	Hs.153534	pumilio (Drosophila) homolog 1	1.33	1.24
	463555	N23574	Hs.123949	ESTs, Moderately similar to ALU7_HUMAN A	1.33	2.25
30	404343			C7002191+g15353023g3pAAAD36811.1HAF155	1.33	1.04
	412383	AW947577		gbc-R02-MT004-140300-031-1-09 MTC04 Homo	1.33	2.06
	404260			Target Exon	1.33	2.53
	413292	AF033922	Hs.76501	light chain protein 2 (zona occludens	1.33	2.81
	422716	A1702835	Hs.124475	ESTs, Weakly similar to YEF4_YEAST HYPOT	1.33	2.30
35	440862	A1351979	Hs.152717	hypothetical protein FLJ13725	1.33	1.08
	403540	AW408505		gbc-th01 ex5.x1 NIH_MGC_17 Homo sapiens cD	1.33	2.18
	431196	NM_012249	Hs.250897	ras-like protein	1.32	1.39
	402754			NM_022459-Homo sapiens hypothetical pro	1.32	1.16
	420798	SS3774	Hs.59536	keratin 10 (epidermolytic hyperkeratosis	1.32	2.02
40	459710	A1701596	Hs.121592	ESTs	1.32	2.70
	459152	AK000735	Hs.4835	eukaryotic translation initiation factor	1.32	2.22
	401353			Target Exon	1.32	2.18
	453394	AW960474	Hs.40239	ESTs	1.32	2.20
	421820	AW652990	Hs.294133	home-binding protein	1.32	1.24
45	444047	A167452	Hs.135255	ESTs	1.32	2.95
	440850	R10492	Hs.122676	ESTs	1.32	2.63
	425908	AA584109	Hs.177390	ESTs	1.32	2.11
	458558	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	1.32	2.05
	447015	A8033029	Hs.16953	KIAA1203 protein	1.32	1.30
50	414015	AA340397	Hs.75553	prolylcarboxypeptidase (angiotensinase C	1.32	1.39
	414843	BE539833	Hs.77492	heterogeneous nuclear ribonucleoprotein	1.32	1.26
	424068	AL121516	Hs.139817	thyroid hormone receptor interactor 12	1.32	2.01
	401195			Target Exon	1.32	2.13
	460147	AW373713	Hs.146524	CGI-145 protein	1.32	1.32
55	422699	BE410690	Hs.119257	emt 1 sequence (mammary tumor and squamou	1.32	1.33
	405172			Target Exon	1.32	2.11
	434087	AF118875	Hs.334676	hypothetical protein PRO1942	1.32	2.30
	416720	H05435	Hs.11110	hypothetical protein MGC2508	1.32	2.18
	426521	NM_0010329	Hs.171391	C-terminal binding protein 2	1.32	1.53
60	424915	AB033017	Hs.8594	KIAA1191 protein	1.32	1.43
	443879	Z38482	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	1.31	2.24
	405180	NM_000249		phosphorinositol-3-kinase, catalytic ga	1.31	1.36
	417365	D50653	Hs.82023	transforming growth factor, beta receptor	1.31	0.98
	420217			Target Exon	1.31	1.31
65	425323	NM_001649	Hs.2351	apical protein, Xenopus laevis-like	1.31	2.05
	409935	AW511413	Hs.273025	ESTs	1.31	1.20
	430233	BE269048	Hs.236344	RAB10, member RAS oncogene family	1.31	1.51
	400172			Ect Control	1.31	1.06
	421742	AW970004	Hs.107528	androgen induced protein	1.31	1.79
70	404273			Target Exon	1.31	2.35
	418204	AW972270	Hs.144054	ESTs	1.31	2.15
	435976	AW298113	Hs.92909	SON DNA binding protein	1.31	2.05
	452497	AA732153	Hs.278965	Homo sapiens cDNA: FLJ21333 fls, clone C	1.30	1.57
	404596			Target Exon	1.30	2.23
75	415080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.30	1.15
	427195	W2123C	Hs.173912	eukaryotic translation initiation factor	1.30	1.34
	436129	AA779847		gbc-th01-R0341 Soares_Josita_N-IT Homo ssp	1.30	2.55
	402138			Target Exon	1.30	2.09
	404229			NM_018938-Homo sapiens protocadherin be	1.30	2.83
	402731	AL042818		E3 ubiquitin ligase SMURF1	1.30	3.32
	458795	AW1183518	Hs.55610	solute carrier family 30 (ion transport	1.30	1.58

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5	436585	AW451715	Hs.184075	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.30	2.73
	417219	AA353073	Hs.220936	ESTs	1.30	2.45
	423125	AA353071	Hs.12579	leucine aminopeptidase	1.30	2.00
	416168	BT157060	Hs.70070	v-type adenosine triphosphatase viral onco	1.30	1.60
	444681	AJ243637	Hs.288316	chromosome 8 open reading frame 9	1.30	0.94
10	406621	X57809	Hs.181125	immunoglobulin lambda locus	1.29	1.02
	436563	AW410458	Hs.5259	chromosome 11 open reading frame2	1.29	1.20
	417250	NS6241	Hs.332115	ESTs	1.29	3.43
	434978	AA321238	Hs.4310	eukaryotic translation initiation factor	1.29	1.91
	448079	R76981	Hs.1508	thyroid hormone receptor-associated prot	1.29	2.01
15	450526	AW190589	Hs.1508	insulin-degrading enzyme	1.29	2.08
	456025	BE543127	Hs.335948	Human sapiens, clone IMAGE:5530861, mRNA,	1.29	2.23
	417809	BT19707	Hs.253550	zinc finger protein 200	1.29	2.39
	454771	AW190593	Hs.273629	ESTs	1.29	2.10
	413895	BE178180	Hs.1278	gb:RC2-HIT600.050400.022-h10 HT0900 Homo	1.29	2.08
20	404649			Target Exon	1.29	1.32
	440876	NM_004987	Hs.1278	LIM and oncogene cell antigen-like domain	1.29	2.02
	405691			Target Exon	1.29	2.00
	418965	A100238	Hs.11482	splicing factor, arginine/serine-rich 11	1.29	2.41
	412824	AW558075	Hs.11261	small proline-rich protein 2A	1.29	1.27
25	420337	BE295598	Hs.135569	hypothetical protein FLJ14708	1.29	1.23
	452221	BE246322	Hs.306121	leukocyte receptor cluster (LRC) encoded	1.28	2.48
	456561	AW512481	Hs.104105	ESTs	1.28	2.35
	422984	W28514	Hs.104105	chorionic somatomammotropin hormone 1 (p	1.28	1.57
	456385	BE057554	Hs.86560	gb:MR4-6TC058-140400-006-g10 HT03588 Homo	1.28	1.06
30	418264	AA326111	Hs.86560	ESTs	1.28	2.38
	420474			NM_004075 Homo sapiens cathepsin S (CTSS	1.28	1.99
	448456	A1521830	Hs.107100	ESTs	1.28	2.18
	450208	W27249	Hs.8709	hypothetical protein FLJ21000	1.28	1.80
	450553			Target Exon	1.28	3.73
35	428915	A1041278	Hs.87098	SmG-related CSP activator protein	1.28	4.25
	443721	AW460451	Hs.263365	ESTs	1.28	1.15
	452047	N35953	Hs.43510	ESTs, Weakly similar to BOK B BINDING FA	1.28	2.30
	440213	AW346253	Hs.7043	succinate-CoA lyase, GDP-forming, alpha	1.28	1.19
	452900	AA587594	Hs.7043	polymyosin, alpha (gene sequence 20)	1.28	1.27
40	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	1.28	2.78
	458911	AA373131	Hs.263322	ATPase, H transporting, lysosomal (vacuo	1.28	1.21
	444280	R40915	Hs.12395	ESTs, Weakly similar to 20C4399A chromo	1.28	2.43
	413631	AA548508	Hs.122244	ESTs	1.27	1.51
	447566	AA310605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	1.27	3.08
45	403016	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	1.27	1.37
	416272	AA178882	Hs.60293	gb:zp38080.r1 Stralagene muscle 937205 H	1.27	2.00
	437456	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.27	3.16
	458327	H58741	Hs.38774	ESTs	1.27	2.35
	403349	NM_001406	Hs.286232	ephrin-B3	1.27	2.28
50	428821	H51282	Hs.286232	Homo sapiens cDNA: FLJ23190 fig. clone L	1.27	2.13
	454555	AW807095	Hs.2106	gb:MR4-ST0052-040103-024-002 ST0062 Homo	1.27	2.03
	456872	A1763903	Hs.2106	gb:z0308.r1 NCL_COP4.CLL1 Homo sapiens	1.27	1.44
	401720			NM_014537 Homo sapiens SRY (sex determi	1.27	2.07
	400082			Eos Control	1.27	1.28
55	420183	W52885	Hs.143408	ESTs	1.27	2.24
	411579	AC005268	Hs.70930	US mRNA-associated Sm-like protein Lsm7	1.27	1.17
	420181			NM_021337 Homo sapiens testis-specific	1.27	2.44
	457118	A1246525	Hs.182469	Homo sapiens mRNA: cDNA DKFZp564K1972 (f	1.27	2.17
	408576	NM_003542	Hs.48423	H4 histone family, member G	1.27	2.78
60	428828	BE245288	Hs.301536	peroxisomal biogenesis factor 6	1.27	3.15
	414909	R83316	Hs.132659	PP2B protein	1.27	1.37
	416114	A1655549	Hs.183858	glucuronidase, beta	1.26	2.48
	455478	AW948172	Hs.183858	gb:RCO-MT0013-261300-021-305 MT0013 Homo	1.26	2.18
	445926	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	1.26	1.35
65	432647	A1807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.26	1.16
	455436			Target Exon	1.26	2.38
	406140			Target Exon	1.26	3.20
	426201	AW182614	Hs.128459	ESTs	1.26	1.17
	433334	A1827208	Hs.231958	matrix metalloproteinase 28	1.26	2.30
70	423262	NM_005479	Hs.128057	frequently repressed in advanced T-cell	1.26	2.61
	422529	AA356694	Hs.54011	ESTs, Weakly similar to MGB4_HUMAN MELAN	1.26	2.11
	445605	A1909088	Hs.27159	hypothetical protein FLJ12577	1.26	3.11
	425050	BE391854	Hs.7870	gb:501205394F1 NH_LMG_C_44 Homo sapiens c	1.26	2.10
	420539	AA182135	Hs.44024	AD251 protein	1.26	2.03
75	427352	AL353367	Hs.284181	hypothetical protein DKFZp434P0531	1.25	1.19
	456535	AA305079	Hs.13482	cytochrome c oxidase subunit Vb	1.25	1.10
	434202	BE382411	Hs.3764	purine-rich kinase 1	1.25	1.14
	455528	BE613180	Hs.265368	Homo sapiens cDNA: FLJ21314 fig. clone C	1.25	2.12
	401718			Eos Control	1.25	2.15
	430023	AA158243	Hs.227726	FGF95-binding protein 2 (13kD)	1.25	1.20
	412841	A1751157	Hs.101395	hypothetical protein MGC11352	1.25	1.39

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5	425655	BC514651	Hs.738	ribosomal protein L14	1.26	1.22
	449530	AB95598	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	1.25	3.00
	418408	X73601	Hs.846505	cyclostin 20	1.24	2.11
	414570	Y0285	Hs.75473	insulin-like growth factor 2 receptor	1.24	1.14
	435987	AA751728	Hs.133706	ESTs	1.24	2.53
10	457216	AA452654	Hs.283937	ESTs, Weakly similar to A4179C neural re	1.24	2.18
	416414	J34977	Hs.84581	X-ray repair complementing defective rep	1.24	1.35
	423217	NM_002094	Hs.1940	collagen, type VII, alpha 1 (epidermis)	1.24	0.92
	421733	AL_119671	Hs.1420	fibroblast growth factor receptor 3 (sch	1.24	2.71
	402329		NM_005505	Homo sapiens poliovirus recep	1.24	1.13
15	447525	AF_51031	Hs.300631	hypothetical protein	1.24	1.07
	445839	BE918938	Hs.141003	Homo sapiens cDNA; FLJ21691 fls, clone C	1.24	2.23
	421936	AB040884	Hs.108954	KIAA1451 protein	1.24	2.15
	433681	A0004377	Hs.200360	Homo sapiens cDNA FLJ13027 fls, clone NT	1.24	2.15
	426177	N65977	Hs.49390	Homo sapiens mRNA; cDNA DKFZp454C2328 f	1.24	2.14
20	404751	T7045		ribosomal protein L5	1.24	1.30
	411445	AW047588		glnk3-C10213-151299.039-008 C0213 Homo	1.24	2.35
	425417	AF068848	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	1.24	2.88
	434508	AB486001	Hs.118012	ESTs	1.24	2.03
	428284	AA535152	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.24	1.59
25	418597	AV001676	Hs.86337	similar to D1U-directed RNA polymerase I	1.24	2.27
	414191	AW250085	Hs.75907	PC2 and LIM domain 1 (elin)	1.24	1.63
	449210	AB35363	Hs.345517	ESTs	1.24	2.18
	439551	W72052	Hs.11112	ESTs	1.24	2.13
	425244	AB54608	Hs.153289	succinate dehydrogenase complex, subunit	1.23	1.06
30	425395	BC146082	Hs.24724	VPM-amplified sequences with leucine-ric	1.23	1.34
	429917	B95684	Hs.211563	B-cell CLL/lymphoma 7A	1.23	2.27
	434943	AB529819	Hs.52309	chromosome 21 open reading frame 50	1.23	2.10
	417010	NM_000225	Hs.86775	phospholipase C, delta 1	1.23	1.21
	425508	W22184	Hs.170171	glutamate-azetidine ligase (glutamine synt	1.23	1.37
35	434055	AF168712	Hs.3725	x003 protein	1.23	1.68
	438353	AB89351	Hs.22253	hypothetical protein FLJ21552	1.23	2.44
	420757	R48131	Hs.26257	ATP-dependent interferon response protei	1.23	2.28
	45018	U54969		NM_018955:Homo sapiens ubiquitin 1 (UBB)	1.23	1.44
	444061	AW855598	Hs.12210	hypothetical protein FLJ13312 similar to	1.23	1.16
40	440112	AA059014	Hs.231029	Homo sapiens, clone MGC:15951, mRNA, com	1.22	2.07
	425572	AW270655	Hs.171774	hypothetical protein	1.22	1.16
	449556			C10032107g(W512582)ref(NF_003234.1) pe	1.22	2.18
	435088	NM_000481	Hs.102	aminocyclitol:serine (glycine cleavage	1.22	1.08
	438588	AW274454	Hs.5318	peroxisomal short-chain alcohol dehydrog	1.22	1.02
45	434454	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endoxy	1.22	1.27
	425869	W15480	Hs.24283	ESTs, Moderately similar to reduced expr	1.22	2.62
	423755	D37454	Hs.19355	KIAA0255 protein	1.22	1.18
	420585	AA275362		gluc8A404-41 NCL CGAP, GC0B1 Homo sapiens	1.22	2.75
	458991	A1743602		gluc8A3812.x2 Soares_NFL_T_GBC_S1 Homo s	1.22	2.39
50	414825	X08370	Hs.77432	epidermal growth factor receptor (avian	1.22	1.00
	434023	A1727883	Hs.148141	ESTs	1.22	2.12
	430801	A1681935	Hs.106588	ESTs	1.22	2.53
	414880	AW247305	Hs.119140	eukaryotic translation initiation factor	1.21	1.16
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	1.21	1.04
55	404780			C120017077-gp1305215ref(NF_038999.1) k	1.21	2.05
	423943			C5010051g(W540322)ref(NF_000785.1) cy	1.21	2.05
	400201			NM_008158:Homo sapiens neural precursor	1.21	1.35
	421005	AW293089	Hs.33283	ESTs	1.21	2.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.21	1.11
60	400789			C110013677-g14078205.gp150054 hypo	1.21	1.56
	412942	BE287535	Hs.74528	adaptor-related protein complex 2, beta	1.21	1.34
	449709	BM41075	Hs.23818	hypothetical protein PPS355	1.20	1.27
	413726	AJ278405	Hs.22510	annexin A11	1.20	1.14
	428465	NM_002660	Hs.7580	fibronectin I	1.20	1.24
65	405163			C5010051g1g71513700(gp1T14151) low po	1.20	1.11
	415887	NM_003375	Hs.78902	voltage-dependent anion channel 2	1.20	1.16
	434408	N26309	Hs.39268	ESTs	1.20	3.20
	449843	AW136925	Hs.98198	hypothetical protein VGC11332	1.20	2.25
	429442	BE287535	Hs.3069	heat shock 70kD protein 90 (serine-16)	1.20	2.18
70	444242	RS2345	Hs.20758	HSPC180 protein	1.20	1.22
	415763	U52819	Hs.78781	vascular endothelial growth factor B	1.20	1.05
	442155	AB905885	Hs.23403	hypothetical protein FLJ22060	1.20	1.18
	408824	L53005	Hs.48375	small nuclear ribonucleoprotein polypept	1.20	1.45
	430012	NM_015373	Hs.227537	chromosome 22 open reading frame 2	1.20	1.03
75	413382	AW021404	Hs.13021	ESTs	1.20	2.07
	415955	A0897275		Target Exon	1.20	2.08
	455552	AA305049	Hs.274530	surin1 6	1.20	2.53
	409898	AL119844	Hs.49475	Homo sapiens clone TUA8 Cid-de chag m	1.20	3.45
	427818	AW811222	Hs.193755	ESTs	1.19	2.99
	405404			NM_002162:Homo sapiens intercellular ad	1.19	1.17

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5	433333	A016621	Hs.71816	v-akt murino thymoma viral oncogene homo	1.09	1.06
	451362	H818180	Hs.221516	ESTs	1.08	2.76
	464717	AW616123	Hs.129593	gb:U4-5T0212-361199-046-bc1 ST0212 Homo	1.08	1.98
	422743	BE304678	Hs.121596	abscornin protein L3	1.08	1.00
	411672	AJ275985	Hs.71414	transcription factor (SMF gene)	1.08	1.00
10	422748	AB011128	Hs.30612	Homo sapiens mRNA for KIAA0656 protein,	1.08	2.45
	428330	L22624	Hs.2236	ratios metalloproteinase 7 (matrilysin),	1.08	2.15
	447703	A420277	Hs.29463	gb:U5412.x1 NCL CGAP P28 Homo sapiens	1.07	2.06
	452420	B5564971	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	1.07	2.03
	455234	R41084	Hs.75627	gb:HK753-1 Adult heart, Clontech Homo sa	1.07	2.08
15	413945	NV_000691	Hs.173179	CD14 antigen	1.07	0.91
	417333	AL157545	Hs.75183	translocin and PHD finger containing, 3	1.07	1.00
	434105	AW952124	Hs.13004	presenilins associated rhomboid-like pro	1.07	1.11
	455630	AV655701	Hs.75183	cyclohexane P450, subfamily 1E (ethoxyc	1.06	2.14
	455424	AW937373	Hs.1592	gb:U5-OT0045-21010-063-406 DT0045 Homo	1.06	2.03
20	438244	AJ785869	Hs.6152	KIA0071 protein	1.05	2.27
	421604	AW293880	Hs.243867	MEGF11 protein	1.05	2.00
	422514	A3008006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.04	2.83
	404068	AW956243	Hs.98074	Target Exon	1.04	2.10
	453065	H59970	Hs.98074	KIA00251 protein	1.04	2.16
25	417590	H59970	Hs.98074	ghyrl504r1 Scores fetal liver spleen	1.04	2.40
	408653	AW410189	Hs.64754	richy (mouse homolog) E3 ubiquitin prote	1.04	2.73
	440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS (H	1.04	2.05
	492929	AA405160	Hs.137267	ESTs	1.04	2.73
	458107	AA180200	Hs.137267	ESTs, Weakly similar to JC5238 galactos	1.03	2.18
30	415403	P07923	Hs.28744	ESTs	1.02	2.43
	455591	BE008018	Hs.184027	gb:U5-3K10147-260400-214-c01 B10147 Homo	1.02	2.08
	428481	AF091036	Hs.38911	KIA0116 protein	1.02	2.81
	407758	BE514682	Hs.38911	S100 calcium-binding protein A2	1.02	2.11
	435450	NV_018545	Hs.3945	CG-107 protein	1.02	2.78
35	442174	AJ890080	Hs.128907	ESTs, Weakly similar to ARX homeodomain	1.02	2.05
	413431	AW245428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	1.02	1.00
	452436	BE077546	Hs.31447	ESTs, Moderately similar to AA8010 X.4a	1.02	2.25
	454412	AW982698	Hs.238094	gb:U5-1T0275-080100-01 H4-51 T0278 Homo	1.00	2.20
	428955	AA393699	Hs.184760	ESTs	1.00	2.18
40	425910	AA830079	Hs.184760	CCAAT-box-binding transcription factor	1.00	2.10
	405710	AA305627	Hs.139336	CK000582g[12741327]ref[X]_008333.2[2] zi	1.00	2.00
	402925			ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	402091			Target Exon	1.00	1.00
	402812			NV_0048307 Homo sapiens capping protein	1.00	1.00
45	422892			Target Exon	1.00	1.00
	403329			Target Exon	1.00	1.00
	427202	N58172	Hs.109370	ESTs	1.00	1.00
	406684	R61377	Hs.12727	hypothetical protein FLJ21510	1.00	1.00
	410555	U92549	Hs.54311	a disintegrin and metalloproteinase doma	1.00	1.00
50	413573	AJ733859	Hs.149089	ESTs	1.00	1.00
	414343	AL039165	Hs.323378	coated vesicle membrane protein	1.00	1.00
	414422	AA147224	Hs.249195	Homoec box A13	1.00	1.00
	417008	AW673606	Hs.80758	aspartyl-PRNA synthetase	1.00	1.00
	421577	SE454541	Hs.109925	single-minded (Drosophila) homolog 1	1.00	1.00
55	423349	AF010258	Hs.127488	homoec box A9	1.00	1.00
	424273	W00400	Hs.144442	phospholipase A2, group X	1.00	1.00
	424649	BE242035	Hs.151461	embryonic ectoderm development	1.00	1.00
	426827	AW087805	Hs.172665	methylcrotonylhydroxylase dehydrogenase	1.00	1.00
	427338	D26057	Hs.174965	KIA04033 protein	1.00	1.00
60	429597	NV_000816	Hs.2142	a disintegrin and metalloproteinase doma	1.00	1.00
	430261	AA305127	Hs.237225	hypothetical protein HT323	1.00	1.00
	431078	HE2827	Hs.249195	homoec box A13	1.00	1.00
	432222	AW314472	Hs.238415	disckey (Drosophila laevis) homolog 4	1.00	1.00
	434892	AW770553	Hs.14553	small O-cyclinase (cycl-Centromere	1.00	1.00
65	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	1.00
	443054	AJ745185	Hs.8939	yes-associated protein 65 kDa	1.00	1.00
	443564	AJ821685	Hs.189713	ESTs	1.00	1.00
	446442	AJ151753	Hs.230350	aminopeptidase	1.00	1.00
	446413	AJ151342	Hs.12677	CG-147 protein	1.00	1.00
70	448705	AW291096	Hs.21814	interleukin 20 receptor, alpha	1.00	1.00
	448807	AJ571940	Hs.7549	ESTs	1.00	1.00
	449448	D07370	Hs.57471	ESTs	1.00	1.00
	449517	AW501016	Hs.20543	serine/threonine protein kinase MASK	1.00	1.00
	449565	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	1.00
75	451844	TE1430	Hs.172510	gb:yc05603.s1 Streptococcus lung (337210) H	1.00	1.00
	452039	AJ922898	Hs.172510	ESTs	1.00	1.00
	452795	AW392555	Hs.18676	hypothetical protein FLJ21520	1.00	1.00
	453096	AW294631	Hs.11325	ESTs	1.00	1.00
	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	453966	BE148734	Hs.53325	transmembrane protease, serine 4	1.00	1.00
	405880			Target Exon	1.00	1.00

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5	430268	AI000737	Hs.237490	hypothetical protein FLJ20730	1.00	1.00
	450377	AB033091	Hs.74313	KIAA1265 protein	1.00	1.00
	433226	AW503733	Hs.9414	KIAA1458 protein	1.00	1.00
	412719	AW018610	Hs.816	ESTs	1.00	1.00
	425289	AW138342	Hs.155530	interferon, gamma-inducible protein 16	1.00	1.00
10	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.00	1.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to CAP1, HUMAN DEATH	1.00	1.00
	438817	AB033109	Hs.153242	ESTs	1.00	1.00
	455474	AW946204	Hs.23440	gR-RC2-MT0012-290300-031-c10 MT0012 Homo	0.99	2.00
	420146	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B [autosoma	0.99	2.33
15	426466	AF151063	Hs.184456	hypothetical protein	0.98	2.20
	421594	RN5689	Hs.21689	Homo sapiens cDNA FLJ12976 fs, clone NT	0.96	3.09
	444654	AW565072	Hs.23440	KIAA1105 protein	0.96	2.00
	406759	N40285	Hs.81182	histamine N-methyltransferase	0.97	2.20
	401936			Target Exon	0.97	2.59
20	434421	A1915927	Hs.34771	Target Exon	0.96	2.38
	412636	NM_004415		desmoglein (DPL, DFI)	0.96	2.15
	442432	BE093589	Hs.38178	hypothetical protein FLJ23458	0.93	2.05
	421838	AA050551		glucuronicid, r1 Soares, testis, NIF Homo sep	0.93	3.10
	447470	BE518624	Hs.263561	ESTs, Weakly similar to ASS331 oncodet	0.92	2.08
25	446869	AW268692	Hs.111335	ESTs	0.91	2.35
	421710	AE007930	Hs.107088	KIAA0461 protein	0.91	2.63
	406805	AI686003	Hs.296031	ESTs	0.91	2.21
	447475	U380797	Hs.158992	ESTs	0.90	2.25
	428892	U62628	Hs.194182	ataxin telangiectasia mutated [ischides	0.90	2.22
30	450222	U75308	Hs.24944	TATA box binding protein (TBP)-associate	0.89	2.73
	401572			C1500138c.g12737057.p01XP_012129.1]	0.88	2.00
	429226	AA813330	Hs.53542	choroacanthocytosis gene; KIAA0986 prot	0.88	2.37
	421979	AW065118	Hs.233160	hypothetical protein MCS3569	0.87	3.70
	407614	NM_001932	Hs.37144	membrane protein, palmitoylated 3 (MAGUK	0.86	2.02
35	417812	R25289	Hs.50547	ESTs	0.86	2.00
	401654			NM_007242 Homo sapiens DEADH (asp-Glu-A	0.86	2.11
	403149			NM_001453 Homo sapiens four and a half L	0.86	2.19
	413300	BE046280		gluc43c3c2-2 NC1_CGAP_R072 Homo sapiens	0.85	2.40
	425168	AW021456	Hs.154919	KIAA0625 protein	0.85	2.18
40	447371	AA334274	Hs.18386	DKFZP564B0769 protein	0.84	2.13
	432601	AI935987	Hs.34447	ESTs	0.84	2.55
	409557			Target Exon	0.83	2.16
	426420	BE383808	Hs.322430	NDRG (family, member 4	0.83	2.14
	429354	AA451666	Hs.269693	ESTs	0.80	2.25
45	417631	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	0.78	2.43
	434368	BE580891	Hs.159210	ESTs, Moderately similar to hK116F5.2 [H	0.78	2.00
	441001	AB914405	Hs.128163	ESTs	0.76	2.08
	429462	AI980356	Hs.127894	Homo sapiens, clone IMAGE:3536432, mRNA,	0.76	2.03
	403010			C21000152.g16226483[bp]C251181YMO3_ERVS	0.75	2.43
50	420344	BE463721	Hs.97101	putative G protein-coupled receptor	0.75	2.42
	448332	AW203110	Hs.171068	ESTs	0.74	2.00
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	0.71	2.18
	450645	AL117441	Hs.301997	hypothetical protein FLJ13033	0.67	2.06
	448514	AD020626	Hs.301866	KIAA0819 protein	0.67	2.03
55	431890	AW72792	Hs.264330	N-acetylglucosaminide amidohydrolase (acid c	0.64	2.00
	417512	X76514	Hs.82229	glycoprotein (transmembrane) amb	0.60	2.00
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434t4247	0.57	2.15
	408077	AL133574	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (f	0.53	2.29

TABLE BB

60	Proj:	Unique Eos probe/seq identifier number	
	CAT number:	Gene cluster number	
65	Accession:	Genbank accession numbers	
70	Proj:	Unique Eos probe/seq identifier number	
	CAT number:	Gene cluster number	
75	Accession:	Genbank accession numbers	

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449079	74834_1	R76561 AA11801 AA1101722 AA058802 BE006483 AA343200 AW963375 BE050425 AA213371 B5627102 AA309094 AW960171 A275045 Z44230 AW243724 A151487 A1376204 R63631 AW970550 CD0116 AA384051 AA122255 A1375041 AW225873 AW205359 AW159219 AW129632 A1541433 A1698869 A1352506 A1373306 AA213708 AA084145 A1300826 AA161022 AA161505 AA117195 AA1-01723 AW514352 R64287 AW27555 A251910 A180303 A875123 AW023075 AW134559 A926196 AA831086 A1638324 F29011 R45355 F03383 C17731 R20584 T50131 A033745 A1043133 AA844424 AW166024 A1831699 A1571057 AA011686 H70852 H70851 T61433 A820546 A827336 A4626704 A1667775 AA071274 AA028041 A1554235 N71035 N70230 AW674412 A871138 A1563555 A1594237 A4649543 A1340231 A1365856 A1868711 W44486 T83736 AA125250 A3434615 H94257 T47633 A1672891 AA595355 R23240 A814680 A50219 AA64262 N67040 AW074273 A3375717 A4655354 A1027942 R33837 H55526 N63928 AH16101 A1186469 A8939677 AAT78429 AA125352 A1595407 C00016 A46316 AW522076 A695945 A1753116 A1750505 A1025232 T75306 A8242548 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A4304178 AA140732 AA452066 W19399 AA256394 H44259 W56767 C0571 C05835 A171498 N58532 AW102617 AA112583 A52246 W36495 AA353575 AAS23671 C08275 AA32500 N53132 AW522568 AW810556 AW818947 AW818655 AW818637 AW818234 AW807055 AW807022 AW845300 AW807036 AW807461 AW846116 AW807070 AW816123 AW815138 AW815299 TA1054 AW875566 AW537733 AW537727 AW537833 AW949054 AW949481 AW548270 AW548203 AW949084 AW949086 AW949086 AW948074 AW548074 AW548117 AW548085 AW548081 AW548098 AW548102 AW548281 AW548080 AW548081 AA918251 A1594389 AW548080 AW548104 AW548119 AW548096 AW548100 AW548112 AW548121 AW948088 AW548105 AW548105 AW548057 AW5481320 AW548108 AW548111 AW548114 AW548115 AW548072 AW548083 AW548095 AW548116 AW548076 AW548077 AW548071 AW949067 AW548107 AW548012 AW548065 AW548084 AW548113 AW548083 AW548062 AW548176 AW946169 AW946176 AW546191 AW546152 AW548186 AW548187 AW548188 AW548189 AW548191 AW548192 AW548193 AW548194 AW548195 AW548196 AW548197 AW548198 AW548199 AW548200 AW548201 AW548202 AW548203 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AW548426 AW548427 AW548428 AW548429 AW548430 AW548431 AW548432 AW548433 AW548434 AW548435 AW548436 AW548437 AW548438 AW548439 AW548440 AW548441 AW548442 AW548443 AW548444 AW548445 AW548446 AW548447 AW548448 AW548449 AW548450 AW548451 AW548452 AW548453 AW548454 AW548455 AW548456 AW548457 AW548458 AW548459 AW548460 AW548461 AW548462 AW548463 AW548464 AW548465 AW548466 AW548467 AW548468 AW548469 AW548470 AW548471 AW548472 AW548473 AW548474 AW548475 AW548476 AW548477 AW548478 AW548479 AW548480 AW548481 AW548482 AW548483 AW548484 AW548485 AW548486 AW548487 AW548488 AW548489 AW548490 AW548491 AW548492 AW548493 AW548494 AW548495 AW548496 AW548497 AW548498 AW548499 AW548500 AW548501 AW548502 AW548503 AW548504 AW548505 AW548506 AW548507 AW548508 AW548509 AW548510 AW548511 AW548512 AW548513 AW548514 AW548515 AW548516 AW548517 AW548518 AW548519 AW548520 AW548521 AW548522 AW548523 AW548524 AW548525 AW548526 AW548527 AW548528 AW548529 AW548530 AW548531 AW548532 AW548533 AW548534 AW548535 AW548536 AW548537 AW548538 AW548539 AW548540 AW548541 AW548542 AW548543 AW548544 AW548545 AW548546 AW548547 AW548548 AW548549 AW548550 AW548551 AW548552 AW548553 AW548554 AW548555 AW548556 AW548557 AW548558 AW548559 AW548560 AW548561 AW548562 AW548563 AW548564 AW548565 AW548566 AW548567 AW548568 AW548569 AW548570 AW548571 AW548572 AW548573 AW548574 AW548575 AW548576 AW548577 AW548578 AW548579 AW548580 AW548581 AW548582 AW548583 AW548584 AW548585 AW548586 AW548587 AW548588 AW548589 AW548590 AW548591 AW548592 AW548593 AW548594 AW548595 AW548596 AW548597 AW548598 AW548599 AW548600 AW548601 AW548602 AW548603 AW548604 AW548605 AW548606 AW548607 AW548608 AW548609 AW548610 AW548611 AW548612 AW548613 AW548614 AW548615 AW548616 AW548617 AW548618 AW548619 AW548620 AW548621 AW548622 AW548623 AW548624 AW548625 AW548626 AW548627 AW548628 AW548629 AW548630 AW548631 AW548632 AW548633 AW548634 AW548635 AW548636 AW548637 AW548638 AW548639 AW548640 AW548641 AW548642 AW548643 AW548644 AW548645 AW548646 AW548647 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	401383	6721135	Minus	155543-157381
	401496	7381769	Minus	82790-83002
	401512	7622346	Plus	136595-136557
	401563	8247910	Plus	51395-51763
5	401572	8570271	Minus	7865-1-7889
	401593	7236957	Plus	10368-10572,11293-12356
	401600	4380746	Minus	27363-27518,28727-28891,29526-29731
	401603	7689965	Minus	116565-116780
	401613	4879062	Plus	22461-22831
10	401654	9097132	Minus	64695-64797
	401660	9100664	Minus	173662-174024
	401720	6465551	Plus	7763-8466
	401784	7246190	Plus	146393-148666,149453-149536,149731-149962
	401835	7139700	Plus	142267-142742
15	401886	7229913	Minus	79215-79363
	401936	3608091	Plus	40617-40943
	402001	5991618	Plus	60052-60223
	402087	6117546	Plus	137069-137213,139678-138828,138969-139050
	402138	7704985	Plus	14173-15108
20	402144	7242328	Plus	116425-116977
	402150	8575087	Minus	76468-76559
	402191	8576073	Minus	69410-69583
	402329	7798795	Plus	15833-16180,16416-18715,22507-22624
	402388	9558577	Minus	47218-47330,49052-48203
25	402371	9558584	Plus	86736-86958
	402378	9823333	Minus	41312-41448,48313-48720
	402440	9796874	Plus	59867-60039,62588-62828,63465-63623,64023-65108
	402474	7547175	Minus	53826-53828,55755-55920,57630-57757
	402617	9798108	Plus	17656-17721
30	402699	7239886	Plus	5635-5687
	402717	9630797	Minus	69466-69945
	402712	8989263	Minus	10941-11138
	402731	9211639	Minus	117613-118004,121110-121211,121327-121457,125478-125623,126540-126863
35	402737	9212184	Minus	13358-13552
	402764	9213730	Plus	15345-16382
	402760	9213869	Plus	136825-136952,137336-137521
	402812	6010110	Plus	25026-25091,25844-25520
	402845	9369288	Plus	160461-160617,160788-161009
40	402869	6434643	Minus	138639-139336
	402892	8066544	Minus	194364-194645
	403010	3132346	Plus	78385-79052
	403149	9759833	Plus	25034-25185
	403328	8440206	Minus	110959-111122
45	403329	8516120	Plus	96458-96598
	403342	7233487	Minus	42312-43750
	403349	8569773	Minus	167815-168374
	403381	9430267	Minus	26009-26178
	403463	9525938	Plus	102596-102879
50	403655	8730083	Plus	65668-65859
	403725	7534031	Plus	86737-85843
	403728	7534291	Minus	34481-34871
	403807	8439933	Minus	182963-185773
	403826	9838209	Plus	121197-121358
55	403885	7710403	Minus	53259-53524
	403943	7711684	Plus	100742-100904,101322-101503
	403988	8576087	Plus	16251-16462
	404029	7871292	Plus	108718-111112
	404058	3548785	Plus	99367-101808
60	404069	3168619	Plus	47310-47450
	404178	7630978	Minus	179075-179383
	404204	3189112	Minus	78958-80321
	404231	8718036	Minus	61007-61322
	404250	9187145	Minus	36099-36212,37909-36075
65	404273	9885189	Plus	97789-98295,99601-99865
	404343	9538093	Plus	122864-122931
	404349	7633858	Minus	61006-61187
	404361	3135305	Minus	26030-26173,27852-27997
	404392	3135305	Minus	29738-29857
70	404397	9509808	Minus	104042-104232
	404438	6994205	Plus	53413-63053
	404430	7139680	Plus	55316-55585
	404530	6479107	Plus	3157-3304
	404596	9558282	Minus	104807-105043
75	404649	9759826	Minus	105227-105309
	404666	7272179	Minus	18577-18993
	404687	9757554	Minus	128456-128565
	404744	9187237	Plus	71776-71852,72885-73019,73700-73822,74692-74890

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	404751	7630939	Plus	113799-114252,114393-114715
	404769	8099713	Minus	175801-176823
	404790	7230958	Plus	38911-38761
	404806	7331453	Minus	100285-101125
5	404955	7387343	Plus	55883-56293
	404977	3738341	Minus	43091-43229
	405000	8957544	Minus	88954-89393
	405022	7330304	Plus	217153-217459
	405053	7651944	Minus	157134-157430
10	405058	7655585	Plus	150740-151555
	405155	9966228	Plus	130468-130723
	405163	9966267	Minus	161171-161239
	405165	9966302	Plus	6461-6945
15	405165	9966302	Plus	40526-40691
	405172	9966752	Plus	153027-153262
	405180	7130743	Plus	65438-65740
	405193	7230072	Plus	129187-129389
	405194	7230072	Plus	190455-190645,193346-193610
20	405245	7240293	Minus	57550-58312
	405368	2275192	Minus	119667-120872,120481-120824,121029-121367
	405376	1552533	Plus	23975-25099
	405418	6997232	Plus	51936-51953
	405436	7406968	Minus	55716-55979
25	405443	7408143	Plus	90716-90887,101420-101677
	405474	8439781	Plus	172006-172175
	405502	9211311	Minus	60360-60584
	405580	4512267	Plus	169232-169647
	405595	7159256	Plus	47585-47688
30	405630	4598116	Minus	103218-103291,106358-106993,110061-110126
	405645	4914350	Plus	7411-969
	405710	8531255	Minus	66209-66932
	405806	7274891	Minus	224961-226780
	405812	4775630	Minus	29424-29764
35	405855	7652031	Minus	60377-60795
	405879	8758747	Minus	54758-55457
	405891	8758795	Plus	41062-41951
	405902	6758795	Minus	82322-83110
	405932	7767812	Minus	123525-123713
40	406039	3369537	Plus	37764-37877
	406140	9168231	Minus	49887-50219
	406181	5923650	Plus	16586-16585
	406231	7417725	Plus	17206-17841,17772-17966
	406248	7417725	Plus	43711-50227
	406274	7543737	Plus	932-1125
45	408355	7107907	Plus	18781-18973
	406404	9255305	Minus	152569-152874
	406467	9795551	Plus	132218-132358
	406557	7711589	Minus	5443-5574,1170-3352
50	406575	7711679	Plus	142034-142473

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TABLE 10A: Genes preferentially expressed in non-invasive bladder tumors

	Playr:	ExAccn	Unique Eos process identifier number	Unigene Title	R1
	ExAccn	Unigene accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title: Unigene gene title				
	R1	80th percentile of T1a tumor Als divided by the 80th percentile of T2-T4 tumor Als			
10	421110	HA250717	Ha.13555	cathepsin E	5.78
	470851	AF156478	Ha.188471	annexin A10	6.23
	451568	Z45946	Ha.376444	cartilage acidic protein 1	5.53
	415511	A1732617	Ha.182382	ESTs	4.72
	428336	AA503115	Ha.183752	microsomal protein, beta-	4.66
15	418028	BC379727	Ha.93213	fatty acid binding protein 4, adipocyte	4.62
	400752			NAI_003105: Homo sapiens scortin-related	3.96
	430315	NM_004293	Ha.239147	guanine deaminase	3.82
	403010			C21000152:g822648.3[sp]C52118[VM03_ERWS	3.56
	404977			Insulin-like growth factor 2 (somatomed)	3.54
20	426567	NM_015895	Ha.171731	solute carrier family 14 (anion transport)	3.51
	400409	AF153341		Homo sapiens winged helix/foxhead trans	3.38
	400844			NM_003105: Homo sapiens scortin-related	3.27
	406061			Target Exon	3.22
25	417275	X63578	Ha.295449	pancreatin	3.03
	402220			Target Exon	2.96
	454219	X75042	Ha.44313	v-rel avian reticuloendotheliosis viral	2.89
	403381			ENSP00000231644: Eoethropic virus integra	2.87
	426586	AF030007	Ha.166196	ATPase, Class I, type B1, member 1	2.86
30	422266	AC355670	Ha.123533	ESTs, Weakly similar to ZN51_HUMAN ZINC	2.89
	434061	AW024973	Ha.263675	NPL009 protein	2.66
	418406	X73501	Ha.84905	cytokeratin 20	2.65
	418818	AA228699	Ha.101307	Homo sapiens HUT11 protein mRNA, partial	2.59
	421594	FA5689	Ha.21689	Homo sapiens cDNA FLJ12576 fs, clone NT	2.57
35	403383			Target Exon	2.56
	435583	AF210317	Ha.95497	solute carrier family 2 (facilitated glu	2.55
	424800	AL035588	Ha.153203	MyoD family inhibitor	2.54
	404606			Target Exon	2.53
	416205	L21715	Ha.83760	Insulin 1, skeletal, fetal	2.53
40	431912	AA60552	Ha.76549	ESTs, Weakly similar to A56154 Abi subcl	2.52
	413786	AW613780	Ha.13500	ESTs	2.51
	421100	AW351639	Ha.124660	Homo sapiens cDNA: FLJ21763 fs, clone C	2.50
	416940	BE82476	Ha.79944	neurop-specific protein	2.50
	420729	AW954637	Ha.230825	ESTs	2.50
45	402844			C1000118:g19561913[sp]NP_065832.1[pr	2.46
	401093			C12000586:g16330167[sp]BA6477.1[1] (A	2.46
	417720	AA208525	Ha.208067	ESTs	2.45
	400267	A1172776	Ha.386201	hypothetical protein DKFZ256401278	2.45
	403816			Target Exon	2.44
	440273	A1805392	Ha.325335	Homo sapiens cDNA: FLJ23523 fs, clone L	2.44
50	418080	AA211589	Ha.208047	ESTs	2.40
	420843			NM_003105: Homo sapiens scortin-related	2.38
	446006	NM_004403	Ha.13530	deafness, autosomal dominant 5	2.35
	401512			NM_014080: Homo sapiens dual oxidase-like	2.34
55	446947	T51454	Ha.67845	Homo sapiens cDNA: FLJ21930 fs, clone H	2.32
	417054	NM_003895	Ha.81162	histamine H1-methyltransferase	2.31
	438295	A1801168	Ha.120910	ESTs	2.30
	436246	AW450963	Ha.119991	ESTs	2.30
	447578	AA912347	Ha.136855	ESTs, Weakly similar to JCS314 CDC28[dc	2.29
60	417381	AF164142	Ha.82042	solute carrier family 23 (nucleoside-ri	2.26
	426228	NM_001110	Ha.172228	a disintegrin and metalloproteinase domain	2.27
	431448	AL137517	Ha.306201	hypothetical protein DKFZ256401278	2.26
	437181	A1306615	Ha.125343	ESTs, Weakly similar to KGA00755 protein	2.23
	415025	AW207081	Ha.72307	ESTs	2.18
65	412610	X90670	Ha.74126	fatty acid binding protein 6, fetal (gas	2.04
	424099	AF071212	Ha.139335	ATP-binding cassette, sub-family C (CFTR	2.03
	433078	AW015168	Ha.121575	Homo sapiens cDNA FLJ12321 fs, clone MA	2.01
	416225	AA577730	Ha.188684	ESTs, Weakly similar to POK259 lentilin	1.99
	411880	AW872477		gblhs303.31 NCL_GCAP_Thy4 Homo sapiens	1.90
70	432316	AA238484	Ha.61265	ESTs, Moderately similar to G708_HUMAN p	1.86
	413804	T54682		glycylaldehyde 2:1 Sirtalagene liver (G3724)	1.88
	432306	Y18207	Ha.303090	protein phosphatase 1, regulatory (inhi	1.76
	405364			ENSP0001259138: Guanine nucleotide-bind	1.60
	414320		Ha.75893	anilin 3, node of Ranvier (anilin 3)	1.52
75	401929	U13616		C17001690:g1605670[sp]NP_020909.1[1] AT	1.83

TABLE 10B

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Pkey: Unique Eos probe/seq identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
411880	1263110_1	A/872477 DE088101 T05990
413804	1390710_1	T64662 DE168190 DE168295

10

TABLE 10C

Pkey: Unique number corresponding to an Eos probe/seq
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1 et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1 et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

15

20

Pkey	Ref	Strand	NL_position
400752	7331445	Minus	38215-38461
400843	9188605	Plus	5863-5970,7853-7784,8892-9023,9673-9607,10634-10769,15254-15403,23827-23958
400844	9188505	Plus	24746-24872,25635-25294
401093	8516137	Minus	22335-23166
401512	7622346	Plus	136399-136557
401929	3810670	Minus	3167-3285,4216-4310
402230	9955312	Minus	29762-29932
402844	3959286	Plus	54958-55313
403010	3132346	Plus	76385-79052
403381	9438267	Minus	25009-25178
403383	9438267	Minus	119637-121197
403816	6962065	Minus	133630-138512,144656-144796
404606	5212936	Minus	22310-23289
404977	3736341	Minus	43061-43229
405384	2281075	Minus	48325-48491,49136-49252
406061	9123861	Minus	38115-38591

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TABLE 11A: Genes preferentially expressed in muscle-invasive bladder tumors

	Pkey	Unique Ecos probe/est identifier number			
	ExAccess	Exemplar Accession number, Genbank accession number			
	UniGeneID	UniGene number			
	UniGene Title	UniGene gene title			
	R1	80th percentile of T2-T4 tumor AIs divided by the 80th percentile of T1 tumor AIs			
10	Pkey <td>UniGeneID<td>UniGene Title<td></td><td>R1</td></td></td>	UniGeneID <td>UniGene Title<td></td><td>R1</td></td>	UniGene Title <td></td> <td>R1</td>		R1
	U23961	HS.136346	protein (DSF-20)		11.22
	U42148	U42683	keratin 6A		10.87
	U01780		NM_005577 Homo sapiens keratin 16 (flea secreted phospholipase 1 (lecithinase), ESTs, Weakly similar to S96504 hypothetical ESTs		9.16
	U46619	U076843	Rs.513		9.46
15	U44381	HS.285713	HS.285713		7.40
	U00049	U004576	HS.37007		7.53
	U43928	Y00757	Rs.624		7.74
	U41183	AW557446	HS.300711		7.40
	U11573	A0079000	HS.70823		6.02
	U41522	AW518944	HS.75358		6.52
	U41905	A005537	HS.75194		6.40
	U41633	AW585544	HS.112242		8.14
	U27337	Z62223	HS.176683		5.51
	U20695	AW63537	HS.100600		5.66
	U41324	AW58694	HS.112405		5.82
25	U18970	AF147294	HS.85914		5.46
	U01761				5.41
	U21116	T19132	HS.101850		5.41
	U48426	D71408	HS.12223		6.32
30	U41522	NM_025584	HS.75358		5.41
	U47326	AA045753	HS.353649		5.37
	U24247	X14008	HS.234734		5.22
	U46526	AW63537	HS.100600		5.66
	U19007	M13595			5.17
	U00663	U24693	HS.239441		5.08
35	U25993	A2279921	HS.19198		5.08
	U33336	A071596	HS.31386		4.93
	U26116	U007611	HS.154672		4.85
	U19594	NM_009223	HS.75358		4.74
	U12338	RS0768	HS.73817		4.39
40	U21626	L10343	HS.112341		4.23
	U48981	A0012113	HS.16530		4.23
	U33470	AW590564			4.22
	U17680	BC141518	HS.82948		4.22
	U46500	U79693	HS.15154		4.22
	U13324	U00571	HS.75284		4.20
	U38729	BC621607			4.15
	U50455	AA117424	HS.25935		4.09
	U13211	BC143846	HS.7551		4.00
	U12429	AW550262	HS.75755		4.00
	U18293	S76895	HS.83942		4.00
50	U14286	AA237830	HS.83988		3.76
	U20695	NM_016129	HS.75358		3.97
	U00688	HS.0266	HS.145609		3.94
	U27446	AA769946	HS.101302		3.94
55	U13441	AS125374	HS.75367		3.91
	U46654				3.77
	U31319	AA873340	HS.202322		3.76
	U50432	AW206005	HS.283378		3.76
	U29679	NM_006290	HS.211600		3.65
	U28330	L22624	HS.2226		3.65
	U00380	AF123650	HS.44532		3.65
	U11103	W87390	HS.109154		3.65
	U12545	X02761	HS.267670		3.52
	U29043	X54942	HS.83758		3.46
65	U00688	AW103364	HS.7277		3.46
	U09957	M21126			3.46
	U14369	M21204	HS.75929		3.46
	U17299	AW903838	HS.81800		3.46
	U14759	AW402482	HS.82212		3.46
	U46535	AW150177	HS.345726		3.22
	U00333	AW514020	HS.7277		3.22
	U17744	NM_002111	HS.177444		3.22
	U27227	AB090507	HS.293441		3.22
	U09142	AF136877	HS.50578		3.22
75	U53331	U204066			3.10
	U00688	AW585332			3.10
	U23696	HS.185289	HS.1076		3.10

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5	414622	A152656	Hs.75699	nicotinamide N-methyltransferase	3.07
	418478	U38545	Hs.1174	cyclic-dependent kinase inhibitor 2A (mc	3.02
	417771	AA084658	Hs.82547	retinoic acid receptor responder (brazo	2.77
	413936	AF113676	Hs.291681	serine (or cysteine) proteinase inhibitor	2.75
	406735	N8725	Hs.54390	metallothionein 1L	2.67
	426553	AA550882	Hs.171655	dual specificity phosphatase 1	2.75
	433623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.81
	423507	AF076464	Hs.5593	THYD protein tyrosine kinase binding pr	2.64
10	422046	NH_015445	Hs.258126	spondin 2, extracellular matrix protein	2.55
	410204	AA243425	Hs.320535	early growth response 1	2.46
	438573	AW659503	Hs.80440	ESTs, Weakly similar to serin protease w	2.46
	420202	AA135557	Hs.95510	putative lymphocyte G1/G1 switch gene	2.44
	422626	AA344632	Hs.116796	reticulohyalin 2A	2.44
	424202	NH_000554	Hs.8272	prostaglandin D2 synthase (211d, brain)	2.44
15	413902	AF007543	Hs.755613	CD35 antigen (collagen type I receptor,	2.42
	434868	RS0032	Hs.152593	collagen, type VI, alpha 2	2.42
	407207	T03651	Hs.335790	troponin, beta polypeptide	2.30
	431635	AW945276	Hs.8441	Home sapiens mRNA, cDNA DKFZ660021 (H	2.29
	430413	AW842182	Hs.241352	small inducible cytokine A5 (RANTES)	2.20
20	424909	S78187	Hs.153752	cell division cycle 25B	2.18
	419938	AF076772	Hs.1279	complement component 1, r subcomponent	2.17
	415819	U77735	Hs.80206	pim-2 oncogene	2.11
	422562	AA52690	Hs.110307	AE-binding protein 1	2.07
	414081	AW959975	Hs.279039	matrix G3a protein	2.07
25	428406	AF742501	Hs.197575	complement component 1, s subcomponent	2.03
	443960	NH_001425	Hs.9959	epithelial membrane protein 3	2.01
	416323	NH_002115	Hs.1152	major histocompatibility complex, class	1.90
	414420	AA043424	Hs.75905	innate-like early response 3	1.90
	415149	X12451	Hs.78056	cathepsin L	1.72
	415213	NH_002553	Hs.78224	ribonuclease, RNase A family, 1 (pancre	1.70
	422148	X15005	Hs.102805	cathepsin, type B, alpha 1	1.69
	425216	AA658030	Hs.23759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.64
	427676	AA594052	Hs.300772	tropomyosin 2 (beta)	1.64
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.59
35	424390	AW815557	Hs.132241	interferon induced transmembrane protein	1.51
	425625	AL133415	Hs.29173	Vimentin	1.46
	425293	AS682743	Hs.94553	Human sapiens, Similar to complement comp	1.46
	407694	U77594	Hs.37682	retinoic acid receptor responder (brazo	1.44

TABLE 11B

Key:	Unique Ecol probe identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers
1	29520_1
50	1
55	1
60	1
65	1
70	1
75	1

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433470 3672_1
 AW1960564 AA092457 T5890 D56120 T92525 A1815987 BE182608 BE182696 AW080208 M06657 AA347238 AV581686 AV179446
 AA304671 AW583735 T81714 AA318968 AW46615 AA345532 AA083489 AA489005 W52095 V23480 H57402 D62836 W25540 W53947
 D62720 D58990 BE519162 AA315188 AA330638 AA113474 W05162 AA088544 J52265 AA306161 H01062 AA113765 BE620957 AW651691
 AA347379 BE615660 BE547180 BE546056 F11933 AA376800 AW239185 AA376086 BE544367 BE619041 AA452515 AA001806 AA190873
 AA1104843 AA159646 F00242 A1940609 A940602 A1189753 T97663 T66110 AW062896 AW062910 AW062902 A051622 A1828930
 AA102482 A1865096 A1819390 AA557597 AA383220 A1804422 A1833575 AW538147 A186103423 AW506600 AW750567 AW510872 A2550777
 A1063510 AW629019 AW513200 AA921353 A1877934 A1148608 A1558569 A4173825 AA4543027 A027865 A10376542 A4454089 AA733014
 A5911381 R75300 R00023 AA441108 AA625058 AA444898 AW375550 AA880018 A1847475 AW205937 A052220 A19386117 A19386111
 A6899452 A242320 N47475 H38176 AA366821 AA113196 AA130023 H39740 T61629 A886973 AW083671 AA179730 AA335757 A1285455
 H83566 A2416013 AA336155 AW999695 T97525 AA343549 T91762 A771981 A285052 A591366 BE392486 BE365952 AA682801
 A882884 A1345840 T84771 AA292949 AA393079 AA056791 D62607 T46574 A1752036 C06300
 BE672807 A1445461 A1848805 AA437343 A854944 A098386 A0984527 BE15674 A894111 A591358 C17504 C17476 C17963 C18304
 A1071625 A1878112 C17732 D57559 H61762 A1720539 A1262930 H27252 A4479712 A1927769 AA291465 AA155661 A1963432 A1967995
 AA427676 N526507 AA252966 AA150448 AW192593 A1855836 A896905 A8871950 A911921 BE619741 BE438796 A161512 A1097001
 AA424384 A1003810 A240388 AW820230 AA92654 BE344033 AW262737 AW008670 AA043216 AW629005 AA138646 AA337722 A0700557
 AA026439 A1806193 A19506153 AA175836 BE591657 A1129574 R08114 A1649504 AA504530 BE337120 A19572331 BE219754 BE349186
 AW15724 A0443271 AW772001 A1798614 A1871727 A17759725 AA507832 AA70033 AA125675 W38161 A1972738 AA045070 AA627886
 AA723200 AA147228 AA030350 A190245 A1075878 T32487 C06123 AA157944 A8100106 W60075 A185160 AA178328 A1867512
 AA182640 A1950527 AW275048 AW103470 A2986935 A1871421 R79130 A0805158 W64510 A333170 A1305456 A662517 T55840
 A1823466 A892846 AA932987 AW191997 A1136658 A1251617 BE041154 A19339104 A1851782 A1724739 R78335 AA411100 AA191349
 A4337886 A1810286 A1757735 A1772283 A4010631 H89093 A1769516 H84895 A1061095 A1950993 A085492 A1245332 V12694
 AW88598 BE156350 AA349330 A1821320 A1789844 AW194272 AA148284 A1963883 C06385 AA487893 A1927217 A018523 A1454545
 A1789522 A1189366 A261359 A1032569 AW338678 A1972695 A1500576 A1872628 A093030 C28771 A1985583 A363829 AW339001
 AA681093 A1866038 W60032 AA803586 A886240 A18242958 AA719173 A1745717 A18673502 A1852462 A234545 A195459 T90579
 A1918453 A1935576 A072627 A18261556 A1915114 A1867445 D57558 A1846740 D57846 A188264 C05782 A172226 A4432033 R21762
 BE157610 A1802640 A1865337 A18545433 A8989662 A865912 AW197954 A344941 X77684 A344943 A19563310 A0888297 A334860
 A194887 A7798415 C11921 A1377596 A1893655 A1744233 C06111 A248307 AA948565 A224807
 A210685 T33681 N77488 H51833 AA147247 R75732 C16450 A79399 A1035755 T49004 H0388 AA411580 R33396 AA410586 T48689
 D62929 R31981 H12496 H02688 AA035218 R75957 A1803529 R77529 R3203 A1801992 A806765 R78948 AA411440 AA597629 A378780
 A171802 T48170 R73096 T55632 H05012 A1939684 H050580 H12839 N58781 AA72532 A1360919 H05051 H05052 BE205286 R68586
 A3304463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 A0035486 R25190 R25110 AA147533

TABLE 11C

Play:	Unique number corresponding to an Ex probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham1. et al., Nature (1999) 402:485-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	NL_position
401760	7249190	Minus	25357-26517,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-86037,86290-86914
404854	7143420	Plus	14260-14537

TABLE 12a: Genes preferentially expressed in muscle-invasive bladder tumors

	Play:	Ex/Accession	UniGeneID	UniGene Title	Seq ID No.
	Ex/Accession	UniGene Accession number, Genbank accession number			
5	UniGeneID:	UniGene number			
	UniGene Title:	UniGene gene title			
	Seq ID No:	Sequence identification Number linking information in Table 12a to sequences in Table 13			
10	Play	Ex/Accession	UniGeneID	UniGene Title	Seq ID No.
	424503	NM_002205	Hs.14969	Integrin, alpha 5 (fibronectin receptor,	Seq ID No. 1 & 2
	402289	X07620	Hs.2268	matrix metalloproteinase 10 (stromelysin	Seq ID No. 3 & 4
	418007	M13505	Hs.63169	matrix metalloproteinase 1 (matrilysin)	Seq ID No. 5 & 6
15	418738	AW388633	Hs.6892	solute carrier family 7, (sclerotic amino	Seq ID No. 7 & 8
	406964	M21305		FGFES3 predicted novel secreted protein	Seq ID No. 9 & 10
	425276	AF060885	Hs.19812	G protein-coupled receptor 51	Seq ID No. 11 & 12
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Oy	Seq ID No. 13 & 14
	410102	AW24808	Hs.279727	ESTs; homolog of PEM-3 [Drosophila]	Seq ID No. 15 & 16
20	425247	NM_006540	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. 17 & 18
	424735	U13875	Hs.272499	short-chain alcohol dehydrogenase family	Seq ID No. 19 & 20
	421159	AI572490	Hs.93765	Homo sapiens cDNA: FLJ21245 fl. clone C	Seq ID No. 21 & 22
	415811	AI755817	Hs.182382	ESTs	Seq ID No. 23 -25
	425481	N78223	Hs.106106	transcription factor	Seq ID No. 26 & 27
	413324	V00571	Hs.75294	corticotropin releasing hormone	Seq ID No. 28 & 29
25	443211	AI128389	Hs.13655	ESTs	Seq ID No. 30
	439506	AW014875	Hs.137007	ESTs	Seq ID No. 31 & 32
	432222	AQ24995		g0am03c03.1 Stralagene schizo brain S1	Seq ID No. 33
	409008	BE298227	Hs.250822	serine/threonine kinase 15	Seq ID No. 34 & 35
30	443171	BE281128	Hs.9030	TGDU	Seq ID No. 36 & 37
	432829	W03777	Hs.57722	ESTs	Seq ID No. 38 & 39
	410583	AW016824	Hs.272068	hypothetical protein MGCI4128	Seq ID No. 40 & 41
	419183	U08869	Hs.89863	cytochrome P450, subfamily X00V (vitamin	Seq ID No. 42 & 43
	425721	AC002115	Hs.159309	urokinase 1A	Seq ID No. 44 & 45
	420370	Y13845	Hs.97224	urokinase 2	Seq ID No. 46 & 47
	437552	BE031836	Hs.268987	ESTs, Weakly similar to U36501.2 [Hsa	Seq ID No. 48 & 49
	428864	AK001666	Hs.185095	similar to SALL-1 (sal) (Drosophila)-like	Seq ID No. 50 & 51
	468034	AW450979		gbtUH-H-B3-ata-4-12.0-U1-s1 NCL_GCAP_Su	Seq ID No. 52
	421110	AJ250717	Hs.1365	cadherin E	Seq ID No. 53 & 54
40	416866	Z33943	Hs.328444	cartilage acidic protein 1	Seq ID No. 55 -60
	408243	Y00797	Hs.824	interleukin 8	Seq ID No. 61 & 62
	440304	BE159984	Hs.126395	ESTs	Seq ID No. 63 & 64
	414918	AI215207	Hs.72222	hypothetical protein FLJ13459	Seq ID No. 65 & 66
	418887	D31771	Hs.85404	mesh (Drosophila) homeobox homolog 2	Seq ID No. 67 & 68
45	426386	AF038607	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. 69 & 70
	430503			C102652?g[544327]sg[404799]FMO5_RABIT	Seq ID No. 71 & 72
	422282	AF019225	Hs.114309	apical protein L	Seq ID No. 73 & 74
	426582	AK001604	Hs.159651	death receptor 5, TNF superfamily member	Seq ID No. 75 & 76
	403444			NM_003105?Homo sapiens sorbin-related	Seq ID No. 77 & 78
50	404875			NM_022819?Homo sapiens phospholipase A2	Seq ID No. 79 & 80
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	Seq ID No. 81 & 82
	431347	AI133481	Hs.251664	insulin-like growth factor 2 (somatomedin	Seq ID No. 83 & 84
	413824	Y14682		glycylalanyl-glycyl-Serine liver (873224)	Seq ID No. 85 & 86
	444163	AI126098		FGFENSH1 predicted RNaseH+ domain-contains	Seq ID No. 87 -89
55	444444	AI149332	Hs.14955	ESTs	Seq ID No. 90 & 91
	427747	AW411425	Hs.180685	serine/threonine kinase 12	Seq ID No. 92 & 93
	419741	NM_007919	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. 94 & 95
	420281	AB23953	Hs.323494	Predicated cation efflux pump	Seq ID No. 96 & 97
	402305			C1900735?g[4508627]ref[NP_003414.1] z	Seq ID No. 98 -100
60	438005	AA628980		down syndrome critical region protein DG	Seq ID No. 101 & 102
	427239	BE270447		ubiquitin carrier protein	Seq ID No. 103 & 104
	413278	BE563065	Hs.833	interleukin-stimulated protein, 15 kDa	Seq ID No. 105 & 106
	424008	R02740	Hs.137555	putative chemokine receptor: CTP-binding	Seq ID No. 107 & 108
	414907	X30725	Hs.77597	pola (Drosophila)-like kinase	Seq ID No. 109 & 110
65	421379	Y15221	Hs.103682	small inducible cytokine subfamily B (Oy	Seq ID No. 111 & 112
	426228	NM_001110	Hs.172028	a disintegrin and metalloproteinase domain	Seq ID No. 113 & 114
	417719	U85560	Hs.81154	interleukin 1 receptor antagonist	Seq ID No. 115 & 116
	401093			C1200536?g[6330167]g[BAAB647.1] (A	Seq ID No. 117 -119
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a)	Seq ID No. 120 & 121
70	44872	BE280074	Hs.22660	cytochrome E1	Seq ID No. 122 & 123
	429173	BE063064	Hs.16065	matrix metalloproteinase 12 (matrilysin)	Seq ID No. 124 & 125
	419478	U39845	Hs.11174	cyclin-dependent kinase inhibitor 2A (me	Seq ID No. 126 -130
	439606	W79123	Hs.85851	G protein-coupled receptor 67	Seq ID No. 131 & 132
	418543	NM_005325	Hs.85952	hyaluronan synthase 3	Seq ID No. 133 & 137
	419878	NM_001327	Hs.187379	conserved helix antigen (NY-ESO-1)	Seq ID No. 138 -141
75	428182	BE386042	Hs.253317	ESTs, Weakly similar to GGCI1_HUMAN G ANT	Seq ID No. 142 & 143
	427335	AA448542	Hs.261677	G antigen 7B	Seq ID No. 144 & 145
	439420	Z15008	Hs.54451	laminin, gamma 2 (nicotin [100K], kalni	Seq ID No. 146 & 147

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404440				NM_021048: Homo sapiens melanoma antigen,	Seq ID No. 148 s 149
433591	Y12642	Hs.3186		hemophyric antigen D complex, locus D	Seq ID No. 150 s 151
408380	AF123600	Hs.44532		chitinase	Seq ID No. 152 s 153
405983	AW247090	Hs.57101		mitochondrial maintenance oxidant (S.	Seq ID No. 154 s 155
424505	NM_002497	Hs.153704		NMA (over in similar gene)-related k	Seq ID No. 156 s 157
438617	AI020799			ESTs	Seq ID No. 158
421478	AB032443	Hs.47258		ESTs, moderately similar to S29530, rps	Seq ID No. 159 s 160
431515	NM_012152	Hs.265883		EDG-7 (endothelial differentiation, rps	Seq ID No. 161 s 162
433159	AB035898	Hs.150587		kinase-like protein 2	Seq ID No. 163 s 164
432441	AW292426	Hs.163484		ESTs	Seq ID No. 165
425728	AF165608	Hs.163530		ropalase 3	Seq ID No. 166 s 167
449045	AL297436	Hs.20186		prostate stem cell antigen	Seq ID No. 168 s 169
431846	BE019924	Hs.271580		uropalatin 1B	Seq ID No. 170 s 171
437044	AL038864	Hs.69517		differentially expressed in Fanconi's an	Seq ID No. 172 s 173
444381	BE307335	Hs.703713		ESTs, weakly similar to S60454 hypothel	Seq ID No. 174 s 175
400393	AA247758	Hs.75136		LVI-1 protein, estrogen regulated	Seq ID No. 176 s 177
452747	BE153855	Hs.81460		ly superfamily receptor LNR1	Seq ID No. 178 s 179
400297	A1127076	Hs.305201		hypothetical protein DKFZ5564C1278	Seq ID No. 180 s 181
428484	AF104032	Hs.184601		soluble carrier family 7 (cationic amino	Seq ID No. 182 s 183
429211	AF152693	Hs.190249		gap junction protein, beta 5 (connexin 3	Seq ID No. 184 s 185
417389	BE260694	Hs.82045		midline (tetraile growth-promoting factor	Seq ID No. 186 s 187
445537	AJ245671	Hs.12944		EGF-like domain, multiple 6	Seq ID No. 188 s 189
423961	D13566	Hs.135348		perlecan (OSF-2os)	Seq ID No. 190 s 191
417433	BE270266	Hs.52128		514 oncogene tyrosinase-associated glycoprotein	Seq ID No. 192 s 193
444781	NM_014400	Hs.11932		GP-anchored melanin-associated protein homolog	Seq ID No. 194 s 195
434666	BE062109	Hs.241551		chloride channel, calcium activated, family member 2	Seq ID No. 196 s 197
425450	NM_001944	Hs.1525		desmoglein 3 (permpagus vulgaris antigen)	Seq ID No. 198 s 199
429103	AF251237	Hs.112208		XACE-1 protein	Seq ID No. 200 s 201
129404	AI267100			ESTs	Seq ID No. 202
430347				NM_005655: Homo sapiens transmembrane protease	Seq ID No. 203 s 204
439738	BE246502	Hs.9598		sema domain, immunoglobulin domain (lg), transmem	Seq ID No. 205 s 206

TABLE 128

Key: Unique Eos probest identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

40	Key	CAT Number	Accession
		130710_1	T8482: BE168190 BE168256
		413804	BE270447 AW4199421 BE2012788 BE2017170 D56355 BE263223 BE408711 BE326243 BE3892439 BE212738 BE261776 BE314300 BE267719
		427239	BE28715 BE151878 BE209251 BE397058 AA210893 BE407519 BE15344 BE322905 AW246201 AW250313 119021 AA355115 AA358373
45			BE296933 BE27838 AF290724 AA380031 AA093618 BE301331 W97220 H73020 AW197895 BE274611 BE314315 BE542407 BE562063
			BE31266 BE27187 BE252503 AA426470 M81670 NM_014501 BE264533 A1884863 A884942 A876877 AA292937 A863533 AW270360
			AA303824 AG871253 AW172042 AA329208 AW674598 AW300535 AW515753 AW515587 AW65485 A855295 AA594105 AA5928110
			AC088519 A185899 AA428516 AC088515 AC031111 AW170655 BE47759 AW2512128 AW15507 AW070749 AW248955 AA975490
50			AA211091 A126057 A8826730 AA95407 AG367867 W74068 A886474 A8827720 A522628 AW000668 W58033 AA931461 BE408131
			M1218 A8678186 A861759 A123875 AW055058 AW272315 A525244 AW245051 A1668239 AW250588 A1953488 A1891144 AW1089131
			AJ471577 AA233554 AA484018 BE044548 Z25667 AW556171 BE37716 BE283400 AA918328 A1953488 AW075033 BE1353581
			AC046389 A250128 AW247038 BE13985 A1907517 AW17206 BE04086 AW032227 A054358 A0543615 A1334861 A250755 A254484
55			AW075025 AW032073 AA302738 A054067 A054217 A054174 A054302 AW053722 A054060 A054079 AW075181 A037473 A312145
			A304734 A1334908 AW071374 BE138502 AW074809 AW301901 A251662 A1307559 BE139228 A254764 AW073049 A0521254 A0802837
			AW171867 A1307442 AW075100 AW073496 AW072486 AG270787 AW21639 AW071367 A061013 AW071289 A251232 A251262
			AW073655 AW072901 A0307493 A255058 A251289 A252165 A271466 A252427 AW073495 AW071420 AG270156 A252928 A252839
			A252868 AW072520 AW073445 A154845 A1802654 A1334753 A185886 AW071311 A080263 A208711 A344028 AW072513 A348921
			AG27478 A1305762 BE138515 AW271034 A33486 A340619 AW40748 BE139260 BE139865 AW302085 AW041872 AW289694
			A204895 AW827539 AW069908 AW440775 AA528756
60			AA62880 A1126603 BE504035
			AG8717 A1826307 A893004 A307393 AW070547 AW979007
			A1125038 A1184745 A148521
			AW405879 AA136653 AA136656 AW419381 AA864358 AA492073 BE168045 AA809054 AW238038 BE011212 BE011359 BE011807
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 12C

Key: Unique number corresponding to an Eos probest
Ref: Sequence source. The 7 digit numbers in the column are Genbank identifier (GI) numbers. "Danham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Danham I. et al., Nature (1999) 402:459-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Key	Ref	Strand	NL_position
400844	9188605	Plus	24745-24872,25035-25204
401093	8518137	Minus	22335-23166

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402316	7328724	Plus	40832-41362
404440	7528051	Plus	80430-81981
404875	3801324	Plus	96589-9722,07722-97831
405053	7107731	Minus	142358-142540

5

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Table 13
Seq ID NO: 1 DNA sequence:
Nucleic Acid Accession #: NM_002205
Coding sequence: 24...3173

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	1	11	21	31	41	51	
	CAGGACGAGG	AGAGAGCAGG	GCTATTGGGA	GC0GAG0GCC	AGAGTCCOCT	CTCAG0GCGG	60
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10	TGCCGCGCGC	A00CAAGGCT	GGGAGCTTCA	ACTTGAAGCG	G00AG00CCA	GCAGTACTCT	180
	CGGAGCGCCC	GSCCTCTCTT	TTCCAGATCT	CGATGGAGTT	TTACAGCGGAG	TACAGCTGAG	240
	GGGTGAGTGT	GCTGGTGGG	GACCCGAGG	CTATTACGAG	CGAGCGAGGA	CGCTCTCAGG	300
	GTGGTGCTGT	CTACCTCTGT	CCTTGGGGGT	CGAGCGCCAC	ACAGTGCACC	CCCATTTGAT	360
15	TTGACAGGAA	AGGCTCTCGG	CTCCTGGAGT	CCTCACTGTC	CAGCTCCAGG	GGAGAGGAGC	420
	CTGTGGAGTA	GAAGTCTCTG	CAGTGGTTCG	GGGCAACATG	TCCAGCACTT	GGCTCTCCCA	480
	CTTTGGAGCT	CGCTCGGCT	TACAGCTGCG	GCAAGAGGAA	GGAGCTCTGT	AGCTAACCCG	540
	TGGGCGCTGT	CTACCTCTCC	ACAGATAACT	TACCCCGAAT	TCTGGAGTAT	GGACCTTGCC	600
	GCTCAGATTT	CAGCTGGGCA	GGAGGACGAG	GTTACTGTCCA	AGGAGGCTTC	ATGCGCGAGT	660
20	TCA0CAGAGC	TGGCGCTGTG	GTTTTATGTT	GACCAAGGAG	CTATTTCTGG	GAAGCCAGAA	720
	TCCCTGCTCG	CAGTCAGAG	CAATATTCAG	AATCTATTAT	CCCGGAGTAC	CTGATCAACT	780
	TGGTTCAGGG	GAGCTCTGAG	ACTGCCGAGG	CCAGTTCGAT	CTATGATGAC	AGCTACTGAG	840
	GATACTCTGT	GCTGTTTGTT	GAATTCAGTG	GTGATGACAC	AGAGGAGCTT	GTTCCTGGTG	900
	TGCCCAAGAG	GAACCTCACT	TACGCGTATG	TACCAATCGT	TATAGCTCA	GGATCTGGAT	960
25	CCCTCTACAA	CTCTCTAGGA	GAACAGATGG	CCTCTCATTT	TGGTATGACA	GTGGCGGCGA	1020
	CAGATCTGAA	TGGGAGGAG	CTGGATGAGT	TGCTGGTGGG	GGACCCCTGT	CTCATGGATC	1080
	GGACCCCTGA	CGGCGGCGCT	CAGGAGGTGG	CGAGGGCTTA	CGTCTACCTG	CAGCACCCAG	1140
	CGGGGATAGA	GC0CAAG0CC	A00CTTACCC	TCACTGAGCA	TGATGAGTTT	GGCCGATTTG	1200
	CGAGTCTCCT	GACCGCCCTG	GGGACACTGG	ACAGGCTTGG	CTCAGTATAT	GTGGCATCTG	1260
30	GGGCTCTGAG	TGGTGGGAG	AGCCACGAGG	GAGTAGGTTT	TGATTTCTCT	GGGAGGCCAG	1320
	GAGGCTGGGG	CTCTAGGCTT	TCCCAGGTTG	TGCAGGCCCT	GTGGGCGGCC	AGGCCACACC	1380
	CAGACTCTCT	TGGCTCTGCC	CTCTCGAGAG	GC0CAGACT	GGATGGCAAT	GGATATCTGG	1440
	ACTTGATGTT	TGGGCTCTTT	GGTGTGAGCA	AGGCGTGTGT	ATACAGGCGC	CGCCCATCTG	1500
	TGTCGCTGAG	TGTCGCTGCT	CGGCTATCTT	CGGCTATGTT	CGACCGAGAG	GAAGCGAGCT	1560
35	CGGCTTAGA	GGGGAACCTT	GTGGCGCTGA	TCAACCTTAG	CTTCTGCGCT	AATGCTCTGT	1620
	GAAGAACAGT	CTGACTCTCT	ATTGGTTTTA	CAGTGGATCT	TAGCTGGAC	TGGCGAGAGC	1680
	AGAGGAGGAG	GTTAGAGGCG	GCATGTTTCC	TGGCTCTCAG	GGAGGAGGAG	CTAGCCAGGA	1740
	CCCTGCTCAT	CAGAGATGAG	GCTCTGAGAG	ATTGCGAGAA	GATGAGATGC	TACCTCAGGA	1800
40	AGGTTCCAG	ATTTCGAGAC	AAACTCTCGC	CGATTCACAT	CGCTCTGAC	TTCTCCTTGG	1860
	AGCCCGAGAG	CCGATGGAGC	AGCCACGCGC	TCAAGCGCAG	CGTACATTTAT	CAGAGCGAGA	1920
	GGCGGATAGA	GAACAGAGCT	CAGATCTTGC	TGGAGCTTGG	AGAGAGGAC	ACTGCTGTGC	1980
	CTGAGCTGCA	GCTGGAGTGG	TTGGGAGGAG	AGAAAGCTGT	GGAGCTGGTG	GAGAGAGATG	2040
	CCCTGAGACT	CAGTCTCCAT	CCCGCAATGT	TGGGTGAGGG	TGGGCTTATG	GAGGCTGAGC	2100
	TTCGAGCTCAG	CGCCCTTCCA	GAGGCTGAGT	ACTCAGGACT	CGTCAAGCAC	CCAGGCGAAT	2160
45	TTCAGAGCT	GAGCTGTGAC	TACTTTGGCG	TAAACGAGAG	CGAGCTGTGT	GTGTTGAGCC	2220
	TGGGCGAGCC	CAAGAGAGCA	GGAGGAGCTC	TGTGGATGAG	CGTCTGTTAT	ACAGTCCCTC	2280
	ATCTCCGCGA	CGTAGAGAA	AGCATCGAGT	TTGACTTCCA	GATCTCAGAG	AGGATCTCA	2340
	ACAACTCGCA	AAGGACA0TG	GTTTCTTTTC	GGCTCTCGGT	GGAGGCTCAG	GCCGAGTCCA	2400
	CCCTGAAGCG	TGTCCTCAG	CGTGAAGCAG	TGCTATTCCG	AGTAAAGCAG	TGGATCTCCC	2460
50	GAGCACAGCC	TCAAGAGGAG	GAAGAGCTGG	GAAGCTCTGT	CGACCTATCT	TATGAGTCA	2520
	TCAACAGAG	CCGAGGCTCA	ATTAGCCAGG	GTGTGCTGGA	ACTCAGCTGT	CCGAGGAGCT	2580
	TGGAGAGTCA	CGAGCTCCTA	GTGTGAGCCA	GAGTATGAGG	ACTCAAGTGC	AGCAAGCATC	2640
	AGCCCATTTA	CCGAAAGGAG	CTCGAGTTGG	ATCCGAGAGG	TTCCGTCGAC	CAGAGCCAGAA	2700
	AAGGCGAGAG	TCCAGAGCGC	AGCTCTGTGT	CCTCGGAGCC	TAAGCGAGGCT	GAAGCGAGAG	2760
55	AGGCTGATGT	TGCTGAGTGG	CGCTGTGAGT	TGGGCGCCCT	GACAGAGACA	GAAGAGCCAA	2820
	GTCTGCAATT	GCAATTCGGA	GTCTGAGCCA	AGACTTCTCT	GGAGCGGAGG	CAGCAGGCACT	2880
	TTAGCTTGCA	GTGTGAGGCT	GTGTACAAAG	CCCTGAGATAT	G00CTCAAGTA	ATCTGCTGCT	2940
	GGGAGCTGCG	CCGAAAGAGG	GTTCAGGTTG	CCAGCACTGT	CGATCTGAGC	AAGGCGAGAG	3000
	CGAGCATATG	CGTGGAGGCT	TAGATCTCTA	CTGTAGCATC	CTGTCTGAGC	CTCTGCTGCC	3060
60	TAGGCTCTAT	CATCTACATC	CTCTACAGAG	TTGGATTTGT	CAAGAGGCTC	CTCCATATGT	3120
	GCGCGCCGAT	GGAAAGAGCT	CAGCTCAGGC	TTCGAGGACG	CTCTAGTGGC	TGAGTCTGCT	3180
	CAATTTGAGA	CTCCATTTCC	TGAAGAGAGC	GTCCGCCGAC	CGTCAATCTA	CGAAAGACA	3240
	GGGAGTCTGG	TACTCTTGGA	AGTGTCTGAG	CGGCGAGGAG	AAATCTCTCT	CCGAGGAGCC	3300
	GAGACATCTG	TGAAGGCGCA	GAGCGAGGCG	GTTGAGGAGG	TGGGATATCC	TCCGCCCATC	3360
65	GCACTGTGGA	GAGCCCTTGT	TACACATATC	CGTCTTCTAT	GATGGGAGGAG	CTCAGATGCA	3420
	GGGACAGAGG	CGGAGCTCTG	CTGAAGGCTT	TGCATTTTGG	AGGATTTTCT	GAAGACAGAT	3480
	GAGACATATC	TGAGAGATTC	AGATCTCTGAG	TCCAGCTTGC	CAGAGATCCA	AAGAAAGCCC	3540
	CCGATTAAGAA	CTCGAGACTT	GGGAGTTTAA	GA0CTCGGAG	CTCTGAGAGC	CGCCACCTGT	3600
70	GTGGCGGAC	AAGAGCAACT	AACATAGCAT	GGTGGCCGAG	GA0AGCTGCA	GGAGGAGTGC	3660
	CACAGAGATA	GATCTCTGGC	CAGGCGCGAG	GGCCGCTCTC	AAGGCGATAT	AGAGATCAAA	3720
	TGGGCGGAGA	TGCGGAGGAG	GATCTCTGAG	GTATCTGAAA	CCGAGAGACA	GGCATTTGCA	3780
	CGATCTGAGG	CGAGTCCAGG	ACTATATTGT	GGGCTGCTCT	AGAGCTGATC	CTGGAGGCGC	3840
	AGTTCAAGCT	GAATTTAGAG	AAGCGAGAGAA	TTTCCAGAGA	CTTGAAGGCG	CATGATTTGC	3900
75	AACAGATCTG	GAGCTCAGG	CTGGAGGAGC	CACAGAGGCT	CGTGTCCG	AGGAGAGGCG	3960
	CGGAGTCTAG	CTGGGAGGCT	GGAGATTTTG	GGTCTGCTCT	CGTAAATGCA	CTGATGCTGC	4020
	CGGATCTCTG	CTGAGCGAAT	CCTTCACTCA	CTTGGGAGCC	AGAGCCAGGA	GGCATTTATTA	4080
	AACCTCTGTT	CAGTGTGCAAT	AAATCTGAGC	CAGTGGCCCC	ACTGAGCCAG	ACTGAGAAAA	4200

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AAAA

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_002196.1

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    2  GFSVBFYRFG  TDGVSLVYLG  PKANTSQGV  LQQAAYILCP  WGASPTQCTP  IEPDSKGSRL  120
    3  LBSISSBSG  BEPVKESYLG  WFGATVRAHG  SGLACAPLY  SHREKBPIS  DFWGTCLYST  180
    4  DNPTRILEYA  PCHSDPSMA  GGQVQKQGS  AETKRGVIV  LGGRSIFWQ  SGILLATQD  240
    5  IARSYPIEL  IHLVGGGLQ  RGRSETYDS  LVLSVAVGE  FSGHTSDIV  AVKPKNTLY  300
    6  GYVTLHOSD  IRLSLVSGE  QWASYGVAV  AATDVNGDL  DDLVQAPLL  MORTPDGRPQ  360
    7  EVGRVYVILQ  HPAGIEPTT  LITLHDSBG  RPOSSLTPIL  DLDODGYNDV  AICAPFGGPT  420
    8  QGVGVVFFPG  PGQGLGSKF  QVLCPLMAAS  HTPDPFGSAL  RGRDLDDG  IYDLVHSPG  480
    9  VDKAVVYRGR  PIVEKASLIT  IFPANIPEE  RQCSLSQHP  ACMLGLCLM  ASKAVWASL  540
    10 GTVTLQDM  QWQKQWGA  LTASAKNTL  TOTLLIQMG  REDCKEMKY  LRHSSEFRDK  600
    11 LSPHIALMT  SLDQAPVDS  HOLRPAHYQ  SKSLBDKAG  ILQCGENIL  CVPLGLEVP  660
    12 GBQHVYVLD  KHALMLTFA  QWVSGGAYE  AELRVTAPE  AYSGLYRHP  GYFSLGSLDY  720
    13 SFRLSVBGA  QTVLNGVSE  ENLFPVSD  HFDQPKSE  DLGAVHYVY  BLNQGPSSI  780
    14 SOGVLELSC  QALEXQQLY  YTVTCLMCT  TNHPINPKGL  ELDPGSLHH  QOKREAPSS  840
    15 SASBPQILK  CPBACPRLR  CELQJMQGE  SQSLQHFVY  WAKTFLQRE  QPFLQCAW  900
    16 YKALMPYRI  LPRQLPKER  QVATVQHTK  ABGSGVPLW  IITLILFGL  LLGLLITLY  960
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Seq ID NO: 3 DNA sequence:
Nucleic Acid Accession #: NM_002425
Coding sequence: 23..1453

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    3  TGCCACGCA  TACCTAGAA  AACTACTACA  CCTCGAAAG  GATGTGAAC  AGTTAGAG  180
    4  AAGAGCAGT  AATCTCATG  TTAATAAAT  CCAAGAGAT  GAGAGATTCC  TTGATTTGGA  240
    5  GTTGACAGG  AACTAGACA  CTGCACTCT  GAGGTGTATG  GCAAGGCCA  GGTGTGAGMT  300
    6  TCTCAAGTT  GGTCACTCA  GCTCCTTTC  TGGCATGCC  AAGTGAAGA  AARCCACCT  360
    7  TACATACAG  ATTGTGAAT  ATACACAGA  TTGCCAAGA  GATCTGTGT  ATTCTGCCAT  420
    8  TGAGAAAGCT  CTGAAGTCT  GGGAGAGGT  GACTCACTC  AGATTCTCA  GACTGTAGA  480
    9  AAGAGAGCT  GATATGATA  TCTCTTTC  AGTTAAGAA  CATCGAGACT  TTATCTTT  540
    10 TATGCGCCA  GGACACAGT  TGGCTCATG  CTACCCACT  GACCTGGG  TTTATGAGA  600
    11 TATCACTTT  GATATGATG  AAAAAAGAC  AGAAGATGA  TCAAGCACCA  ATTATCTCT  660
    12 CATTGTGCT  CATAAAGTT  GCGACTCCT  GAGGCTCTT  CACTACACA  AACTGACAC  720
    13 TTGATGTAC  CCACTTACA  ATCATTCAC  AGAGCTGCC  CAGTCTCGC  TTTCGAGAA  780
    14 TGAATGAAT  GGCATCAGT  CTCTACAGC  ACCTCCCCC  GCTCTACTG  AGAAGACCT  840
    15 GGTGCCACA  AATCTGTTT  CTTCGGGTC  TGAGATGCA  GCAAGATGT  ATCTCTCTT  900
    16 GTCTCTCAT  GGCATCAGCA  CTCGAAAGG  AGAATATCT  TCTTTAAG  ACGATATTT  960
    17 TTTTAAAGA  AATGATTT  GGGCATCAG  AGAATAAGG  GTACAGCA  GTTATCAAG  1020
    18 TTGCGAAGA  TCCCATGTA  ACCCTGAC  TGAATTCAT  TGTCTTCTG  CAGATTTAT  1080
    19 CTCTCTTCA  TCAATTTGG  ATGCTACAT  TGAAGTTAC  AGCAGGACA  CGTTTATT  1140
    20 TTTTAAAGA  AATGATTT  GGGCATCAG  AGAATAAGG  GTACAGCA  GTTATCAAG  1200
    21 AAGCATCCAT  ACCGTGGTT  TTCTTCAC  CATANGBAA  ATTATGTC  CATTCTGTA  1260
    22 CARGAAGAG  AGGAAACAT  ACTCTTTC  AGGACACA  TACTGAGAT  TTGATGAAA  1320
    23 TACCATCT  ATGACAG  GCTTCCCTAG  ACTATAGCT  GATGATTT  CAGAGATTGA  1380
    24 GCTTAAGTT  GATGCTGAT  TACAGCAT  TGAATTTTT  TACTTCTCA  TGAGATCAT  1440
    25 ACAATTTGAG  TTTAGCCCA  ATCCGAGAT  GTTGACAC  ATATTAGA  GATACACT  1500
    26 GTTACTTTC  TTAGCGAGT  AAGGAGAGA  CAGATATGG  TTTTATAT  AATCATATA  1560
    27 GTTACTTTC  TTAGCGAGT  AATCCAGAT  GTTGACAC  ATATTAGA  GATACACT  1620
    28 ATATTCTCA  TATGTTTAT  TTAGCGAGT  AATCCAGAT  GTTGACAC  ATATTAGA  1680
    29 GAGAGATG  AGCCTTCAG  ATATCTGAT  GTGTACGTA  GATGTTCT  GGAATCTCT  1740
    30 ACTTGCTTT  GAATTCAGT  GAACAGAT  AAGAAATAT  CATGTGCMT  AAGTGAAGA  1800
    31 ATGATTTTC  ATAGATGAT  TATTACTTC  TCAATAAAA  GTTTATATT  GAGCTGTTT  1860
    32 CTT

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Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_002416

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1      11      21      31      41      51
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    2  KETQGMKPL  GLRYTKMLT  DTLRYWKKR  GQVDPGHPS  SPFGPMKRX  THLYTRIVY  120
    3  TPLPRDAV  SAIBALKLV  BEVPLTPSR  LYBEGADIM  SPAYKERDP  YSPDGHSL  180
    4  AHAYPPGPI  YGDHPDDOB  IUTEDASDT  LFLVYANRI  HSGLGHSAN  TSLALFLYN  240
    5  SPTELAFGL  SLYNKHGDS  LSPPPASTE  PLVPLKSV  SGBHMKACD  PALSPDAIS  300
    6  LKRLVLPD  RYFRSESN  PEPHELSA  FWSLPSLD  AAYEVNEDT  VPIFKNGHW  360
    7  AIRGNEVQAG  YPKIHTLGF  PPIRKILDA  VDSKPKICY  PPAADYKRF  DENSQMSHQ  420

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PFRLIADDFP GVEPKYCAVL QAFGPFYFSS GSSQRFDPN ARMVTHLKS NSMLHLIC

Seq ID NO: 5 DNA sequence:
Nucleic Acid Accession #: NM_002421
Coding sequence: 72..1481

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 15 GGAAACGAGA TGCTGAAACC CTGAAGGTGA TGAAGCAGCC CAGATGTGGA GTGCCGTGAT 360
 TGCTCAGT TTCTCTCACT GAGGGGAGCC CTCTCTGGG GGAACACAT CTGACCTACA 420
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 CTTTCACT CTGAGKATAT GTCAACCTTC TGACATTAC CAGGCTCTCT GAGGATCAAG 540
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 20 CTGAGAAJAA TCTTGTGAT GCTTTTACAC CAGGCGCAGG TATTGAGGG GATGCTCAAT 660
 TTGATUAGA TGAAGAGTGG ACAGACAT TCGAGAGTA CACTTACAT CTTGTGCGG 720
 CTGTGAAT CGGCATCTT CTGGACCTCT CCGATCTAC TGATATCGG CTTTGTATGT 780
 ACCCTAGCTA CACTTCACT GGTGATGCTC AGCTAGCTA GGTATGACT GATGGCATCC 840
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 TTCTCTTCT CTGGCCACAA TGCCCAAAT GCGCTGAGC TGCTTACGAA TTGCGGACA 1080
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 40 GATCTTCC AGATGTGCA ACTCTGACGT TGATCCGAGA GAGCAGCTTC AGTGCAGAAC 1800
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 ACAGAAATAG TGTTTTATGT TTGGATAAA GTCAAGCTTC TTCTACTGT TTT

Seq ID NO: 6 Protein sequence:
Protein Accession #: NP_002412

1 11 21 31 41 51
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 YTFDLPRADV DHATKEAGFL MSVITPLTF KVSBDQNDIM ISPRDEHRD HEPFDGPGN 180
 55 LMAHAPQFPO IGDAHFDEB ERMTHNFRY NLRVNAHEL SHLGLDSEI DGLMPLFPI 240
 FTSFVQLAG TLDIDGATY GRSTGKPGI GPTTACAGC KLTFAITTI RGEVFFKDR 300
 FYSVTSFPG FRTVKHIDA LSEETKNTX FVANKMRYE DEYKASMDPG YPMIAHDFP 360
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Seq ID NO: 7 DNA sequence:
Nucleic Acid Accession #: NM_014331
Coding sequence: 1..1506

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 70 GGAATCTTCA TCTTCTTAA GCGGCTGCTC CAGACACGG CAGCGCTGG CATCTCTTG 240
 ACACATCTGA CGGTGTGATG GTTCTGTCTA CTATTGAGG CTTTGTCTTA TGCTGAATG 300
 GACACACTA TAAGAGATCA TGAAGTCAAT TACAGATAA TTTTGAAAT CTTTGTGCTA 360
 TPKGCTCT TTGAGAGT CTGGGTGGA CTCCTATPA TAGCCCTCTC ACCTACTCT 420
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 75 CTGACCTTG GATCTAAGT CATTTACGCT GTGGCATPA CTATCTAGT GGTCCCAAT 540
 ACATATATG TCAATATAG CCTGTGAGT ATGCAAGTCA TTAAGGTCA AAGCAGAGAC 600
 GCAATCTTA TATTTATAG CCGTGTGAGT ATGCAAGTCA TTAAGGTCA AAGCAGAGAC 660
 TTAAGAGCC CTTTTCAGG AAGAGATCA ATGATATAC GGTTCGACAT GCTCTTTAT 720

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 25
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Seq ID NO: 8 Protein sequence:
 Protein Accession #: NP_055146

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 LPAIVPVVE LLIRPAATA VISLAFGRV LEPFFIQEI PELAIKITA VGITVFWLN 180
 SMSVSWARI QIFPTFCELT AILLIIVQV MLIQKQTN FKPAPGSRD SITPLFLAY 240
 YOMAYAGWP YNFPVREVE RFEXTPLAI CISMALVTG IQLTQVPTT TIMABELLG 300
 KAVATFPEB LQVLEPLAV IPVALAGGK HKGVFAKSE LFTVASRKH LPEILSMIV 360
 KKITPLAVI WPLPLDML PSGLDGLLN FLSPARMLP GLAVAGLTV KYCPDPRFM 420
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 Coding sequence: 1..546

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 CAGTCTGCA AAGCCAGAA CTGTGAGTA ACAGTGTACT CAGAGCTCA GCGAGCTGAG 480
 AAAACCTTTG AAATCTGTT CATGGTTCCA TCAAGCTTA TGTACTGGAT CCACATGGA 540
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Seq ID NO: 10 Protein Sequence
 Protein Accession #: F08NESH

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PCT/US02/21338

1 11 21 31 41 51
 5 HALGSSAPVA LQGNHITPAA PDAKICLAW FQVPLGLFPE LVQRLLQDAR TIRFVPAAL 60
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Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: E05 sequence
 Coding sequence: 461-3286

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5 CGCAGCAGG CACAGCCCTG GACAGGCGAG GCCACGGGCT GCGGACTGCG AGCAGGCTGA 3900
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 AAGTACATTC TCTGTCTAT TGATACGTGA GTTTCACCA TTTTTTTTTA ATTCCTGCG 5520
 30 AATAACAGG ACCACAGAA GTGACTCTAG CTACTTAAT GTTCTCTGT TTTATATCG 5580
 CCAAGACAG CCGTATGCT TGAGAGGCT TCGGCTTAA GCGCTTCCG AAGTATTTA 5640
 GTCCACAAA CCTTTAAAT TAGACTGAAA CTGCCAGAT CAATCTTAA TGAGGAATT 5700
 CTGTACCCC TACTGATGG TATCATTTT TAATTAATG TTGCAANTT GTTTTATGA 5760
 ATAAAAGAA AAGACTGCT GTCTTT

Seq ID No: 12 Protein sequence:
Protein Accession #: B0S sequence

40 1 11 21 31 41 51
 MASPRSSQPP GPPPPPPPPP ARLLLLLLLP LLLPLAPGAN GHARGAPFP PSSPPLSIMG 60
 LNPITREYAK GSGTGVLPFA VELAIQDIRN EBLARPFIID LRLYDREIN AKGLAATPDA 120
 TIKGHHILAV PQGVCPSTVS TIASSQDNR LVQSPRANCT PHLADKEKTP YFFETVPSRN 180
 AWPALKLL HNYQFERSVT LQDVQFSE VMDLTGLVY GEDIEISDTE SFSNPCTSV 240
 45 KLLKNDVRI ILQGFQDQNA AKVFCAYEY NNYGSKYQVI IPMYEPFWM EOVTFEANS 300
 RCLRKHLAA NXYGLVDFSE PLSKKIKTI SKTFPQYER EYNNKRSVG PEKPHOYATD 360
 GIWIAKTLQ RABETLABAS KHKRIGQFWY THTLQIIL NANNENPFO VQGVVTHG 420
 BRNGLIFVQ FQDSREYVQ EYVWADYLE IINDIRFQG SEPPKQNTII LEQLKRLSP 480
 LYSLILALTI LQMINASFL FFRHNRHKK LIXMSPSYN NLLILOGLMS YASIFLPLGD 540
 50 GSPVSEKTE TLTCTVTHIL TVGTTTAPGA MFAKTHVHVA IFKQVHKKR ILIDKQLAVI 600
 VGGNLLIDLC ILICQNVDPD LKSTVEKSH EPQAGRDLS ITPLEBENR THTTTLGIV 660
 YATKGLGLF GCLFANETH VSTPLADSK YIGSVYVQV IMLIGAAVS FLTRDQNHVQ 720
 PCTVLLVIFP CSTTTLCLWF VPRLITLTH PDAATQNRFP QPTQKQKED SKTSTSVTSV 780
 55 QNASTRLBS LQSBHRLHN KITELDKLE EYVMOLODTP EKTYYIKNH YQELNDLHL 840
 GNPTSTDDG KAILGNHLDQ HFGLOHNTFE PSTRCDPIE DINSPIHQR KLSGLPLIH 900
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Seq ID No: 13 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67-363

60 1 11 21 31 41 51
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 65 ATTCAGGAGG TACTCTCTCC TAGAAACGTA CCGCTGACCT GCATCAGCAT TAGTATGCA 240
 CCGTATATC CAGAGTGTCT GAATAAAGCT GAATATPCT CTGACAGCA ATTTGTGTA 300
 GGTGTGAGA TCAATCTACG AATGAAAGAG AAGGTGATCA AGAGAGTCT GATTCAGCA 360
 TGGAGGCTA TCGAGATGAT ATGAAACAG GTTAGCAAGG AATCTCTTAA AGATCTCTC 420
 70 TAAACACAGA GCGGAGCAAA ATGATGACG TCGTCTCAAG GATGAGCACA CAGAGGCTC 480
 CCGTCCCATC CAGCTCCCTA CATGAGCATAT ATCTCAGCGC ATATATGCTC TACGTATGCA 540
 GTTACACTTA AGCTAACCA ATGATGTCTA CCAATCTCAG TCGTCACTCT CCGTATGAGA 600
 GGTTAATCT CATCTATCTA ACTATATGAT TAACTACTC ACCCTGCGAC ATCTATGATA 660
 75 GCTCTACTGA GGTCTATGAT TCTTATGGA TGTCTGACCC CTGCTTCAAA TATTTCCCTC 720
 ACCCTTCCCA TCTTCCAGG GTACTAGAGA ATCTTCTGCG TTTCGGTFTT ATCGAGATCT 780
 TACATGATC AATAATCTAA AGGTATGACA ATCAAACTCG CTTTTRANG AATCTCTT 840
 ACTCATCA CTGACATCTT CPTCTCTCCA AGGCGCTGCA ATCTCTTGA TGCTACTCTA 900
 GTTCAATC CAACACATA CCGAGAGCTA GAATATCTG AATATGATC TGTAAATAT 960
 CTTATTTAT GAAAGACAT ACAAGATATA AACTCTAGAT GTATATATC CTAATATAT

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TTTCAATGTA CATGGAATA CATGTAATTA AGTCAATATG ATCAATAGAGT AACGAGAAAA 1020
 TTTTAAAAAT AACAGATAGT ATATGCTCTG CATATTCACAT AAGAATAATG TGCTGAATAG 1080
 TTTTCAAATA AAGATAGAGT ACTCTCTCTG AATATTATAG

5 Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
 10 MHQTAILICC LIFLILSGIQ CVPLRGTVRC TCISISNPV NPSRLKLEI IPASQPCPV
 EIIATHKKKG EKRLINPESK AIIHLKKAVS KENSISRF

Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 241..1272

1 11 21 31 41 51
 20 GCGCAGAGCG CCGACGCTCC CACGCGCCCC AAGAGGGGCG GCGACGCCAA GCTCTGCGCT 60
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 TGCGCCACTT CGAGCAGCTG GCGCGAGGTC GTGGGAGGTC AGGCTGTGCA GATTAGGCC 180
 TTGAGGCGCA AGCGACACAC CTACATTAAG ACACCGGTSA GGGCGAGGGA ACCAGTGTTC 240
 ATGTGTGACG GCGCGACGGG GCGGCTGTGC ACAGCCGGGC GGGAAATCAT CTCAGCAGCG 300
 GAGCAGCTTCT CCATGATGCG TGCTCTCCGC AACAAAGTCA GCGCGCGCTT TGGTGTGACT 360
 25 CTTGCTCTCG CCGGCGAGGT GAGCATCTCT GTGGGAGTGC CTAACGGGTG GTGTGGGCTG 420
 GTGTGTGGCG CGAAAGGATC AACCTATCAG GCGACGACAC ACGAAACCCA CACATCACT 480
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 30 TCGGACCTT GGGGATGAGA CCGAGCGGCG TCGAAGTCCC TCTCCACCTT CCGGACGAGC 720
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 35 GCGCAGCCA CTTCTCGTCC CTTCTCTCTT GCTCTCTCTT CTTCTCTCTT TCGCGCCAG 960
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 GCGGCGCTGC GAGGCCCGCG GCGGCGGGCG GATTGCAAG TCTGCTTTGA GAGGAGTAC 1140
 40 ACTGCGGCTC TTGTGCGCTC GCGACACACG CTGTTCTGCA TGGGTGTGTC AGTACGATC 1200
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 45 AGAGTTACA CTCTGATACC TGAACACACC CTAAATCTCT GAGCAGCTCA AGAGAACTT 1560
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 50 TTTCAGCAG TGTAGGAG TTGAGATCTT ATCAGAGATG GATATGATCT TCGTGGGTT 1860
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 60 AAGGTGAAA CCGCCACTCT CAGCATGATG GAGCATGATG TTGAGAGATA GTTCTTGCC 2460
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 80 AATGTGACA AACTCTAGAA CAGACACAAA GCGACATAG TGGAGAGACA AATAGAGGAG 3420
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AATAAAAAA CTTTAGAAGG TTTAGAAATAT ATGTAGGAG AGAAAGAGAA AAAAAATACAT 3660
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 CATATGAGA CAGCTACAAA TCCACCAAGS AAAAAATTT CAAGACAAA ATAAAGAGG 5700
 GAATTAJAC AGACCCAGA ATATCAAGT CAAGTGATG TTGCAAAA TACAGAGAA 5760
 GCAAGAGG GAGGCTTAA TGATTAAGT GTGCTTTAA GAATTAAT TTATTAAG 5820
 TACTATTACT TAGGCTC

Seq ID NO: 16 Protein Sequence
 Protein Accession #: XP_044166

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1 11 21 31 41 51
 NVYTORREDVA TARREI19AA EHFSEIRABE MEGSAGFVGA PALPGQVITR VRRPVVVLG 60
 VVGKGTATIE RIQQQNTYVI ITPSRDRDPV FEITGAPGVV ERAREIETH IAVRTGKI LE 120
 YHNENDFLAG SEDAAIDRSY SEDMRVHPOI CKPLSTFRN SLOCTIGBYV DSFPBAPRG 180
 SOGGFPVGG YLFPYGVGVK QPVYTVNABT SPFLHAGQBN ATTPVFLPSV AGSSSSBNAK 240
 ARAGFPKMR SPATGAPLES AGLPREFPQS PLQCFKELQZ QILASPKGRK DCHVCFSESE 300
 TADLPQCHH LFWCECAVRI CRETDFPCPV CHITATQAIR IFS 360

Seq ID NO: 17 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23-1489

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1 11 21 31 41 51
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 TGTGCGCCGG GAGTTCACAC ACCCTCATGC GAGAGAGAGG GGGCCACAGC CCGTGGGCTC 180
 AGCCCTGCCC CAGATACCGG CAGCTGCCC GAGGCCCCCT GAGGCCCCCT GCGCTCCGAG 240
 GAGCTCAGG CCGTCCGCT GTGGCCTGCC GAGCCCTCTT GATGGGCTGA GTGCCCGCAA 300
 CCGACAGAG AGTGTGTGTC TTCTTGAGCG GGCCTGGAGS AAGACGAGCC TACCTACAG 360
 GATCTCTTGG TTCCATCCGC AGTTGTGTGCA GAGAGAGGTT GGGCAGACGA TGACAGAGGC 420
 CCTAAAGGTA TGGAGCGATG TGAGCGCATC CAGCTCTGCT GATGSGGAC GACTGTGCTT TTGATCGGCC 480
 TGACATATG ATGACCTGCG CCGGCTACTG CATGSGGAC GACTGTGCTT TTGATCGGCC 540
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 TCAACACCTA TATGAGACAG CTTGGCCAC TGTCACTCTC AGAGACCCAG GATGGGCGCC 840
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CCCCGACCC CTCACUAGC TGGGCTGTG GAGGTCCCG GTCCATGCTG CTTTGCTCTG 1260
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CAGCAACCCG GTTGTAGACA GTCCCGTCCC CCAGACGCC ACTGACATGA GAGGTTTCC 1260
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TGACGACCTG GGCTTAGGG CAGGCGCACT TCTCGAGCTC AGGTCTTGGT AGGTGCTGCG 1980
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CAGACGCTT CATCTGCT CAGGCTGAG TCTCTCTGCA GACCTTTTCT CAGCACTGCT 2160
ATCTCTCAA GGCATGTAA ATGTGTGAC AGTGTGTATA AACCTTCTCT TCTTTTCTT 2220
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Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_005931.1

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1 11 21 31 41 51
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LVQBGVRCIT ABLAKVNDP TPLFTTVEIE GRADIMIDEA RYHNGDLFP DGRSLANA 180
FPFKTBKGG VAGDHTVY TPLDQTDLL QYAHMRGIV LGITPTAAK ALMSATFTFR 240
VPLSLRPPC RQVLLVQGF NPTVTSRTPA LGPQAGIDTN ETAPLEPAP PDACEAFDA 300
VSTIRGELFF FKAGFVRLR GQLQPOPYTA LASRMHGLP SPVCAAFDA QHIMFQGA 360
QYVYVDEKLP VLGPALTEL GLVRFPPVHA LVNGPEKNI YFRGEDVHR PHFSTRVDS 420
PVRATIDNR QVPSIDAAP QDADYATFL RGRLYHRFDF VYKALEGFF RLVGDFPFC 480
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Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_005794.1
Coding sequence: 434-1276

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1 11 21 31 41 51
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CTTCACTCTT GGGGCCAGCA AGACACGAA TGACCCGAA GGAATGACA ACTCTGACA 180
CACCACCTTT AAGACAGTA ATACTCACG CAAAGGTCG CACTTCATC CTGAATCTA 240
GTGAGGCCA GACAACATA ATTCAGTACA CATTTTGGT ACTTGAGAA GACTCTCAC 300
TATCCAGAG TGCTGAGACT ATTGCCAAG AGTGAGACTA TTGCCAGTG GTGAGCAAT 360
CACCAGCGG TGAAGATCT ACCTATCGCC AAGTGGCTG ATTGACAG AGCATCTCA 420
GACACACACC ACTATGCTT CAGCAATTG CCGGGCTAC CAGGCTGCT TGCATCTG 480
TGCTAGCTTT TCTGTGGA TGACGAGAG CCGATGAGC AGGAGGGCT TCTGTCTAA 540
CGGCTACCC GTGTGACG GATCCACAG TGCGATCGG TTGGCATCG CCGAGCTCT 600
GCGCCCGGAG GGGGCCAGC TGATCATGAG CAGCGCGAG CAGCAGAGC TGACCGGCG 660
CATGCGCAG CTGACGAGG AGGGGCTGAG TGTGCGGAG ATTGTGTC AGCTGGGAA 720
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CAGGAGAACT CATCACTG CAGAGGATGT GAGATCGAG GACTGTGAG GAATCTGTC 1200
CTTCTGTGCT TCTCAGATG CAGCTATGCT CAGCGAGAG AAATCTGCG TGCGAGCTA 1260
CTCACTGCG CTCTGAGG AGTGGAGGCT GTCTGTGAC TGTGTGCCA GCGCGAGAG 1320
CTGAGGCGT GTCTAGTGA TCAATTGGAT CTGAGAGAGA GTCTGCAAT TGCGAGAT 1380
AGCAATTTG GGGCTTACT ATGCTAGGCT TGAGAGAGAA GAAACACCT TGCGATCT 1440
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Seq ID NO: 20 Protein sequence:
Protein Accession #: NP_005785.1

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75

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1 11 21 31 41 51
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ARVV IISRRQ QNVDRMAKIL QGQGLSVAGI VCHVGKABDR BQWAKALRH GSHVPLVCS 120
ADNVPLVST LQTSRQIWR LLSVHRSPA LLGQLPLVR EBRGACNLIV SSIAHRPVRV 180
ALGVNVRT ALLGLPFLA LRLAPKIDRV MCVVPIIIT DFKSVKENE SLGNFKRHH 240
QJQRIGESD CAGIVFLFCS DELSYVRGHR IAVAGYSTR

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Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: B08 sequence
Coding sequence: 77-904

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	GGAGCTGGAC	TGCTGTGAG	AGACTACAC	CATGTGCGCT	CGTATCGCG	AGTCTACAGA	180
10	CAGATACGAC	AATGTCTAT	TTTCTATTT	ACGCGGCATC	TGCAATGTCT	TGTTTGTCA	240
	GTATCGAAC	GTGCTTCAAC	GTGCGACTTA	CTTAATCTTC	ACTCTTTTGG	TGTATGATGG	300
	AATTTGATCC	GTCTACTTCC	ATGCGACCTT	TACTTTCTTG	GTGATGATGG	TGTATGATGG	360
	TGCGATCCTT	TGGGTTCGTA	TGTCCTTCT	ATGCAATGCG	TTCCCGACGA	GTATATACCC	420
	AAAGATCTTT	GGGAATGACC	GGGTAGGTT	CAAGTGTGTG	GTGATGTGCT	TGCTGTGCT	480
15	TACGACGTGC	TGGGCTTGT	TGACGCTGC	CATCAACAAC	ATCTCTCTGA	TGACGCTGGG	540
	AGTTTCTTGC	ACTGCACTGC	TGTCGTCGCA	GTATTAACAG	TGTGACACGA	TGGGTGTGTT	600
	TAACTGGGCG	CTCTCTCTGC	GGCTCTGGG	CGCTTTTCT	GAATCATGAG	GAATCATGAG	660
	CGAGCTTCT	TGCGAGCTTC	TGTCATCTTT	GAATCTCCCG	TACCTGCACT	GCATTTGGCA	720
	CATCTCTATC	TGCTTGTCT	CTTACTGGG	CTGTGTATCG	TTTGCTACT	TGTATGCTGC	780
20	CTCAGAGATT	CTCAGAGAG	GGCTCTCTGC	CAAGTCTTGG	CCCAATGAGA	AATGAGCTTT	840
	CATTGTGCTC	CTGCTATG	GGCTCTCTGC	CTTATGCGC	CTCATGAGT	GGCTCTCTCT	900
	GTGATGCGAA	GATGTGTGAT	GGCTCTCTGC	CTTATGCGC	CTCATGAGT	GGCTCTCTCT	960
	TGCTAGGAG	CAGCGCAAG	GAGTCTGAAT	AGTTTGGGTG	TGGGTATCT	TTTCAAAAT	1020
	CTATTCTCTG	GGGCTCTTAA	TTTCTTGAAT	GTCTCTTGTG	TGTAGGATT	TAACTTTCT	1080
25	CATATGTCAC	AAATATCTCC	TGCCCCCTG	CAATTTCCCA	TTTCTTTCT	AGTATTTAA	1140
	TATTTTCTG	CGATCTCTG	TTAAATCTT	CATCTGTCCA	CATCTGTAAA	TTTCTTTCT	1200
	AGGATTTCTG	GATTTTGTG	AAATTTTAAA	AAAGTCCCT	CTCTCTCTCT	AATGTTCTG	1260
	TGGACCACT	GGATTCACAT	CAGCAAGGG	AAAATGTCT	ATTCTTTTCC	CAGAGATGGA	1320
30	AAATGAGGG	CTTAGGAGCA	CTAGAGAGG	CTTTCTCAG	ATCACTTCCA	GATGAGTGA	1380
	CTTCTTGGG	TGCTCTCTCA	ATGCTCTCTG	CAGACAGCT	CTTGTAGGGA	TGAGAGCTG	1440
	TACATATCAT	CTCTCTCTG	AGAAAGCTGG	CTCTGTCAG	ACCCCAACAT	TCGCAAGGCG	1500
	CTCTGAGTG	GACTCTACTG	ATGACAGACA	GACCCCTCGA	GAGACAGAGC	CTCTGACTAC	1560
	TGTATGAGAA	GATGCGCAG	ATTCTCTTT	GGGTAATG	TGTATGAGAA	AAACCAAGCA	1620
35	GATGAACAC	AGTCTCTG	TGTGTGTGAA	AGGCTATCT	TTTCTCTCTG	ATTCTCTGAC	1680
	TACACAGGT	TTTACATGCA	CTGTGAATC	CTTTTACTAC	TACTCTCTGT	GAGATATGCA	1740
	GAGACTTCAG	ATRAACGTGA	AGCTAATGAG	TAAACACCTC	TTTGCCAAAA	CTCAGATCTC	1800
	ACTTTAGGCG	CTTCTGTGAG	ATGAGCAGAA	TTTTTAATA	CTGAGCAGAA	TTTTTAATA	1860
	CTGACATCAC	TTCTCTCTG	CTCTCTCTG	CTCTCTCTG	AGCTCAAAAT	CTCAGAGGAA	1920
	GAGAGATAT	GGCATGAACA	TTCCACAGCA	CCACCATCT	TTAAGACTTG	ACCTCTGTAA	1980
40	GTTTACGAAA	GGGCTCTCA	CAATGTGTGT	GGGGTCTTG	GTTCGAAAT	TGAGAGCAAC	2040
	ATGAAGTTT	TGGAACGTT	TTCTCATTTG	AAAGCTCCAG	TAGCTGTGAC	TATTTCTGAA	2100
	ATTACCTTCA	AGAGCTCTAC	CTCTCTCTG	TTCTCTCTG	CTCTCTCTG	CTCTCTCTCT	2160
	CACGCTCTCA	GTGAGAGTG	CTTCTCTCT	TTCCACAGAT	ATCCAGCAGC	TCACTCTCT	2220
45	CAAGTCTCTG	CAGTGTCTAT	GACTCAAGG	GGCTCTTGG	GTCTCTCTG	CAGCAGGCTA	2280
	AATCTGTCTG	CTTCTGAT	TTTCTCTCT	AATGTGAGAC	TGCTCAAGAT	GAATCTCTCT	2340
	TTCTCTCTCT	TGATGTGAAG	ATTCAAGAC	CATCTCTGAG	GTGACGTGTG	GGATATGAA	2400
	ACCTCAAGGA	TATCTATTT	AGCTCAAGG	TGCTCTCTCT	TGTATCATCT	CATTTTGGG	2460
	AGAGGTCAG	ACAGGTGTGT	TTCTCTCTG	GCAGAGTCA	TGCTCTCTCT	CTCATATGT	2520
	AGAGTTTGG	AAAGTGAAGA	TTTTTCAAC	ATCCAGAAC	CTCTCTCTCT	CTCATATGT	2580
50	GTACAGACTC	CAAGGTGAAG	ACCCCATGTA	GCATCTGAA	TTGAGATTTA	AAAGAGATG	2640
	ACTTATCTCT	ACACTCTCTG	TTTCTCAAT	AAATGAGTTG	TGAGAGAGCA	GAACTCTGTT	2700
	CTTATGAGAA	AACTCTCTG	GAACCCAGT	GTGTGAAGTA	AATGTATGT	TATTTAAAT	2760
	ATTTAAGCTT	AAATTTATGG	CTTACTACTA	ATAATATATG	AGTGTGAGTA	AATGCAAT	2820
	AAACAAATGG	TAAATTTCCA	GTGAGAAAGA	TTAGTGTGTT	AAATGATGTA	TATTTGTT	2880
55	TATATGATTT	TTATATATAT	ATGAGAGAG	TTTCTCTCT	TGATCTCAGG	CTCTCTCTCT	2940
	ATTACATGCG	CTGAGATGCA	GTGTGTGAGT	CATGACTCAC	TGTAGCTCT	GTCTCCAGAG	3000
	CTCAAGTAT	CTCTCACT	CAGCTCTCCG	AGAGCTTGG	ATGATCTGTG	GGTCTCTCA	3060
	CTCCAGCTCA	ATTTTGTAT	TTTTTCAAG	AGATGTGGTT	TCCACTATTT	GGCAGCTG	3120
	GTCTCAACT	CTGAGCTCA	AGAGCTCTG	GGCTCTCTG	CTCCAGAT	GGTGTGAA	3180
60	GGCATGTGCG	CTCTCTCTG	GGCTCAAAA	TATTTTAAA	ATGATCTGTG	AATTAAGAT	3240
	TGTATGATTT	TCTATATGAT	CTTCTGTAGA	CTGAGAGGT	TGATGAGACA	GACTCTCTGT	3300
	TAACTCTCTT	GGGTTCAGAG	TCTAGATTT	TTTAAAGCA	AATATGAGTA	CATTTCTATT	3360
	TTAGATGTAC	CTTATCAGG	ATGGATCTCT	CTCTCTCTG	TCTATGAGTA	TAAATCTCT	3420
	AGAGTGGGG	GTTTGTGATA	TATTTTAAAG	GGGCTCTTTT	TTTTTTTCTT	TTTTTTTCTT	3480
65	TTTAAATGT	GAGAGAGAGA	ATGTCTCTCT	AGAACTGTGT	TTTAAAGAGA	TGAGCTGAGA	3540
	AGGAATATGT	GAATGAGGTA	TATTTGAGCA	CGAGACAGCA	TAACTTCTAT	TTTGAAGAGA	3600
	AATCTCACTA	GTCTCTCTG	ATGAGAGATA	ACCCAGAGAA	GAGAGATAT	ACCATCTTAA	3660
	TTTAAATGT	GTCTCTCTG	ATGAGAGATA	TATTTAAAG	CATCTCAAGT	TCTTAAAGCA	3720
	AAATTTGGAA	ACTCAAGAGA	AGTCAAGAGA	AAAAAAAGT	ACCCATATTT	TCTATTTGCC	3780
70	AGGTATATGT	CTTGTATATA	TTTGTGTTG	GTCTCTCTCT	TTTTTCTCTT	AATTAAGTGT	3840
	TAAATTAAGT	CTTGTATATA	TTTGTGTTG	GTCTCTCTCT	TTTTTCTCTT	AATTAAGTGT	3900
	CAATTTGATG	ACTTCTCTCA	GAATTTGATG	TATCTCTCTA	CTTATGAGTA	CTTATGAGTA	3960
	TGATTTGATG	TACTGTGAT	CATGAGTGA	CTACTGATCT	TACTTTTATA	ATCAGAGCTA	4020
	ACATGAGTGG	GTCTCAAAA	GTATGAGTGA	TAACTGTACT	TTTTGAGTGG	CTCTCAAGTA	4080
75	TGCTTGTGTT	AGTCAATATA	ATCAGTGTG	AAATATGTA	CTTATGAGTA	TTTTGAGTGG	4140
	TCAAGATTGA	AAAAATGAT	AGTTTATTT	ATAATGAT	GGGCTCTCA	GAATCTCTCT	4200

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Seq ID NO: 22 Protein sequence
Protein Accession #: B05 sequence

	1	11	21	31	41	51	
5	NGAHHWDLQ	QAGSSEVDHC	EDHYTIVPAI	AEFYNTISW	LFHILPPICM	CLERQYATPC	60
	NSGIVLWTL	LVVGVGEVY	PHATLSFLOQ	MLDEIAVLW	LKALAMWFP	RYLPLKIFH	120
	DRGRFYVYS	VLSAVTTCLA	FKERIAHIS	LATLVQVCTA	LIILAEKRD	HWYFLKLF	180
	SLWATWALF	CHLSBBAKCS	LLSERPFLF	ICKHMLICL	ANYLQVCYA	YFDAASPIHE	240
10	QGVPIKPHN	EKAHFIQVVP	VSLLCANKKS	SVKIT			

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
15	TGAAGTACT	CTGTTTAATG	TCAATATATC	GAGATGTTCT	GTGGAGCCAG	AATTCAAAAC	60
	CCGATATAGC	AGGAGGACAC	ATTCTTGATC	GOTATTTTAT	TCTATATTTT	TTATTAGTTC	120
	CAATCCTTAT	GACTCTGTTT	AAATAGAGTA	TCTGCATTAT	TGTGCAACCA	CTTCTGAGAT	180
20	CTCATCACAT	ACCTGATCCG	ATTTAACTTC	AGTCATATCC	TCTATTAATT	TTTGTGAAAT	240
	TGCTATCTTA	AGTTGAGAST	TCTCTGTGAG	TATTCCTAT	TTTCTCTCT	TTTAAATGAT	300
	ACCTGTGCTA	AGTAAATAG	CTAACATATT	GGCATCAAC	CATTGCTAT	TGAAGCAGCG	360
	TTTGAATGAA	ATTGTTTGT	CATTGACAC	TGTAAGAATC	TCAATTTGTA	AGATANTACT	420
	GAATAAGATC	CTGACTCTTA	TGTATGCTTG	GCTGTCTCTG	AACTCCAGCT	CTATCAGACT	480
25	ACTCAATACA	TTCGCTCTTT	CCAACTATTA	TCTCCTATT	CAGAGAAAG	TTTTTGGA	540
	GGCTCTCA	GGTCCAGCA	ATTCAACAT	TCTCTAAA	ATAGAGATT	CTTTTAGATA	600
	TGAGCAATGA	AAATTCAAGC	AAACAATATA	CTTCTCTCAT	GTCTCTTGCT	TTTTTAAGAT	660
	CTGAACTCA	AGATTCAAT	GGATTTTTCAT	TGAATTCAC	CAGATCCGC	TCTGCTGACT	720
	TGGTCTGAAA	TGCACATTC	TGCATTATAT	TGACCCCTAT	GAATCACTG	GCTGAGCAAC	780
30	CAKAGATCA	ATCAAGATCC	AAATGTTAAA	CTCTGCTG	CTTGAGATT	TCCGTCTTCA	840
	CATCAAGCA	TTTCACTGCC	GTGACCAAT	TTTTAATGA	TGTGCTCATG	GTTTGCAAGA	900
	TTTCAATTA	AAGACTTTCC	TGGCTGACT	TCTCAATGA	GTTTCTCTGC	TGCTCTC	

Seq ID NO: 24 DNA sequence
Nucleic Acid Accession #: B05 sequence

	1	11	21	31	41	51	
40	GTGTGTAGTC	GGGTATGAGA	ACGATTGCAA	GCAAAAGCAG	CTGAGGAGCG	CTGTCCAGAG	60
	AGTAGGCTCA	GTAGCAGAAA	CTGCAAAATC	TGAGAGAGG	AAAGTTTCAG	CCTGTGCTCG	120
	GAAGTGTGTT	TAGCATGCTG	GAGCTGGTGT	TCTGCTTGGT	AGCCTTACAA	CTTTGGCCCA	180
	ACTACTTGGC	CTCTGGAGCT	CAGATCTCTC	CTCTTTAAAA	TGGTGTAT	AAATGCAACC	240
	ACCTCTGTGT	AGAGAGATTC	TGTAGAGACA	AAATGAGATC	ATCCAACTAA	GCGTGGAACC	300
	CTGTCTCTGG	TAGCTCTCTG	GAAGAAGTCC	TATGATTAT	ACTCAACCTA	CACCTCAAGT	360
45	AAAGGAACAT	CTACACACAG	AGGAAATGAA	TAAACATGAG	TGAATTTCTC	ATCTCCATTC	420
	CCACAGCTCC	CCATCTTACT	TGCGAAGAG	TGCTCTACAC	TGAATATGAG	TTTATTTTCC	480
	CTGTGTGCAA	AGACAGTCT	TTTCTGAAA	ACTGAGCTGC	GAATATATCT	GAATATATGAG	540
	GGTCTCCGGA	AAAGGAGCCT	GAAGCCCCCT	TTGTAAATTC	TGCATTAGCG	TGCTCTCTCG	600
	GCAGACAGGA	AACTCATCTA	GAGAACTCAG	CCAGAGAAAG	TCTTTAAATG	GAATTTGTGC	660
50	AAAGCAGAGG	CAAAATGCAAT	AAAAATTCG	TGACGGCCTT	GAATATCTTT	GAATGAGAA	720
	CCGAAATGTC	CAGAGCAGGA	GGATTTTAA	ATTTTGAATC	TGATGTGCTC	TGTGTTTCTC	780
	CAGACAGGTT	ATTCATGAGG	CTAAATATA	TGCAGAAATG	GTATCTTCAG	ACCAACAGTA	840
	CAGAGGGGAT	GCTGTGAT	TTCAATGAAA	ATCCATTGTA	ATCTTGAGGT	TGAAATCTTA	900
	AAAGACAAA	GGACATGAGA	GAGTATATAT	TGTTCTTGA	AAATTTCTGT	CTTATATCTA	960
55	AAAGAACTC	CTATTTTTPA	GAGAAATGTT	GAATCTTCC	AGATGTGAGT	AGCTCCCAAC	1020
	AAATCTTCT	CCTGAAATAG	GAGATAAATG	TTGGAAGAG	GCATATGAT	GAGATGTGCT	1080
	ATAGAGGTGG	AGTTTCAAGA	CAGGCAAGCA	TACATATAG	TCAGATGTT	TTTCAGTAT	1140
	ATCTTTTACA	ATGATTTGCT	TACAGTGCTC	AATGACAAAC	CATTTCAT	GAAGGTGCTC	1200
	TTCAATAGGC	AATGTGTTGA	TGCATATAT	TGACATGCT	ACTTGGACCA	CCATATGATC	1260
60	TAAAGAGAG	AAATATTAAG	AATCACTCAG	CAGAACCTCC	AACTTAGATA	GCACTTTCCA	1320
	CAAAAGTAA	TGAGGGGATA	GACTGAATGT	AAATGAGTAT	AGGTATATGA	TGAGATCTCA	1380
	GAGGTGTTTG	CACAATTAAT	CAGATATCTA	TTTTAAACAG	AGTCAATAGG	ATTGGAACATA	1440
	ATGAAATATA	TAGAAATAAA	TACCGATACA	GAGTGTGCTC	CTCTGTTAT	CTGAGTTTGT	1500
	AATCTGCTCT	CCACAGACT	TGTCAGATAT	ATGACATTTA	AC		

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: B05 sequence

	1	11	21	31	41	51	
70	GTGTGTAGTC	GGGTATGAGA	ACGATTGCAA	GCAAAAGCAG	CTGAGGAGCG	CTGTCCAGAG	60
	AGTAGGCTCA	GTAGCAGAAA	CTGCAAAATC	TGAGAGAGG	AAAGTTTCAG	CCTGTGCTCG	120
	GAAGTGTGTT	TAGCATGCTG	GAGCTGGTGT	TCTGCTTGGT	AGCCTTACAA	CTTTGGCCCA	180
	ACTACTTGGC	CTCTGGAGCT	CAGATCTCTC	CTCTTTAAAA	TGGTGTAT	AATAGCAACC	240
75	ACCTCTGTGT	AGAGAGATTC	TGTAGAGACA	AAATGAGATC	ATCCAACTAA	GCGTGGAACC	300
	CTGTCTCTGG	TAGCTCTCTG	GAAGAAGTCC	TATGATTAT	ACTCAACCTA	CACCTCAAGT	360
	CCTGTCTCCG	TAGAGAGTCT	AATGACAAAC	CATTTCAT	GAAGGTGCTC	CTTATATCTA	420
	CCTCATCTCA	CTTCTGAGAA	GTTGCTTAC	ACTGAAATTC	TTGTTTCTT	AGCTCTCTCG	480
	AAAGACAGT	CTTTTCTCCA	AAATGAGAAC	TGGAATATAT	CTGAAATATC	AGCTCTCTCG	

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GAAGAGGAC GTGAGGCC CTTGTAAAT TCTGCATTAG CGTGTCTCC TGGCAGGCG 540
GAGACCTCAT CAGAGAGTCC AGCCAGAAGAA AGTCTTAAAT TGGAAATGTT GCAACAGGAG 600
AGCAATGTCA TTAAGAGTCT GCTACGCGCC ATGAATGCTC TGTATGTGAA GCGCGAAGAC 650
TCCAGCAGAG AAGAGTTTAA AGATTGTGAA TCTGATGAC TCTGTGTTT CTGAGACG 720
TTATTCCTAT GCGTAAATAA AATGTGAGAA TGGTACTTTC AGACACACAGC TGGCAGAGGG 780
ATTGTGTGGA ATTTCATGAA AATCACTATT GAACTTGGAG GTTCAGATCT TAAAGAAAGA 840
AAGACATGGA CAGAGAGTAAT ATTGTGCTTT GAAATTTTCA TGTCTATATC TAAAGAAAGC 900
TCTATTATTT TCGTAATCTT TCGAATCTTT AGAGCTGAGT AGAGCTGCC AGAATCTTT 960
CTCTGAATAT AGGAGATAAA TGTGTGAAG AGGCAGATGA TTGATGATGC TGATGAGAGT 1020
GGAGTTCAGA CAGACGCAAG CATACATAAG AGTCAGATATG TTTTTCATTA TTATCTTAC 1080
AATAGAGTTT CTTCAGTGG TCAATGAGAA ACCAATTTTCA TGTCAAGCTT GCTCTAATAG 1140
CGAATGTTTT GATSCCATTA TGTATGATCT TTACTTGTGAG CATATGAGAG 1200
AGAAATAATA AGAATATATA ACCTGAGAAC GAACTTGAAG TAACACTTTC CAGCAAAAGT 1260
AATGAGAGGA TAGACTGAGG TTAATAGGGA TCAAGTATGT GATGAGATCT CAGAGAGTGT 1320
TGCACAATAA TGCAGACTACT CATTTTAAAC AGAGCTATAG GAGTGGGAC TATATAAAGT 1380
AATAGATATA AATACCATCT AAGATATGTT CTTCTTGCTGT ACTGGGTTT TGAATTTGAG 1440
CTCCACAGAA CTTTGTGAGT ATATGAGTAT AAAC

20 Seq ID NO: 26 DNA sequence
Nucleic Acid Accession #: NM_013282.2
coding sequence: 85..2466

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1 11 21 31 41 51
CGACTCTTAA GAGCATGCGA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTGTCT 60
GTCCCTCCCC TCAGCCCGGA CACCAAGTGG ATCCAGAGCT GGACACTGGA CCGAGGCCAG 120
ACCCACACGG TGGACTGGCT GTCAGAGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAATATC 180
CAGAGAGCTGT CAGCATCTGGA GCGAGCGCTG CAGAGAGCTGT TCTACAGGAG CAAACAGATC 240
GAGGACGCCC ATACCTCTTT GTCATGACAG GTCCGCTGTA ATGACAGACT CAGACAGCTC 300
GTCCGCGTGA CCGTCTGCTT CCCCACAGCC ACCAGAGAGC GGAATCTCGA GCTCTCCGAC 360
ACCGACTCCG CGTCTCTGCT GGCACAGAT GAGTCAGACA AGTCTCTCAC CCAAGCGGAG 420
CGCGCCCGCC AGACTGAGAG CAGGCGAGAG TGTGAGAGCA TGTGGAGTGA GAGCGAATG 480
GGGCTGTACA AGGTCAATGA GTACCTCGAT GCTGCGTGA TGTGGAGTGA GAGCGAATG 540
GAGGCGCAGG CAGTCTGTGA TCGCGGAGAG GTCCCTCCCC GAGACAGACC CTGAGCTCC 600
ACCTCCAGGC CCGCGCTGGA GAGGAGCTC ATTTACACAG TGAATATAGA GACTACCGC 660
GAGAGAGGCG TGGTCCAGAT GAACTCCAGG GAGCTCCGAG CCGCGAGCCG CAGCAATATC 720
AAGGAGAGCG AGCTGAGAGT GGGCACAGGT GTCATCTGCT ACTACAGGCT GAGCGAATG 780
CGAGAAATCT ACCGACAGCT GGTGCTGGGG GATGATCTC TGAACAGACT TGGATCATC 840
TTGCTGAGCG AAGTCTTCAA GATTGAGCGG CCGGATGAAG GAGGCCCATC GGTTCAGACTC 900
CCCATGAGAC GAGAGAGGCG GCGTCTCTGC AAGGCTGTGA AGGACAGGCT GACAGACTCT 960
TCCGAGTCT GCGCTGCGA CTTGTGCGGG GCGCGGAGAG ACCGCGRCA GAGCTCATG 1020
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TCACAGCGGG ACTCGAGGAG GGGGAGAGCC TGTGTGGGCC GCGCGAGGA AGTTGATCT 1320
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CAGTCCAGG TCAGCGAGCT GGTGTTCGAT CCGGCCAGCG TGGCTGGCAT ACAAGCGCG 1440
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AACCGTACG ATGAGACTTA GAGGTGTGAT GGTGAGATCT TTTCGAGGA CAGAGAGCT 1740
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GAAAGCTCTG CCAACAGAGA GAGAGAGAGG GAGAGACAGA AAGAGGAGGA GAGGAGAGG 1920
CAGAGAGGGG GCTTGGGCTC CCCCAGGAGC CCGCAGAGCA AATGAGAGG GAGTCTGAG 1980
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CAGACAGAA TGGCTCCAGG GAGAGCTCTG TCCAGTGGG GCGAGAGCTG TGACTGAGGC 3120
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 CTACAGAG GTTTTATTT TAATTTTT TCTCTTAAT GACACATTT TCTAAAGA 3480
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 TTAGATCTC AGATAAATG TTTTTCAG ATTTGAAAA AAAAAAA 3828

Seq ID NO: 27 Protein Sequence
 Protein Accession #: NP_037414.2

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 NMIQVRTMDG RQTHVDSLS RLTKVEELR KIQELHVEP GLQRLFYRG QMEDGHTLFD 60
 YEVVLNDITG LVRQSLVLP HSTKRESEL SDTDSGCCG QSESDKSSTH GEAAATDSR 120
 PADENHNDIT ELGLYKVEH VDARDTNGA WFEACVVRV RKAPSRDEPC SSTSPALBS 180
 DIVIRHYKID YPESVYQHS SDYFAKART ILRWQLEVO QYVPLVWPD WFKSRQWID 240
 AILBRKSTR TABELVANY LQDSIAKRC IIPVEVFKE ERPGSGSPHV DNPBRKSGP 300
 SKCKKDDVN RLRCVCAEL CQGRQEPFK LWCDECMHF HIYCLDPLS SVPSDEMYC 360
 PECRNDASEV VLAGERLRES KKKAKASAT SSSQEDWAGQ HACVGRTEC TIYVSNHTG 420
 IGTPIGTVMH RFRVQSESS VHRPVGATH HSESGAGSL VLAQVDEDV DHRPFTTNG 480
 SGRLDSGK RTADGSCQK LNTVRALL NCAPINDOR GAEKEDHRS KPVRVVRNK 540
 GKNSKYAPA EGRHYDIYK VKVYKPKKK SFPLVRYLL BRDDDEPQM TGEKDRKK 600
 LGLTHQYEP VLEALANREK EKNRSKRESE EQOEGVQSP RTGHWGRKK SAGQGSBRG 660
 SPRTSKKTK VEPYSLTAQ SSILREDSN AKLANVEAS LKRPASGSP FGLFSLRYS 720
 TPQICCGSE VFRPTITVQK HWKQCDLER SPRAGVNSCP ACRTDLGRSY ANQVNPQLT 780
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Seq ID NO: 28 DNA sequence
 Nucleic Acid Accession #: NM_000756.1
 Coding sequence:186..776

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 AGAAACTCAG AGACCAAGTC CATTGAGAA CTGAGCGAA AGAGAGGGA GAAGGAAAA 60
 GAGAGTGGG ACAGTAAAG GAAGAGAGA CAACCTCAG AGAAGCCCC CAGAGACCTC 120
 TCTCTGCGA GAGCGCGAG CACCGGCTC ACTGCGAGG CCGTCGGGA CGAGATGCC 180
 CTAGATGCG GTCGCGCTG CTTGTGCTC CGAGATCTC GCTGCGTCT CTCCGCCCTC 240
 GCCGCCCATG CAGGCGCTC CTGAGCGCG GCGCGTCCC GAGAGCTCG CAGCGCCGC 300
 AGACCTCA GCGCTTGAT TCTTCCAGC CCGCCCGCA CTCGAGCAG CCCGCGCAGC 360
 CGAGAGCTG GCGCTCTGT CTCGCATGG CTGAGAGTA CTCTCTCGC CTGCGGAGC 420
 TCGACMGAG CGCGCGCTC CCGCTTGCG CCGCTCTCT GCTCTCTCG CAGGCGAGC 480
 GCGCGCCCC TTGCGCGAA CAGGCGAGC CCACTTTT CCGCTTGTT CTGCGCAGC 540
 TGTGCTGCC TCGCGCTCG CTGAGCAGC CGCGCTCT CCGAGAGCC GGCCTAGGA 600
 ATGCGCTCG CGCGCACAG GAGGACCGG AGAGAGGAG GCGGTCTCG GAGCTCTGA 660
 TCTCCCTCG AGCATCTTC CAGCTCTCT GCGAGTCTT GGAATATGCC AGGCGCGAGC 720
 AATTAGCA CCAAGCTCAC AGCAACAGA AACTCATGA GATATTGG AAATAAAGC 780
 GTGCGTTGG CCAAAAGAA TCTGCATTA GCACAAAAA AATTAAAAA AATACATAT 840
 TCTGTACAT AGGCTGCTC TTATGCACT TGTATTATT TMTATAGCTT GAACACAGA 900
 GCGAGAGAG GAGAGAGCTT ATGCGCTTA CTGAGATC ACATAAGTA TCAAGTCCA 960
 GCGACACAC AATTTATTC GTTTCTCTA CTTTAGTTC CCGTTCCAG GTGTATTATG 1020
 TGTGCTTTA AAGAGATGT AGACCTGTGA GAAAAGTCT TGTGTAATA AGCAGACAGA 1080
 AGTCATCAA TTGTTTTGT TGTGCTCTA GCGCAAGGA ATGCATTTT CTGTGGTGG 1140
 TAAGACTAAA TCTGTAGCT CTTGAAACR ACTTCTCTT GTAAAGTCT CAGTAATAA 1200
 ACATCTTCC ATCTCTGTT CATTGTGTT GTGTAAGGA ATGTGATA CTATTATTTT 1260
 TAATAAAGT TCGAAAGT

Seq ID NO: 29 Protein Sequence
 Protein Accession #: NP_000747.1

65
 70
 1 11 21 31 41 51
 | | | | |
 NPLPLVSG VLVVALLPC PCRALLSRP VHGARGQPH POPLDPPPP PQSRPQPPQ 60
 APPLVLEMG EYFLRLGMLN KSPAALPSA SSLCAGSGS RPSPEQATN PFKVLALQL 120
 LPRRLSDSA ALARSGARHA LGHREAPER DRSSEPPIS LDUTPHLLS VLRMARASGL 180
 AQAASNRKL NEIGK

Seq ID NO: 30 DNA sequence
 Nucleic Acid Accession #: CAT cluster

75
 1 11 21 31 41 51
 | | | | |
 ATTTCTTGAG ATGCTCTCT TTGAACTAT GCMCTCTCC TGATACTGG ATGCTTTCG 60
 TCTGACTGAT GAAGATCCTG AATACCAAG AGGGCCCTC AAGGCTCTT AGAGGTACG 120

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CTCTAGGAA CCTTAAGCCA GAGGAGGCT TCCTACATC ATCTCTCTG ACATCTCTCC 180
 GTTGAAGAG CAGTCAGACT TCTCTTTGC TCCTCAGATC TAATTTGGG GTTTAAGAGC 240
 TGAGGTTACT GGGGGAAGTC TTTTACACA TCTCTCTTAA AGATCCGGG GTTCAGATTT 300
 CATTTGTTT GGGTCTAGT AGAGATGAT TATGACGAA AAGCAACTC TCACTCTTCC 360
 5 AGAATAGGT TCAATTTTA CTTGCAACT ACCAATCTG TGGCTGGT TCAGCATTA 420
 AACTCTTAA ATTTCACTTT TTCTCTTSTA AATGAGTAT ATGACAGTA CACTACTCAA 480
 AATGCTTTG TGAAGATTAA AARGTTAAC ATAAAGATT CAGAGAGTG TCTGCGATAT 540
 TGTGCTGAT AAGTGTATT TTATTTATG CTGATTAAC CAGTAATTA ATTATAT

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 134..1917

1 11 21 31 41 51
 15 CAGCTGAGC CCAACCCCA CCGCAGCGC ATCCCTGCG CAGCTGAGT GGTCAAGGCC 60
 TCAGAGAGT GTGCTCTTC CCGAGCGCTA CAGAGAGGG CAGTCTCAG CAGCTGCGG 120
 AATCCTTATT GGCATGTCTC TTAGAAGCCA CCGCTTCCC AGGCAAGACA GGCCCAAGG 180
 20 GAGTGTCCG AGGGCGGTC CCGGAGGCC CTTGGGTCCC AGCACTTCA CACACTCTGA 240
 GGCAGAGAC GGCCTCTCTT CTTCAGTGG AGACTCTAA AGACAGATA CAGGGGCTT 300
 GATTGAGCT GAGTCTGAC CAGAGCCAG AAGTCTCGG ACCAGGAGT CCGCCAGCCC 360
 AGACCTTCC CAGAGCTTA GAGGAGAGG AACCGGAG AAGATCTAG ACCCTCTGCC 420
 CCAAGCCGG ATGCCCAAG GCGCCGACA CCGCCCGCG CAGAGCCGC CTGGCCCGC 480
 25 GGCCTCTCT TCTGGAGGC GCTCACAGCC GATACCCAG GATGCGAAC CAGAGAGTG 540
 CCAATCTCT CAGCTGCTG AGCAGAGCT CCGTCCGCG GCTCTGGGG ACCTTCAGG 600
 GAGAGCCCG GGGAGGGGG GAGCCTCTG CCGCCGAGC GGGGAGCTA GAGAAAGCA 660
 GAGAGAGGC CAGAGCTCA TGTGTTTTCT CAGAGGCCC GGGGTCTGG GGTGTGTGA 720
 GGGGCCCGG AAGCCAGCT CCGGAGCCT GAGCCCGGC AGGGGGGCG CCGTCCAGG 780
 30 GGGCTGAGC CAGCTCAATT GCTCTGACT GCTGAGCTC GAGCAAGAC AGCGAGAGC 840
 CAGCTGAGT CAGCTCTGAT AGCCTGTAT GAGCAGACA CTCTCTGAG TCTGGAGGA 900
 CCGCTGCTC TACCGCGGC TGAGCGGCG CGACCGGAG CGCATCTCA CCGTGGGAGC 960
 GCGCCGGAG CGGGCGTGC TGGGCTCTCT CTATCTGCC AGCTTACG AGGGGGGCG 1020
 CTGAGGCTC CAGAGGCGC CTGTGGGGA GAGACTCTC GAGCTGCGC CTGTCTCTG 1080
 35 GCTCTCTCT GAGCTCTCT AGCTTTTCA GAGCTCGGAG AACACTCGC GGCCTCTGAC 1140
 CAGCTGCCC GAGAGCGCC CCGTTCTGG CTGCGTCTC TGCACTATG ACAACTACT 1200
 GTTCTGAGC GGGAGCGCT CTGGCTCTG TCGCAAGGC GCTCTCTCA AGAGTCTT 1260
 CTCTAGAC CTTCTAGCA AATCTGAG CAGAGTGG CCGATCGAC AGGCGCGAG 1320
 40 CAGCTGAG CTGTGCGCC TGACAGGCT CTTCTATGC ATGGCGGAG AATCTCTGA 1380
 CAGCTGAG TCTTAGACC CCGACAGA CGCTTGAGC CCGAGCGGC CACTTCCGC 1440
 AAGCACTTC CTTGTGCC ACCAGGCT GCGCTGCGT GGGGCACT AGCTCACCG 1500
 GGTGACTTC TCTACGCC TCGTCAAGTA CAGCCCTTG AAGGATGCT GGAAGAGT 1560
 45 CCACTAGT GCGAGGCC GCGCTCTGC GAGCTGCTG GACTTATG GCTCTCTG 1620
 CCGCTGAG CTCTGCGGC CCGTGGGCG GCGCTGAGT GCTACACA CAGTACCGG 1680
 CTCTGAGC AGGCTGCT CCGTGGCTCT GCGCCGCC CCGCCACTG ACTGACAG 1740
 50 CTTGGGAC ACCATTACT GCTGCAAGC CAGGTCAGT CAGCACTTA GGTCTCTG 1800
 GGGGACTGC CAGTCTCAG CTCTGCCCC TGAGGACCG CTGCAACT CACTCTGAT 1860
 CTTGAGCT TTGCTCTGA CTCTGCCCC TGAGGACCG AGACCTCT GGGATGGCC 1920
 GCGAGCAGA GACCAAGAC TCGTCTCTG CTCTCAGG AGACCTCT GGGATGGCC 1980
 55 TGAGGACCG GCGCTCAGG AAGGGCTG GATCGAGT TCGTCTCT GTTCTTGA 2040
 AACTTCCC TCTGCTTA AAGGTCTG ATATTGGA AGCCGAGT CCGTACCT 2100
 CTTCTCCC CTGCTGAC AGCGAGCT TCTTCAGT CATCTGTA CACTACTA 2160
 GACTCTCA GCTTCTGAC ACCCGCTCT TCTGGAGT CCGATTCCC TAGAGCAG 2220
 GACTGATG TGTCCAGA CAGAGACT GCTGCTGA GCTCTCTA GCGAGAGAG 2280
 GAGGGGTAG AATCACTCA CACTTCTAT GCTCTCTG CAGAGCAG ACGAAAG 2340
 60 TCCCGAGA AGCTCTGC CTCTGAGCT TCTGCTCTG CTAAGGCT CCGCAGTAC 2400
 CAACCCGTA GCTATCGG TCTGTTTTG ACTTGGAT TCAAGGCC TAGAACCT 2460
 GCGCTGAA CTGCTGCT GTTCAGGCC TGTCTCTG AGCTCTGC CATACCCCA 2520
 GCGCACACA CCGCAGGCC ACTCCAGCT CCGGCTCT TCGGCTCT 2580
 AGCCCTCT CAGAGAGCT CTTCTGAGT CAGCACTCC GATCTCTAA ATGAGCGTG 2640
 65 CCGTCTCT TGTCTATAA ATGTGAGCA TGAAGCTCT TCCACAGA GAGTTTGGG 2700
 AGACAGATC AACTATAGA GCACTGCA CCGTCTCG CAGCTCTG AAGTCTGAT 2760
 ATGCTTTTC TCGCTATG CTTCTTGA GCTCTCTG GAGCTCTG AAGTCTGAT 2820
 GGTCTGCT GACTCTTCA CCGTGAAT GCTCTCTG GCGCTTTTC TGTTTTTAT 2880
 TCTATCTCA GACCACTG CACCAATAC ATTTTAATC ACCGAAGCA

Seq ID NO: 32 Protein Sequence
 Protein Accession #: XP_054631.1

70 1 11 21 31 41 51
 1 KPRCPQPPA RPPGPAAS SARESPVPO LKRSRCEIA PSSGQVRPA ASGDPQGPAP 60
 YRCPGASGRS GALTGRQBEA RLKMLVLPQP GGRGVVGRPR KPSSRALEPA TAANLRRLD 120
 75 LSGCLVLAFL AQGGREPLGA QETVALMSD LRLVLGDEPL YRLSAURHS KTLASLQRT 180
 RAVLVGLVLP SLVQGRSRL PRPGGRRP AALPVSLPL ALILVRLVGR NTRPLVLP 240
 EBAPELQSG CTNVTYFLA GILIRSLAIA WCNSEHFLY PLTNISQVR PQMGRAQLK 300
 LVALLELLTA TGGCELYSNE CYDPRTDANT PRAPLPGT PLRIRAVACR GLVYVGGHL 360
 FYRLRYSPV KDMHCEYSN ASHRSSDIV ALQGLYRPF LRLGGAAMV RYNTVTGMS 420

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RAASLPLPAP APLHICHTLH TYICNFPQVT ATFTVSGGTA QPQAKELQPF PLOSTGVLSR 480
 FLI/LFPEPR LQTSLS

Seq ID NO: 33 DNA sequence

Nucleic Acid Accession #: CAT cluster

5
 1 11 21 31 41 51
 CCTCTGTCTA ACCTTACATG AAAAAACCGG TTTCACACGA AGCCCTCTAA AAGGCCAAGA 60
 AATCCCTCTG CAGACTTTAC AAGCAAGATG TTTCCTAACT GCTCTATGAA CAGAAAGGTT 120
 AAACCTCTGG AGTTGATCCA ACACATCACA ACCAGCTTTG TGGAGATGAT TCTGTCTAGT 180
 TTTGAAACGA AGATATGCTG TTTCCTGCTG TGCGGAATTC AGCCCTCTGAA ATCTACACTT 240
 GCAATATGCA CAATATAGAT GTTTCAAATC TGCGCTGTCT AAGGGAAGCT TCMACTCTGT 300
 GAGTGTGAATG CACACAACAC AAGGAAGTTA TGGGGAATTC TCTGTCTAG CTTTACATGA 360
 AAGAAACCCG GTTTCACACG AGGCCCTCTA AGTGTCTMAA ATATCCACAT GCMACCTTAA 420
 CAAACAGAT GTTTCCTAAC TGTCTATGTA AAGGAATTC AACTCTTAG AGTTGAACCC 480
 ACACATATCA GAGCAAGTTC TGAGATATGAT TGTGTCTAG TTTTATACGA AGTATTTCG 540
 TTTTCTGCCT TTGGCTCTCA AGCCCTTGAA ATCTCCACTT GCACAAATCCA CAAAAGAGGT 600
 GTTTCAAACT TGTCTCTCTT AAGGAAGGTT TCMACTCTGT TGTCTTAAAT CACACACAC 660
 AAGCAATTTA CTGAGATTC TCTGTCTAG CATATATGTA AAGATCTG TTTCCACACA 720
 AGSCATCTAA GAGTCCGAAA TATCCACTGT CAGACTTTAC AAGCAAGAGG TTTCCAGAA 780
 GGCTGTATGA AAGAAAGGTT TAACTCTGT GAGTTAAACA CACA

Seq ID NO: 34 DNA sequence

Nucleic Acid Accession #: AF011469.1

Coding sequence: 257..1468

25
 1 11 21 31 41 51
 GGAAGACTGT GTCCTT7GGG TCGCAGGTGG GAGCGACAGG GTGGGTAGAC CGTGGG9GAT 60
 ATCTCAAGTG CGACGAGAGA CGCGGGGAGC AAGGGCGGCG TGGTCTGAGT GCGCGAGGCT 120
 CAAGTCCCTCT GTCCCTCTCT CGTCCCTGTA GTCTCTCTTA GGAATCTGCT TGTACTATAT 180
 GCGCTCTTGC ATCCCTCTCT CGTCCGAGAG AGCCCTCTTA GGAATCTGCT TGTACTATAT 240
 TACGCTAGCA GGCATCATGTC ACCGATCTAA AAGAAACTCG ATTTCAAGAG CTGTTAAGGC 300
 TACAGCTCCA GTTGGAGGTC CAAAAGCTGT TCTCTGTACT GGCACAAATTC TGTCTCAGA 360
 TCCATTAACCT GTAAATATGT GLLAGATCTA CGCGCTCTTG TGTCTCTTCA ATCTCTAGA 420
 GCGGCTCTCT TTCTTAAGCA CAAAGAGTGT CTGCGAGCAG AGCCCTCTCT AGAATCAGAA 480
 CGCAGAGCA TTGCGACCAA CAGGTGTACC TCACTCTGTG TCGAGGCGCC TGAATTAACAC 540
 CCAAAAGAGC AAGCGCCGCC TGCCATGCGC ACCTGAAATAT AACTCTGAGG AAGAACTGCG 600
 ATCAAAACCG AAAATATGAG AATCAAAAAG GAGGCACTGG GCTTTGAGAG ACTTTGAAAT 660
 TGGTCTGCTCT CTGGGTAAAG AAGAGTTTGG TAAGGTGTAT TGGCAAGAGI AAGATCAAG 720
 CAGGTTTATC CTGGCTCTTA AGGTTTATAT TAAAGCTCAG CTGAGAAAGC CGGAGGTGGA 780
 GATCAGCTCT AGAAGAGAG TAGAATATCA GTCCCACTCT CGCATCTCTA ATATTCTTAG 840
 ACTGTATGGT TATTCCATG ATGCTACCGC AGCTAGACTA ATTCTGGAAT ATGACCACT 900
 TGGAACAGTT TATAGAGAAC TCGGAAACT TTCAAAATTT GATTAAGAGA GATCTCTAC 960
 TTATATAACA GATTTGCGA ATGCTCTTTC TTACTGTCAK CGAAGAGAG TTATTCTATG 1020
 AGCAATTAG CCGAGAAACT TACTCTTGG ATCAGCTGGA GAGCTTAAAT TTGCAATATT 1080
 TGGGTGGTCA GTACATGCTC CATCTTCGCG GAGGACACT CTCTGTGGCA COUTGACTA 1140
 CCTGCCCCCT GAATGTATTG AAGTGTGAT GATGATGAG AAGTGGATCT TGTGGACCT 1200
 TGGAGTCTTT TGGCTGAGT TTTTATGTTG GAGCTCTCTC TTTGAGGCA ACACATACA 1260
 AAGACCTAC AAAGAATAT CAGCGTTTGA ATTCACATTC CCGATCTTGT TAACAGAGGG 1320
 AGCATGGAG CTCATTTGTA GACGTATTGA GCATATCCG AGCCAGAGGC CATGCTCAG 1380
 AGATATGACT GAACACCCCT GGNCTCAGC AATTCATCA AATCATCTCA AATCATCTCA 1440
 CAAAGATAT TAAAGTACAG ATCTATGAG ACCTGCAAG GAGGAAGATCT CTTGAGCAG 1500
 GGTCTGCTTA TAACTGCTCA GMACTGCT ACTGAAATTT ATTTTACAT TGACTGCTCG 1560
 CCTCAATCTA GAACTGCTCA CMAATGAT TTGTTTACT CAGCAAGTGT GCTTAACT 1620
 CCGTATGAG AAGGCTCCAC ATCAATAMAC ATGACACTCT GATGAGAGG TAGCCACA 1680
 AATTTGTCTA CTTATACGCG TGTCAATCT GAGGCGGCT TTGCACTGCA CGGCCCCCT 1740
 CAGCCTCTGG TACGCTGCT GCTTCTCAG GAGGCAAACT CAGAGCCTGG CTGTGGGAGA 1800
 AGTGAACACT GTGCCCTGAC CCGATCATGT TAAAGAGCTG TGCAATTAAC CTGTGTATAC 1860
 CAGTGTAGAT GTGTAACTTA TGGGTTAGG GAGGCTCGGT AAGGCTTGT GATGTATCT 1920
 GGTATCTTTT TAAATATGTA AATTAAGAT ATATGACAG ACTCTGCTG TGTCTCTGCT 1980
 TAGTCTCTCT TAACCACTTA TCTCCCATAT CGGCGACCCG GGTAGGCTG ATTGGTTTC 2040
 ACCTCCATTT AAGGATTTGG TTGGATACA GAGAGGCCCA TGTGTCTCAG AGCTGTATG 2100
 GCTCTATTTT TTAAACACT TGGATCTATA GACTGTGTGT AACTCTTAA TATCAATA 2160
 AATATGATC TAGTCTTAA AAAAATAAA AAA

Seq ID NO: 35 Protein Sequence

Protein Accession #: AAC63902.1

70
 1 11 21 31 41 51
 MDKSKENCIS GPWKATAVGG GPKKRVVITQ LQCNRLPLVN SQGQGVRLCP GNSRSRVPLQ 60
 AQKLYVSHSK YQKQKQKQL APSVFNHVR PLANTQKSKQ PLPSADENIT EERLAKSKQN 120
 HENKFKVAL SEIFIEGRDLP KGRKGNVILA REKQSKFLIA LQVLPAKALE KAGVHQLRB 180
 EVELSHLEH ETLRLGYGV HDATRVYVLI EYALDQTVYR ELQKLSKFB QRTATYITL 240
 ANALSYCHSK RVIRHDIKEP NLLGSADEL KIADPQWSHV APSERTTLG GTLDYLFPM 300

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IEGRNDEKVE DLNLSGLVLCY EPLVGRKPPFE ANTQSTKRR ISRVETPTPD PVTEGARDLI 360
 SRLLEKHP9Q RPLRLSEVLBH PWITANSSKP SINCQKESAS KQS

Seq ID NO: 36 DNA sequence
 Nucleic Acid Accession #: NM_016267
 Coding sequence: 67..843

1 11 21 31 41 51
 10 CGCAGCGAGG ACAGAAATCAG GTGATGTCCT AGAATTAAAG GCTGTCACTT GTGTCTATCA 60
 CTCCACATGG AAGAATAAAG GAAGACTGCG ATCCGCTCTG CCGAAGGCGA ACGAGAGCT 120
 APTAGAGGCG AATGGAATGA CAGTTGTGTC GTTTTCATCG ACTTCGAAAG GACATCAGC 180
 AGGTAATGCG ATGAGACACTT CTCGAGGCTG CTGAGCAATA TCGAGGAGCC CCGAGAAATTG 240
 ACCGCTCGGA GTCCAGAGTGA AGGTGTGATG CTGAAAACAG ATGATAGCAT GTCTCCAAAT 300
 15 CAGTGGGGTT ACTGCTCTCC ATGAGAAAGG CCGAACCGCG AATACCTCTT CCGAACGGCT 360
 GCGCGCACT CACATCTCCA TGTGCTGTGT CCGATGGTGT TGAATCAGTT CTGAGCTTC 420
 CTGAGTAGGA GGGGCTCTGT TCGCGCTGGG GAGCTGTGCG ATTCTCTCTC CCGAGCGGCG 480
 ACCAGTCTCT TAGAGGCTGG CTACTCTCAT CCGTTCCCGG CTGGGCACTT GGTTCAGAG 540
 CCGCAGCTGG ATGAGAAAGG TGAGCTCTCT CTAGCTCTCC TCGAGCAAGA CAGATGCTTA 600
 GCGGCTCTCT AGCAACTCTC GCGCAGGGAG AATGCGACG CTGGCGAGT AGCTGGAAGC 660
 ACAGGCTTCC TCTTCAACTC GCGCCGCGCG TCGATTCACT ATAGAGAACT ATATGTATCT 720
 OGTGATCTCG CCGATACCGG CCTTCCAAAT GAAACTCTTT CAGAGTTAGA GACACTGTGG 780
 AATATCTCAC TTACACGACC AAACGACTGG GCGCACCCAC ATGATATCTT GCGATCTTT 840
 TGTATGAGTT GAGAGGAGAA GACAGCACTT GTCTTAAGAC AGCGACGAGA GACATCTGTT 900
 20 CTAATGCTC CAGATAAATA TGAGAGCTGC TCACACCCAC TTGCTCTCCC AATCTGTTPAA 960
 ACGAGCTGCT GTCTAGTAGT AGCTCAGTAC TTGCGCTGTG AAATCCGAG AAGCGCGGCG 1020
 TGTCAATGTT CCGCATCCAC ACGTGTGCTT CTCGCTGTGA CACACTCAGA TGTAGATAAA 1080
 TAATAAAAT GTACTTTTTT GAAAAAATAA AAAAAAATA AAAAAA

Seq ID NO: 37 Protein Sequence
 Protein Accession #: NP_057351.1

1 11 21 31 41 51
 35 MEDMKTAIR LPEKGKPKIK TERNISRCVLF TTPQDLSVV VDEHFRALS NIKSQELTTP 60
 PSSGSGUWL KNDGNSPFG WYSGSWTEP QPSVPVTHA AKGLKVPSP HAVHGFPSL 120
 AARRAVRPG ELHSHRSLG TSLRPNYGH PFPAHLYPE PQPKQSEPI LELLQDRCL 180
 ARHQGSAR ENHNPQGLAG GTLLFLNPP GSVHKKLVY SRGATSLD NETLSELETP 240
 40 QKYSVLTPPN HNHGPHYLIQ RL

Seq ID NO: 38 DNA sequence
 Nucleic Acid Accession #: AK058088.1
 Coding sequence: 252..1772

45 1 11 21 31 41 51
 AGGAACCAA GCGAGCTCC CCGTGTCAAA GCACCTTGCG CATAAGAG AAAGAGGGGA 60
 GCGCCCATG TGATGAGGCG TTCGAGGCTT CAGCTCGAA AGCGCGCCCC AGCTCTCTCG 120
 TAACTCAGAG GCGATGTGA TGAGATTTCC TCACATCGAG ACATCTCCCC TGTAAACAG 180
 50 CATTGTGTT CATGATAATG TCGAACACCG AGAAGCTCG GCTGGAGCG CAGGTCACTG 240
 GCTCAACGA CGGTGGGGT TTGCGCAACG AGCCTTTCTC TGAGGACCTG CTCCTACTTT 300
 CCGAGATGTC CAGAGCTCTG AGCATAGACT TTGAGAGAGC TTGAGAGAGC CCGACAGCT 360
 TACGATTTTC GAGAGAGGAG AGATTTTTCT TGAGAGATT CTGAGACAG GACATCCAA 420
 55 GTGCGAACG AGATGTACTT CTCGATGCGC TGAGCTCAA ATGAGAGCTC CATCAGCCCC 540
 GCGTTTTTCA GTCTGAGACC CTGAGCAAGC CTCTACTGAA AGCGCTTGCG CAGGACCA 600
 CAGACCGCTT GAGAGAGCTG GAGAGAGCTT TGAGAGCTCA CTAACACTCA CAGACCAAG 660
 AAAAACTCCC TCGACAGAG ATCGATCATT CTTTGAAGT CATGACCCA CTGTGACTA 720
 60 AAGTGGCTT CCGCACGCGC CTGAGAACG TCTCATGAG TGAGTGGAG ATTAAGCTGG 780
 AAGCACTACT GGGATGTGCT GCTTCGCGCC AATCTTCCA GTTCAGTGC CTGTTTCAA 840
 GGTGTGTGTA TGTATGATA GCGACATCA AGCGAGGCG ATGACATGAA TCTTACGAG 900
 CCGCTGTGAA GTACAGGAA GAGCACTCTT CCGTGTGCG CAGAGATGCG CCGGATAGTA 960
 ACTGTGTCG TGTAGAGG AGCAGATCC ACCTCGCAA AATCTCACAG GACCTCTCC 1020
 65 ACAAAGTCT GAGTCTCCCC AGGTATTATA CTTTATGAA ATTCCATCTT CTGAAAACAA 1080
 TGCTTTGTGT GGTCTCTCTG CAGCTGAAGT ACAGAGTCA GGCATATGCG ACTTATGAAA 1140
 CCGTATGAGC ATTTTTAAAG AGCTTCTCTG AGACATGTG CTTCTTGAC GCGGATGAG 1200
 GACGAAATCT GAGAGGCTC GCTCTCTACT TGCTTCTGCA CGGCACTCAC AAGAGCAAGG 1260
 ATTGAGAGT GCTGCGGAC CTTAATCTCT TCCGAGAGTC ATGCTCGAG CAGTATTACG 1320
 70 TCAACATTA CAGCGACGTC GAGATGGGG GCGACATGCT CCGACTGAAA GATCTTACCA 1380
 CCGAGCTTGT AGATATTGGG CTGCTCTTTA AGCTTCTCTG CAGAGAGATA TACACTTAT TCMAAGCA 1440
 TGCTCTCTTA TGATGTTCTT TTTAGATTA AGGACCTGA ACCTGATACT ACCTCTATA 1500
 GTTTTACAT CCGAGAAATA AAGCACAGAC ACTGGAATC TCGCTCTGCG GTCTACGAGC 1560
 ACGACAGCT CAGCTCTGGA CGCGAGCGCC TGATTAAGTA TGATATCAGA CAGAGGCCCC 1620
 75 TGATTGAGC CAGTACAGAG GATTTGAGTA CAGACCGAT CAGCGAGAG TTGCTTTGA 1680
 CAGCTGATC CTGCAAGAGC GATCTCTTGA AATCTCAAC TTGAGGAGAT CCAATCATG 1740
 TAGATTTCG ATTCACTCTT CAGACATCTT GAGAGTTCC AGAGAAATCT ATGAGATTTT 1800
 CCGCCACTG GTCTCTAATA AAGAAATAA AATGACATA AAGGAGC

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Seq ID NO: 39 Protein Sequence
Protein Accession #: BAB1658.1

5	1	11	21	31	41	51	
	MMSNTHKAR	LERRVTGSTN	RWRLPKQPPS	GELLSLSQMC	KALSIDPEEA	LHNPORLCIS	60
	QIQKFFPEF	SNKIDQSORA	DVILECLGPK	HELBQPLRPO	SPTIAKLVIK	ALAGVTHPL	120
	RELEELRAQ	SNKTKRPS	AKRILISLK	NEPLVTKVAP	APALREKWS	EVVEIKEDLL	180
	GVLASAILQ	PSGKPCQVD	VIWAGLPSF	TRKPTTAGCK	YKEBLITGC	EKNLEBNLVP	240
10	LGSTQIHILK	IQPDLHLVL	KSPRLPTFS	PHLLKTMLLM	VFIQIANVYIQ	AIPTTYVMT	300
	FFKSPFENC	FLDRIDGRSL	RPLFLCLRILH	GITKGDQLV	LHLEHFPFES	WLDQTVVHY	360
	HALBNQDMV	HLKDLATVA	RPGLFQDHR	TTYSKTLAT	GFPPKISLK	LDITVSFTM	420
	QRIHITDLS	TSAPVHHV	SGARLVKY	ETRAGLVGD	KMEPFTNQI	KQKPLTFS	480
	CKSHLKIC	VGIPITVSPA	PIFFAS				

Seq ID NO: 40 DNA sequence
Nucleic Acid Accession #: NM_032899.1
Coding sequence: 186..1070

20	1	11	21	31	41	51	
	GGCAGGAG	TTGCTCAGG	CAGCGGTAAA	TCACCTCTTG	GAGGTGCCCT	GCAGGCCGCT	60
	CCTGGKAGG	CGCGGCTCC	CGGCGGTGCG	GGAGGCCCC	TGCTCGGTG	TGTGTCAT	120
25	TTGCTTCCA	CATCTGGAG	AGCTGACGTG	CGAGCTCC	CGAGCACAC	CGAGGACG	180
	GAGGACATAG	CCGCTCAGG	CAGCTGAGCA	AAATCCGAA	GCGTCTGGA	GATCTCAGA	240
	GCAGAGGCT	CGGCGACCT	AGGCTGACCT	TTAGTGACAA	GAGAGTGC	CGCTCTGCA	300
	CGGACCCCT	CTTGAGTGG	GTTTCTGAAG	CCTACTGGCG	GGTGCTCAG	CAGAGAGCG	360
	AGGTGACAT	CTTGTCTCG	GTGAGGCC	AGTACATCA	GCGCAGGCC	AGGAGGCC	420
30	CGTGTCCCC	AGACACCTG	GGAGGGGCG	AMCAGAGCG	TAAGAGCT	GACTCATCT	480
	CCTCAGCTG	CGGACATCT	TTCTCTGTG	CTCAGAGCG	CAGCAGCGC	CGCTCTCTG	540
	ACAGCTGGC	CTGAGCTAG	AGCCGTCAC	TGAGAGGAA	ATCCGAGCC	ACTGTATCT	600
	TCCAGACCT	CAGCAGCAC	ACATCATCG	AAGCTGCG	CGCTGCATC	AGCGAGCTA	660
	CGGAGACCT	TTCCATCG	AGTGTGAG	GAGAGATATA	CTGTGCGTA	CGAGCGAGA	720
35	CAATCATCG	CGGAGATCT	GAGGATTTCA	TTATCTGGA	GTCTGATTT	GTCTGTCTG	780
	GATCTCTAG	CTTCACTGG	CTCTGCGAC	ACGTGACCG	GAACTATCT	TCCAGTTCA	840
	CAGCGCAGC	GTTGAGCTG	TTTGCAGAG	AGTTCCCGCA	CCTCTAGCC	TGCTCGAGC	900
	CTGTGATGG	CGTGAATCC	CGCGGCTGG	TGCGGCCCT	CGCGGCTCG	GGAGCGCG	960
	CCAATGCC	CCTTAGGAC	AGCATGGCT	CGCGAGTGG	CGGACATCT	TCCACCCCT	1020
40	TCAAGGCC	CTTGGAGC	AGCCAACCG	GTACCGGAC	TGAAGCTGA	GATGAGTTA	1080
	GATGACTGG	GCGCGGCTA	ACATCTCAA	TGGATTTC	CATCTGCTG	AGAAAGTTA	1140
	AGGAAAGCA	AGCTTGCA	GTACAGAG	CTCCAGACC	CAGTTTCA	AGAGCTG	1200
	CTGTGCTG	TGTGACCT	AGTCTTGG	GATAGGAG	AAGCTCAG	CAGGAGAG	1260
	CGCCCTACT	CTTGACG	CTCATGAC	AGTCTCCCT	CGTGTGCT	CTTCTTAC	1320
45	AAAGGTGAG	TTTCTCTCT	CTGCGGACC	TGTAACTGT	GATGCGCTG	CTGCTGGAG	1380
	GTTAGTGAG	GAGTGGCG	GGAGTGGAG	CATGAGCAG	AAGCGGAG	GTCACTCTT	1440
	GGCAGAGCT	TTGAGACCT	GGTCTCAGT	TGCCACATG	AGACACTCT	CGATGTAA	1500
	CGTCTCTCT	CGAGCTGG	GTCTTAGCG	ATGAGCAGAA	TCCCGCATC	CGACCGCAC	1560
	AACCCACAT	GGATATGAG	TGAGCAGAA	ATAAACCTTT	TGTTGTAAA	AAAAAANA	1620
50	AAAAAAA						

Seq ID NO: 41 Protein Sequence
Protein Accession #: NP_116288.1

55	1	11	21	31	41	51	
	MRSRHILGI	RKLEEDVKS	WVRPARADPS	DNESARLATD	ALLDQGSBAY	WRVLSQBEV	60
	DFLSVEAQT	IQGAREPFC	PPDTLQAGAA	GTKGLDSSL	QSTQTFVFA	EGSEFALLHS	120
	WABAEKPLK	ESKSAATVFP	TVKRNIRDL	VIRCIHTRSQ	KISIRSVBE	TVCKASRKF	180
60	TQGIREFKI	SDRFVLSGS	ISPTMLGVH	IRVILSHFPS	QAVLPQEP	RHLVASKEV	240
	MSLAKSLVA	PVFGAGAFAY	GRLSSSGSA	SDRTSSSPPS	GRSAGSHPT	RITD	

Seq ID NO: 42 DNA sequence
Nucleic Acid Accession #: NM_000782.2
Coding sequence: 405..1346

65	1	11	21	31	41	51	
	TCCAGAGGGA	CAGGAGAAA	CGCAGGCCA	CGAGCATCTC	ATCTACCTC	CTTGACACCT	60
	CCCGCTGGCT	CGACGAGGC	CTAGAGTCA	GCCTTGGGA	CGACAGGAG	GACTCCCGAC	120
70	TTTCCCTTTT	CAGAGATAC	CCGACACAC	GAGCACCTC	TTCCAGCCC	TGCGGCGAT	180
	CAGAGAGGCG	ACAGATCTC	TAGAGCTCT	TAGAGCTCT	GCGTGGTGA	GCTGCGAG	240
	GTCTCTCTC	TGCTCTCTC	GCTCACCTC	GTCCTATCA	ACGACATGC	CTCTTCTCT	300
	TTCTTTTCT	AGATATCT	AGCCCGGACT	CCCATAGCA	CTCTATACA	ACCTCGGCC	360
	ACCCCATCT	CTCTCTCTC	CGGCTCGG	TGTCGCCG	TGCATGAG	TCCCATATCA	420
75	CAGAGAGGCC	CTGCTTGCC	GCTTCTCTG	AGGACATCG	CAGTCAAG	CGTCCAGC	480
	GACTCTGAC	ATCAAGGCG	TAGAGCTCT	CTCAGACCG	AGAGTGTAC	GTCTGCGCC	540
	TGACACTCT	TGAGAGACT	CAGAGACCG	CGCCCTGCG	GGGCCCATC	AGTGTGAC	600
	TGCTCGGAG	CTCTCTGAG	ATTCTCTGA	AAGGGGCTCT	CAGAAACAG	CAGACACCC	660

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TGGTGGAGTA CCACAGAGAG TATGGCAGA TTTTCCGAT GAAGTTGGGT TCCTTTGAGT 720
 CGGTGGACCT GGAATGACGA TCCCTGCTAG AAGGCTCTTA CCGACATCGA AGGTGACCC 760
 AGCGGCTGGA GATCAAACTG TGGAGGCTAT ATGCGACATA CCGGAAGAGA GGTCTGCGG 840
 TCGTGATCTT GGAAGGGGGA GACTGCGACG GGTCCCGGAG TGCGTTTCAA AGAAGACTAA 900
 TGAACACGAG GGAAGTGATG AAGCTGAGCA ACAAAATCAA TGAGGTCTTG GCGATTTTAA 960
 TGGGCAAGAT AGATGAGCTC TGTAATGAAA GAGGCCACGT CGAAGACTTG TACAGCGAAC 1020
 TGAACAAATG TGCTGTTGAA AGTAACTGCC TGCTTTTCTA GAGAGAGTGA TTGAGGCTCT 1080
 TCCAGAGAGA TCGAGGGAAT GAGCTGTGGA ACTTGATCAT GGCCATCAAA ACAATGATGA 1140
 GCACGTTTGG GAGGATGATG GTCACTCCAG TCGAGCTGCA CAGAGGCTTC AACACCAAGG 1200
 TCTGGCAGGG ACACACTCTG GCTGAGCACA CCAATTTCAA ATCAGTCAAA GCTGTATATG 1260
 TGAACAAATG TGCTGTTGAA AGTAACTGCC TGCTTTTCTA GAGAGAGTGA TTGAGGCTCT 1320
 ACAGAGATGG GCTGTTGAAA GAGCTGTGGA ACTTGATCAT GGCCATCAAA ACAATGATGA 1380
 CGGTGGAAAC GACAGCAAC AATCAATATG GAACTCTCTA CAAATTTATC CATTAACTCC 1440
 AAGTGCAAC AAGAGCTCTT AAGGAATCTA AAGTGTATT ACCTGAGAAT CAGAGGCCAC 1500
 GGGAGAGAGA TTTGGAGAAT ATGCGATATT TAAAGGCTTG TCGAAGAGA TCTATGAGAG 1560
 TATCCGCGAG TGTACCATTT AGACTGCGA CTCTTGAGCA GCGACAGMTT CTGTGTGAGT 1620
 ATGCTTTTAC CAAGGAGACA GTGCTCATCG TAAATACCCA GGTCTTGAGA TCCAGTGAAG 1680
 ACAATTTTGA AGATTCAAGT CAGTTTGAAC CTGAGCTGTG GCTTCAGAGG AAGGAAAAAA 1740
 TTAATCCTTT TGCGCATCTT CATTTTGGGG TTGAGAAAGG AATGTGCTT GGTCCGCCAT 1800
 TAGCAGAGCT TCAACTGAGT TGCGCTCTTT GTTGAATATG CCGCAATAC GAAATCTAGG 1860
 CCAAGAGACA TGACCTTGTT GAGATGCTAC ACTCGAGCAC CTCGTGCCCC AGCGGGAGAC 1920
 TCCCATGCG GTTTTGGCAG GATATAATAG CTCGATGATG TGATATTGCG TAACATCAT 1980
 TCCAATCAG GGAAGGCGAG TGATGTGCGG GATCCAGGCG ATTCTACAGG GTTACACTCT 2040
 GBTTTACACT TCACTCTGCT GAGCAACATG TTAGAGTGGC TGAGAGGCTG 2100
 TTTCTGCTTG CATCTTCACT TGAGTGAAGG GAGGCTGCG ACTGTGCAAT CAGTGTGAGG 2160
 TTACAAACCG TTTCAAGCCC TGTACACACA TCTCATTTTT GAATCTTTAA TCCCAAGAA 2220
 TAAATTTACA TTTGCATCAT AATGACTATC AACAGCTTAA TTTTCTGGGG CTGGAGTAA 2280
 TACTGACATC CCAATTTACT TACTCTCTCT TAACTACTA CTTAGAGAGA TCTGAGTAA 2340
 TAAATATGTA AGCTCTGAGT TAACTCTCTT AAGATTAAT TACTGCTCAT GAAATTCGCT 2400
 TCTTCCGACA TGGAAATAAA AACATTTATG GAAACATGGA GAACTCTCT TTTTATAAAA 2460
 GGAATTTTAC GAAGTCAAC TGAATCTTAG ACTATGATTT CACTGGAGCA TATATTGTTA 2520
 GAGGACCTTA AATATGTTTA TTTTATAAT TGATCTCTCT TATGAGCTTA GGTTAAGAT 2580
 GAAGCATATA TTTTATAT GTATGAGCTG ATATAGAGCT CAGACATGTA TGATGTGTTG 2640
 TTTCTGCTTG TGAGTCTGCG GTATATGTTG TGATGTTGTT ATGATGTAAT TGCTCTCACT 2700
 AATTTTATTA TATTTGCAAT ACTGATTTTA GATCTGTGTT TGACGGGCAZ GTTTCAAGT 2760
 TTAGTCAACG CTAAATAAACA TTAGCTGTGA CTTTAAATTT ATAAATGAT TTGCTCAACT 2820
 ATATAGCTTT TGCTCATGTA ATGAGCAGG TGTAAAGCT GCAAAATTA GATGCTGTT 2880
 ATATAGCTTT TGCTCATGTA TTTGAATCTC TAGGAAJAT ATGATTTCAAT AATATTAATA 2940
 TGCAAGAGAA TGCTATGCAAT ACTTATAGGA CTTAAAAAT GTGTTTACAG ATGTTTAT 3000
 TGTCATATTT TTTATCATCT CTTTTCTCTA ATGCTACTTG TATATATTC TGTTATTTG 3060
 ATAAATATTT CTCTCTACAT CATATTTTGA GAATATTTCA GAATATTTCA TTTATGCTT 3120
 TTTAGATTA TAACTCAQCT CTGTGATAT TCTATCTGTA TACCTTGAAA TTTCTGAGAA 3180
 GTAAAAATTA AAGTTTATTA ATATT

Seq ID NO: 43 Protein Sequence
 Protein Accession #: NP_000773.1

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MSPPISKSRSLAAPIQLQLRS PRQPRFLVTS TAYTSQPQRS VPVCPILTAGG ETQNAALPG 60
 PTHNPILLASL LQIKRAGKGL QKHDTLVYKH KYKYLIPRKH LGSFESVILG SPCLLEALYR 120
 TESPORLEI KPNHAYRDIR RSYVGLLEIE GEMWVRSSA POKSLAKRSE VRELIDKINE 180
 VLAFPRKIRID TAEKAGSHVE DLSLELRHS FELLCLYLS KPELLQJNA GSEAVFIMA 240
 LKPMHFFGR MMYTVLELKH SLATEVMQKH TLAWDITFKS VLAICDNRLK KYSQGTSBAP 300
 LCDIYHQRLR SKKELAAAT ELGLAAVETT ANSLMILYN LSHNFQVQKH LKRTGSVLG 360
 ENQRFREEDL RHPMLKACL RESMRILTFQV FPTTFLDEA TVLSHVALPK GTVLMHATV 420
 LOSSEDRFED SSQPRFERHL GSEKIDVFA HLPVQVGHUM CTGRRLALQL LHLALNIVR 480
 KYDIQATNWE PVNLEHSLTL VPSRELPAP CQR

Seq ID NO: 44 DNA sequence
 Nucleic Acid Accession #: NM_007000.2
 Coding sequence: 1-777

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ACGGGCTCTG CCGCAGCAGC GAGAGCGGAG AAGGATCTC CAGTTGTGGT GGGCTGCTA 60
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 GTGACAGCGC ATCAGTCACT GTATACATCA CGATGAGGAG TCTCAGCGCA GATATGCTC 180
 TCTGCTGTGG CCTGAGATTCG CATCTCTGCG GCTCTCTCTC TCTCATGAT AGCCATTTT 240
 GGTGTGATGT CCGATCATCTG CCGAGCGGAG TCTATGCTCC TCACTACTCT GGTGCTCATG 300
 CTCACTGCTC ACATCTTGGA GTGCGCTCC TGCACTCACT CTTACACCCA CCGTAGCTAC 360
 ATGGTGTGCA ACCCATCTCT GATCACCAG CAGATACGTA CTTCTACAG CCGAGACAG 420
 GACACAGGCG GACAGGAGCT CCGACTCTG GAGCCTCTCA TGTATGAGCA AGATATCTG 480
 GGACATCTGA GTGATACATG CTGAGTGAAC TCTGATGAG CTTCTGGAG GGCATCTCG 540
 GAGTGTGTGT TCCCTGGAGT CCAACTGTAC TGTCGCGGGA GGGGAAATCT CATCCCCCT 600
 AACAGAGGAG GCTCGCGCTT GGGGACATG GACTACTTGT TCACCAAGG CTGCTTGAAA 660
 CATCATGAGC AGGCATGACA CAGCTACAG TGGGATATCT CTGTGTTTGG GTTGTGCATC 720

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CTGATGTGGA CCGTCCGGGT CATGCTGATA GGCATGTATT TATACACAT GCTCTGAGGG 780
 ACGAGAGGGG AAGGCAACAT ACACACCCCG GACTCCCTCG CATCTCTCTC CTGCTTCTCT 840
 CAGTGAGGCT GATGAGCTGG CTACGCTCTC ACTCCGACAC GTCCCTTAGG CTACGCTCTT 900
 TCGATCTCA AGATCTCTTT CGAGGTCTCT GAGCTCTACT GTCTCTAGG TGTGCTCTGA 960
 5 AACCCGAGGG CTCTGTGTGA CATATCTCTTA GCCATCTTT CAGGAGGACT CTCCATGATC 1020
 CCACTCCCA TTCACAGATA CCGTCTCTGT AGCTCTCTGA CCGCTCTCTT CATCGCAGGC 1080
 ATGACATTC TGTCTGAACT GTTGTGTGAT GGCATTGTAG CTCTGTAGAC GTCTATTGGC 1140
 TATACGATTC TGTACGAGTC ACTTACTGCT CCACTCATC ACCGAGCAG GCGCTAGGCA 1200
 TATACGATC ATCAATATA TAA

Seq ID NO: 45 Protein sequence:
 Protein Accession #: HP_008931.1

1 11 21 31 41 51
 15 MASAAABAS KSPFVVQLL VVGHILLAS GLSLPARTIW VTADQHYTFP LNPVSGKGV 60
 FAGAHILFC SPFDFWLAGT GYGAALCRIP SWULTYLVLM LIVTFIRKAS CITSYTHUDY 120
 KVSFSLITK QMLTFYSADT DQGGELTRLM DRVMIEQECG GTSFPMWVN PTAAPRAATP 180
 20 EVVFPWPLLC CRYATNFPL NEEGCRILGHM DYLPFTKCFE HIGALSDST WGISWFPFAI 240
 LMVTLFVMLI AMYFTFNL

Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_006760.1
 Coding sequence: 39..593

1 11 21 31 41 51
 25 GAAACCTGCG CAGACCTTAT TCCACCTCCG AGCCGAGCAT GGCACCCCTG CTGCGCATCC 60
 GAGCATGTGC CTGATGCTGT ATTCTGTCTG CTCTCTCTCT CCGAGGCTCT CGAGACTTCA 120
 30 ACATCTGAG CCGTCTCTGT CTGCTCTCCG CCGCGCTAAC GAGAGGCTCG CTGGTGCTCT 180
 TGCCGCCCTG CTACCTCACA GGAGGCAATG CCACACTGAT GTGCCGAGAA GCCAATGACA 240
 GCAAAATGCT GAGCTCCAGC TTGTGTGCTG CTCTCTGCCG TGCGJCHACR GAATCTGFTA 300
 GTGTGTGGA CAGTGTGCTG GCGTCTCAGC TCACTCTGCT CAGTCTATAC CAGGTGACA 360
 35 ACCTCTCC AGGACACAA CTCTACTATT CTACTACTAG GAGAGAGGGG ACAGGCATCG 420
 ATCCGAGCG AGAGATCCCA ATGTCTACAC TCCCTCGAAG GAACAAGGAA TCCATTGGGC 480
 TGSGTATGGC CCGCACAAGG GGCATAGTGG TCATCAAGTT GCTGCTCTCT GTGCGCATGT 540
 TCCCTGTGCT CTGTGGGCTTC ATCATTTGCC TGGCACTGGA CTCCGACAG TAAAGAGGCA 600
 TGCCGAGCG AGCATCTCTC CCGAGAGGCG GAGGACACCA TCCAGCTCCG CAGCCGCACT 660
 40 GCGCCGAGCG CCGAGGCTCT TGCTGCTCCTT GTGCCCTCTG CCGCTCTCTC CTGCGCTCTT 720
 CTCCCTCAGA GCGCTCTCTC CCGCTGTGCC CTCTCTCTGC CCGGATGCC TCACCTTCCA 780
 ACATCCATT ATTCTCTCCA CCGCATCTCT GTCAGAGTGG ACTTCTCTCC CATTTCACA 840
 45 GTTAAACAC CCGCATACA ATTCCCATAT CTTTCACTGA ACTAGTCC TATAATAAG 900
 GCTGAGGCTG CATCTGCCA AAAAAAAAAA

Seq ID NO: 47 Protein Sequence
 Protein Accession #: HP_006751.1

1 11 21 31 41 51
 50 MPFLLPRLTL PLILLILLAL SPQADFNHS SLGSLLPAL TBSLUALPP CHLTGGNATL 60
 HVRANDKRV VTSPVYFPC NRRRLVSVV DSDAGFVTR LSAVQTNLV PFTKFIAYL 120
 VKETVATSS REIPTSLTR NMSISGLGM ARTGGMVIT VLLSVAPLL VLGFYIALAL 180
 GSRK

Seq ID NO: 48 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 200-2932

1 11 21 31 41 51
 60 ATTGCTGATG GATCAGTGAG CCGTGTGTCA TCCAGGTGAG CTGCTGTAGC TCAGATAGTG 60
 ATACTTCTCT TCCAAACAGC ATAGAGAATG ATTGAGCCAC AATATATCTG AAGAAAGGCG 120
 TCGCTCAUAT TCTGCTGTGA AGGATATAT CACCGTTCAC AGCATATGCA CCGCATGCTC 180
 65 GCTGTCTGAT CAGGGGAAAA TGAAGFTGG AGTCTGTGTG CTCAATCTCT TCTTCACTCT 240
 CACTGACGCG CAGCGTGGCT TCGTGGGGA AATATATGCG ATCAAACAA AAAAAAGCT 300
 CACTGTGATV AAGAAAAAC ACTGAGGCC AGTGGAGAA TATCAGCTCG TCGCTGAGT 360
 GAGCATTAGA GATTCCAGAG AGGAAAGAG TTGAGAAAT TTCTGTAGC TCTTGTAGCC 420
 70 TCATATATA TGTTCACATG GGTAAATTAG AATTATCAGA GCAAAAGCTA CCACAGACTG 480
 CAAAGCCCTG AATGAGTCC TCGCTGTGAC CTTGGAAGAC AGCTACACT GTTCTCTCC 540
 CTATGCTCTT GATCCGCCAG ACTGTACTCT TCAACAGCTT GAGGCACTCC CAGCTGTGA 600
 75 AATTCATCTC ACACACTCTA CAGCAGATGT CAGTCTCTCT GAGAGACGA AATATGAGG 660
 CAGTCTGAA ATTAATGAAA GOTTTCAGAA TGACTTTTGA TGACTTCTT CTGTATATA 720
 CTCGAATAT CTGAATGGAA TCGAATTTCA ACTTAAAAAA GATATGAAA GAAATCAAG 780
 TTTTGAATG GTTCAGCTCA CCGAATTTC AATGAGAGC ATGTTTCTTG GTTATGAAAT 840
 TTTTGGTCCC AGCATGCAAT CTGAGCTCTT GTGACAGCT TCTTCTGAG TCTTTCAGAG 900
 TAAAGACAC CTTCACAGC TTTTCTCAT AGAGACGCG TCTTTCAGAG TCTTTCAGAA 960
 AGCCCATGTT AATGACATTG TCTTTGAGAT TGGTTCAGG GATGATGAAT ATACCGTGCC 1020
 CTGACGGGT GCGTACAGGG GATACATCAC AGCCAAATGT GAGTCTCTTG GTTGCGAGTT 1080

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CATCAGGAG ACTTGTGTC TCTCTGCT TGAAGAACTG AACAGAAATT TCGATATGAT 1140
TGTAGGCAAT GCGACTGAGC GAGCTGTGCT ATCTCTTGTT CAAATCTTT CTGTATCAT 1200
TCGGCAAAAC CGCTACAAAC CAGTGGGAAA TCGCTGTTCG GTGGTGTGTA TCTTCAGGAA 1260
TATTTCAACT CTGTCACTGG CAGAGCTTTT CAGCTGTGTC AATTACAGA TGGAGAGATT 1320
CATCACTATA GCTGACATA TCTTATATC AGCTTCAGTA ACCAATCGA CAGTCTTACT 1380
CGCGAGAGAA AAGATAGGCA GCTCACTGTT ACTAGAGACA TTGAGAAACA CAGCACTCT 1440
GTGTGCTCG ACAGCTCTTC CTCTTAATTT TCTCGGAAA TTCACTGAT GGAAGAGAT 1500
TCTCACTGAC AAGAGCCGAC TCAGAGGGG TTACAGCTCT CAGATTAAGA TGTGTCCCA 1560
AAATAGATCT ATTCCTGAC GAGAGCTGTT GTTAATTGGG TCAGACCAAT TCGAGAGAT 1620
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CAAAATTGA AATGCTCAGG TCATGAGACC TGTGATATCC AGGTTATTC TAAACTATTC 1740
CAATAATGAA GTTTTCTTAT TTTTTCGAA GATGAGTCA AACTGAGCC AGCTCATG 1800
TGTGTTGAG GATTCCTGCT ATTGCTGAG GAGAGATCA GCTCTCAC CAGTGAATGA 1860
AACTCAAGC ATGTGAGCT GGCATATGAC TCACTTGACC TCCTTCTCCA TATTGATGCT 1920
ACCTTTTGT CCGCTCTAGA TCTTCCGCT TGTAAATGAG ATCACTATG TGGAGCTGG 1980
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CTTATGCT GATGCTGAG TATGTTGG TGGCAGAGT GACACACGG TGAACCTTC 2160
TGGAGTCTGC ACGGCTGCT TGTCTTTAC ACACCTTCT TACCTCTCT TGTCTCTCT 2220
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CCAGCATTT ATGATGCTA TGGATTTT CCTGCTTAT GGGTGGCTT TCAATTATC 2340
TGTCAATCC ATTCCTGTA CGAAAGTAG CAATACCTA AAAAGGAAG ATGTTGTGTT 2400
GCTTAACTG TCGGATGGA GAAACCACT CCTGCTTTT GTTGTCTCT CACTGCTAT 2460
TGTGCTGTC AACTTGTTT TGGTGTGCT AGTCTTCCA AGCTCTGGA GCGGCACT 2520
TGGGGAAGA CTGAGTGGG ATGCAAGCC CACCTGAT CCGCTGGGA AGACCTCT 2580
CATTCCTGC CCGCTGAT GCTGCACTG GAGCTTTGGA ATGAGAAC TAAGTGAGC 2640
CAGAGACTG CTTGCGCAT TTTATTTGCT TTACTCAAT GCATTCAGG GATTITAT 2700
CTTATGCTT GGAATCACT TGGACATGA CGTGAGACA CTTCTTTCA TGGATTTTC 2760
TGGCTTAAG TCTGAGAGC AACGAGAA CAAAACTCA TCAGATGAT TCTCCAGC 2820
GAAATCTCA AAGCTGAT CCGCACTGA AACAGAGCT CATATGAT TTTCTAGC 2880
TGGAGTCTC TCGCAACA TCAAGTAC TCAATTTGCT TCAATGAT AAGGACAGA 2940
ATCATAAAT CAGAGAAAA TTCCAGAAC AACTGATCT TTAGAGACA ATGTCAATG 3000
AGAAATATG CTCAGTATC GATGCGGTTT TCTGATTAG GGGTCTGGA ATAAAGCAG 3060
AATGCTCAT TGGCTTCA

Seq ID NO: 49 Protein sequence:
Protein Accession #: E0S sequence

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1 11 21 31 41 51
MKVGVNLIS PPTTQHGQ PLAGNDGRT KKELVNKKK ELGFVEVQL LIQVYRDK 60
EKRLDNLFK LRLPELWSE GLILIRAK TIDGNSLNF LQCTCEDTT NFPESCILD 120
KCLITAGL PGCHELMIL SDFNFCST KINOTPLINE RPTNDLASS SAIYSKTAG 180
LEIQLKVAIE RIQGFSEVQV TFRNGSIVA GYEVGSSSA SELLSAIEN AEAATAIK 240
LFEEDGSEF VPIQACNDI VPGRSKDEB YTPLCSGYR KINTAKESS GQVIRCTV 300
LSLLEIAKIN FSNIVGHATE AAVSPQVHL SVIIRGPFPT TVGNANVS ILWTSLELE 360
ASHPFVSTH MEDVISLAIN LAGSAPVTH TVLLREKYA SRLLSTLEN ISTVPPTEL 420
PLRPFKPID WKGIENVXQ LKXGYSYQIK MCPNTSIFI RGVLEISQDQ PQRSLPETII 480
SMASITGNI LPSVGNQAG VNGVISTVI QNYSINEVEL PFKISEHLS QHCFVMDPS 540
HLQNDAGCH LWNFTQIVT QCTHTSFS ILMSFFPST FPFVNNLITY VGLISITSL 600
ILCLITFALF WKIETSGES HTRKICWNT ALSLIADNV PTGATVDTT VNSGVTAA 660
GTFEFPFLF LPSNMLAI LAYRIILVF HMAQHLAWA VQFLGYOYC LIISVITIAV 720
TQPSSTYRK DYKLNNSIG GSKLAPVFP ALAIVANVP VVLVLTKLM RPTVBLERL 780
DDKATIIRO KSLILLTEL GWTGPIQGT IVDGKLAH VIFALMLAP QPFLICPFL 840
LDSELRQLFL HKLSALSNK QTEKNGSDD SAKPLPSKPF NFNQNGHYA FSHTDSSDN 900
IMLTQVSNH

Seq ID NO: 50 DNA sequence
Nucleic Acid Accession #: E0S sequence
Coding sequence: 63-1224

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1 11 21 31 41 51
CAGGAATTG TCGCGAGAG GGCATAAAC TGCGCCTCT CGCGGCGCCC GATGCTGCA 60
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ACGACGAGC GAGCAAGAG ACCCGAGAT TTGCAGATG GCGCCCAAG GCGCCGCGG 180
CGCGAGACT GGGGCTCCA GTGAACACC CAGGAGAGG CAGATGCGG AGTGGAGAT 240
AAGCCAGAT AAGAGAGG CTGAGAGG AAGACAGAT CTGTGAGAA TGTCTGCG 300
ATTCTTAC CATCTCTG TCCCGAAC ATAAGAAAA TTGCGTAA ATCCCACT 360
TCTTCATAT GATGAGAGC GAGGAGCTG TGCCTCAGA AGACTCTCC GAGATGTAT 420
TGAAGCACA GCGGACCAT CCGCAUATA AGGACATCA CAGAGAGAT GCGGCGACT 480
CAGAGAGAT GAGAGAGAG CCGATATGCT GTACTTAA GACAGAGAC 540
CCTGCGACC CACGCGGCG GACATACCA AGTATGCCA AGGCAAGTG GGCACACT 600
ATTGAGCTT GCGGAGACTA CGGAGACCA AGTGGAGCT GATTCAGG AGCGAGAT 660
GACTCCGCG CCGCGGCTT GGTGACAGA GATCTCTG GTCTCTCG CAGATATCT 720
CTCTCGACA GCGAGAGAT CAGAGATCC AGCTACCA CGAGATGCC ATCCAGTGA 780
ACATGTGAG CTCGACCTT CTCCATCCA GCGGCGCAG GCGGCACT CCAAGACT 840
TGGCAGCCA CATGCTCG CAGTTCTG CAGCTGTAC TTTGCTCAG CAGAGACT 900

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GAGCCAGG TCTGTCTCTG GATGCTTGA AAGAGCGGA GCTACCTCAC GCCAACATCC 960
 CTTCTGCCAC CAGCTCCCTG ACCAGAGGGC TGGGACCCCT CACTCTGAAG CCCGATGGGA 1020
 CCGAGTGCT CCGGAACTCT ATGTCCGCC CTCCGAGGCG TTGCTCTCTT CAGCGCCCGG 1080
 GCTGGPCTCT CTTCGAGAGC CATTCTCCA CTCTGGGCT AGACACATCT ACGAAGAGGA 1140
 AAGGGAAGCC ACCGAACTCT TCCGSGGTGG ATCTCAACC CAAAGAGGAG GGGGCGCTCT 1200
 ACGAGACAA GTTAAATAC TTGAGCAAGG TTCTGGGAC TGATGACTCC ITGCGATGCC 1260
 AACTCGGCTC CCACTCTGGA GAGAGACCTT TGTGTGCTCT TGTCTGTGTT GTCACCTCTCA 1320
 CACCAAGAG CAGTCTGAGC CATTCTTCCA ACCGATCTCC CAGGCTGAAG GCAGAACCCG 1380
 AGTCTTTTC CAGTCTTCA GACAAATGCG GCGCCGCGCA TGGCTGCCC CATGCACTCT 1440
 CTGTACTGTA CCGCAATAGT GAACGAGTCT TTTCTTGA GAGCAAACTT GTCTCTGTAA 1500
 CCACTCTGT AGGGTCACT CAGAACTCTT CTTCGCGGAC TAATCCCAAG GAGCTACAG 1560
 TGTGCTCTTT GCGGAGTGAC CTGCACTGTC GCGCTCTCTC AAGATGAGG CTGAGACG 1620
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 GGAOCCCTGA GCGAAGGTCA GAGACCTGTA AATTGACAGA GTTGGTGGAG AACATGTGAC 1740
 AAGCACACAC TGATCCCGAC GAATGTCTCA TTGCGACCG AGTCTTAAGC TGTCAAGACT 1800
 CCTCAAGAT CAGTCTTAAG ACCGACACCG GAGAGGAGC GTTCCAGTGT ABGATCTCTG 1860
 GCGAGACTT TCTCAAGAA GTTAACTGTA AGTCACTCT TGGGCTTCC CAGACACAA 1920
 CAGCAITAA GAGCGAGCAT TGTGCGCCCA CTGCGGAGAA GAGGTCTCACT AATGCGGTGA 1980
 TGTGCGAGCA ACATATTGG ATGCAATGAG GCGGTCAAGT TCCCAACACG CCCCTGCGAG 2040
 AAGATCCCTG TGACTTTAAG GTTCTTGAGC CAATGACCT GGGTGAAGAC GCGCAACCG 2100
 GGCCTATTC CAGTATGAT GTGATCGAA GATCGATGT AGAGGAGTCT AGCTCCAGG 2160
 AAGCTCCAG CAGCTCCTCC AAGGTCCGCA GCGCTCTCC CAGCATCCAC TGGCATCAC 2220
 CCAAGCTAGG GTTTCGCA GTGCTCTCTT TAAATGCGCC AGGGAAGTGT GGTCTGCCC 2280
 CTTTAACTCT CAGAGCGAG CAGGAGCGAG AAAAGCTTCT GTTGAAGAGC GATGCTCTGA 2340
 CACAGGACTCT ATCCCTCTCC ATGGAGAGC AGAGTATCA GAGCCAGAC CAGATATCT 2400
 TGGAAACAC ATCTCTCCG CACTCTCTCC GCGCAGTAG TCAAGCGGAA AGCATCAAGT 2460
 CAAAGTCTCC GATCTCTGAG AGCAAAAGC AGAGCTCTGA GAAACGCGC ACTGAGATGG 2520
 AAGGTGGAG CAGTCTCCT TCGACCTTA TCCGAGCCG GCGAGCTTAT GTCAAGATGG 2580
 AGGTCCTGG CAGATTCTG GAGGACTCT CATTCTCCG AAGATGAGC CATTGTGAT 2640
 CAGCGAGC AGCGAGCAG CAGAGCAGC ATGCGTCCG ACAGTCTCCG AAGAACTCT 2700
 GGTCTGCTAG CAGCTCTGAG CAGCAGAGC GAGACTCAC TGGAGAGAGC CTTTGTGTG 2760
 GCAACATTTG TGGCGGAGCT TTATCACCA AAGCAACTC AAGAGTTCAC TACATGATAC 2820
 AGCGGCGGAA CAGTAATCA CCGCGCGGT GAGGAAJTT GAGGAGTCT ATCCGATCA 2880
 CTCTGTGAG TACGAGTCT CAGAGTCT CAGAGTCT TCCGAGGAA ATCTCGGCC 2940
 CTCTGAGAA TGTGAGCCT TTATGTGTGA ACAAGTAC CAGCATGCTC AATGGCGTCT 3000
 TGGCTGTGAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGTCTCTC ACGCTCCG 3060
 TTTCTCTGG GAGCACTCT GTTGTGAATA AGCAGCTCT TCCAGAGTCT GATGCTCTCC 3120
 AGTCTGGAT CAGTCTGAG GTGAGTCA CAGGTCTAC TACGAGTCT TCCAGAGTCT 3180
 AGTCTCTCA CTCTCTGAA GAAACAGAG TTGCGGTGAG CTAAGGAGCA ACTGGGTG 3240
 AAGAGCAAT GCGAGCAGAG TGAATCTCT AGATCTCTCT TTGTGTTTGA AGAATCTCAT 3300
 TCTCTCTCT TTCTTTCTCT TACTGATAT CAATGAGT TACTACTT GTTGTGAGC 3360
 ACAACTCAG GAAATGCTCA CATCAAGAT TTGTGTTGAG CAGCTCTTGA AAAAGTGG

Seq ID NO: 51 Protein sequence:
 Protein Accession #: NP_065169.1

1 11 21 31 41 51
 MSRRKQAKPQ HINSEEDQGE QQQQQQTFEP ADAAPAPAA BELGAPWHPH GSDVASEDE 60
 50 ATVKLRARE TSVCKECQAS PPSISEFLH KSKCTANIPV LINDSEDPF PSEDFGAVL 120
 SHGPFSSQK DCHENEGDS TDKKPEQDAE SVVYLKTLA LPTTPQDISE LAKKRVANFN 180
 VTGLAGDTR GVADNRSDA FLAPVFGANS IVVLLQLIC LQQQQQ/QQIQ LTGQIRIQWN 240
 MWASIALESG GMAEDTKLT GSMHQQVYSA AVALLSOKAG SQQLSEDLAK QAKLPHANIP 300
 55 SNTSLSPGL AFPTLKPDOT RVLPWNSRL PALLPQAG SVLPQSPPTV LADITGKIK 360
 GKKPILSAVO VPKGQKAL KSKGVCYSV PDSLSLQIH LSHNTGERPP VCSVGRHPT 420
 TKNLKVHTR RHPQVLANPQ LFARPDOKYA AGNIPIYALS VPPIDIEPL SLDSKFLVLT 480
 TSVGLPQLLS SGTNPDLTQZ GSLFDLDLQO PPSSEKQET LPGVQPNYNS PRAGQ/QSG 540
 TPEPSEHTLK LQQLVENIDK ATTDPRNICL CRVLBQJSS LAMVHTHTS EPPKQICG 600
 60 RAPTSGMLA TRLKTLKCTT SIKTSGEPT CQKQFNAMN LQGHIRNBMG GOINPTPLPE 660
 NPCTPUSBP MTVGNGSTG AICHDVIESI LQWREVSQGE APSSSKVPTV PLFIRISAP 720
 TLGFAMASL DAPGKVGAP PHLQKQSSR NSVSEEDLIT NDSLSLWGD EYGRSEPLT 780
 BTISFQALSF ANSCABSLIS KSPDASKAE SSENSTYMS GRSLSPFTV PAPTPTV 840
 VPGTVPFPT LSPQRTPLLA AGRQKQKXN CTCTGDNFS SASAGLHER TTGKPEFVC 900
 65 HLGFAFTIK QNLVITVTH GANNISARQ SKLAIENTNA LIGTQKRVB EIPFKELIAP 960
 GUNVDVFNK QYTSMBGLIG AVKTNESVI QSGGVPLTV SLGATSVVNN ATVSKNDGSQ 1020
 GSISALVRKP SATDGVKIQH PPHLEENKI AVS

Seq ID NO: 52 DNA sequence
 Nucleic Acid Accession #: CAT cluster

70 1 11 21 31 41 51
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 75 CTTGTGAGGT GAGGACACAT ATCAACAGT AGTTCTTCAAG AAGATCTGAG TCAAGTTT 180
 ACTTGAAGA ATTCTCTTCT CACTCTGDS CATCAATGCT CTGAATCTC CCACTTGCAG 240
 ATTCACAGAA GAGAGTGTTT CAAATCTGCT CTGTGTAAAG GGAUCTTCA CTTCTGTAGT 300
 TGAATACACA CAGACAGAG AAGTATCTGA GAATCTCTCT GTCTAGCATG AATGAGAGAA 360

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ATCCCGGTTTC CACGAGAGGC CTCAATGAGG TCTATATATC GACTTCGAGA CTTTGAACAC 420
AGAGTGTGTTT CTAACTGCTC TATGAAAGAAG AAGGTGTAAG TCTGTGAGGT TGAACGACAA 480
CATCACAAA GAGAGTCTGT AGAGATGATTC TGGTCTATTT TTTTAGGAG ATATTTCCTT 540
TTTACGCTTT GACTTCAGAG CAGCTGAAAT

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Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_001910.1
Coding sequence: 58..1249

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GCCCTCAGAG AGGATATCGT CCTCAAGAA GAAAGTGGCG GCACGAGCG AGCTCTCTGA 180
15 GTTCTGAGAA TCGATTAATT TGACATGATG CGAATGTGAC GAGTCTGCTT CATGAGACAA 240
GATTGCCAAG GAACCGCTCA TCAACTACTT GGAATGCGAA TACTTGCGCA ATATCTGCTT 300
TGGCTCGCA CCGAGAACT TCACTCTCAT CTTGCAAGCT GGCCTCTCCA ACCTCTGGGT 360
CCCCCTCTGT TACTGACTTA GCGCAGCGCT CAAAGAGCAC AGCAGTTTCC AGCCTTCCCA 420
GTCCAGACAA CACGAGCAGC CAGGTCAATC TTCTCTCAAT CAGTATGAAA CGGAGAGCTT 480
20 GTTCCGAGATC ATTGAGAGCG ACCAGTCTCT TGGTAGAGAA CTAAAGCTGG TTGTCGACAA 540
TTTGGAGAA AGTGTACAG CAGCAGACCA GACCTTTGAG GATCGAGAGT TTGATGGAGT 600
TCTGGGCTGG GGAATCCGCT CTTTGGCTGT GGGAGAGTGG ACTCGAGTAT TTGACAACT 660
GATGAGCTAG AACCTGTGAG ACTTGGCAAT GTTTTCTGTC TACTGAGGA GTACCCGAGA 720
25 CCTGAATTTG GTCCAGTCA CAAAGCAAT TGAATTTTGG AGCTATGAGC CACTCCCAAT TCTCTGGAG 780
TTGGGAGGCG ACTGTTATGT TGTGCTCGSA GGGCTGCCAG GCGATTGTGG ACGAGGGAC 900
GTTCCTCATC ACTGCGCCTT CGGACAGAT ATTACAGCTC CAARAAGCCA TTGGGCGAGC 960
CCCGCTGGAT GAGAGATATT CTTGAGAGTG TGCCAGACTT AACCTATGAC GGAATGTGAC 1020
CTTCAAGCTT AAGAGAGAT CTTATACCTT CAGCGCAACT GCTTACACCC TACTGAGCTT 1080
30 GTTGAATGGA ATGCAAGTCT CAGCAGATGG CTTTCAAGGA CTTGACATCC ACCCTCGAGC 1140
TGGGCGCTCG TGGATCTGGG GGGATATGTT CATTGAGAG TTTTACTGAG TCTTTGCGG 1200
TGGGAATAC CTTGTGGAGC TGGGCCAGC AGTCCCTTAA GAGGAGGCTT TGTCTGTG 1260
CCTGAGCTGT TGGATCTTGG AGCTGTGGAG ACTCTTAACT ATCTTAACT CACTCAAAA 1320
35 ACATGAGAT ACACACACAC ACACACATAT ACACAGATCA AACATTCGCA ACATTCACAC 1380
ACTCTCCACA CCGTCATGAT GAGAGATATA GTTATATCAT TCATATTTTG TATGATTTG 1440
TGTATTGAA TATGAGACAT GATATACACTT GATATATGAA AATTCGAGC ATATGACAAA 1500
CGAGAGATCA TGTATTAATA AATCCCTTGG CAATCCGACT GAGCCGAGC AACCCATCCA 1560
CACAGCGCCA GGCCTGTTTA TCTACATGTC TGCCCAATCC TCTCTCGAG TCCCATGCTT 1620
40 GTACCTGGAT CATTCTAAAG CAATTCGCGA GCAATTACAT ATTCTTCCA TAAATATTTT 1680
TACATCTCTT AATATACGA TCGGATTTCA AGCATCTGCC ATTGTCCGCG AATATTTGG 1740
CTGTTTGTG AGTGTGATC TTGTATTATG GATTCAGACA AGGCGCATAT ATTGCAATTA 1800
TTTGAATGTT CTTGATGCT CTTTCCATCT ACAGAGTTTA GCAATTGGA AGTTTGTG 1860
TTGAATCTCC GAGGTGATCT TGGACATGTT TCTCTGAGCT TATCTTCTT ATAAATTTGT 1920
45 AGTTAGATCT GAGGTGCTCA TTTTGTGACA AAAAGCTTTC CTAAGTGTGT CTGATATCT 1980
CTTGTGATCT CCGTGTGAG GCGAGATAT GCGTGAGCTT CXTATTTGCT ATGTGTAAGA 2040
CTGCTGGTGT GGTTTGAGT TCTTGCTTTT AATCATCAT TCACAAAGTTC AGCATTTT 2100

Seq ID NO: 54 Protein Sequence
Protein Accession #: NP_001901.1

1 11 21 31 41 51
MKILLILLV LLELGAQGS LHRVPLRHP SLKKHLRAS QLSFVKSIN LMIQPTESC 60
55 ENDCGAREE IYLDMEYGT TISGSPFON FTVI FDTGSS NIMVFSVCT SPACKTHERP 120
QPRSGSTYS QGRFSIQY TGLSLGIIA DQVEVELTV VCGQPGESVT EPQPTPDAS 180
FDLILGLQY SLAVGGYTF FDMNAQMLV DLPMSVYME SHFGAGAGE LIPQYHSS 240
FBSLNNWVF TGAQYVTF TGMVGGTVM FGSGLQALV DYTSLITGP SEELKQLQA 300
TGAATVDEY AVECANLVM PDVTITING PYTLSPATY LLDVFDKQF CSBSPQGLDI 360
60 HPPAGPLXIL GVPTRFYFS VFEGNNRNV LAPAVF

Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

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1 11 21 31 41 51
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70 TACACACGCA AGTTGATCAA GTTCCGCAAT AACCGTATG AGGATCTGCT GAGAGATGAG 180
GTCAACGTGA CCGCTGTGCT GCGCGAGCTT TTGCGGAC GCTCTGGGC CTTGTGTGAC 240
AGAAAGGCT CTTGAGGCTA CTTCTATCAC ATTCCCAAT ACCTCTAGCG TATGTGGGCG 300
CCTGATGCC TCAATGAAAT GGACCTCGAG CGACAGTACC TCTCCGAGG CATCTTGGCG 360
CTCAGAGATG TGGCTCTGTA GCTTGCGGTC ASCAANTATA CAGGCGGCG AGGCTCGAG 420
75 GTTGGCGGCT AGCTGAGTGC CAGTGGCTGG GATCTCTTCT GCGACATTA GAGTGGGCT 480
AGCTTCTCTT TCCACACGCG GGGCGATGCG ACCTTTGTGG AGCTGAGGCG CAGTGTGGGT 540
AAGTGGAGC CCGACAGCA TGGCGAGGT GTCGCTCTGG CTGATCTGAA CTTGATGCG 600
AAGATGAGCA TGTCTATGCG CACTGAGAT GCGCCACAGC GCTCTATCTT GGAATGAGC 660

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 AACATGECCT AGCCAGATCT CTGACACAG CCGCTCTTCC GGT CATCTCTC TAGAGAGACAC 840
 GAGACGCCCC TCATGAGAGA GCTCAATCCG CGGACGCGCT TGGAGCTGGA GGGCGGAGGC 900
 ACAGGGGGGTG TGGTGAACGA CTCTGACGGA GACGGGATGC TGGACCTCAT CTGTGCCCAT 960
 GAGAGATCTCA GCTCTGACGC GCTGTCCGTC TTCGAGAGCA ATCAGGGGTT CACACACACAC 1020
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 TGTGAGATGG AGCCGCGTGG ACACCTTGGC CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG 1200
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 GTGCTGAGGA TCGTCTACCC CCGGAGTAGG CAGACATCTC TGTCCAGAGC CCGACTGGAG 1320
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 ACACCTATGG AAGCTACAGG TGGCGGACCA ACAGAAAGTG CAGTCCGGGC TACGAGGCCA 1440
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 CCGAAGGCCA TCGTGTGACA CTACTTACTT AACATTTAGG GAGACTCTGA AGCCNAGCC 1800
 CTGTGCTGGC CAGATGACTG TATCAACAG AGAGAGGCTC CTCTCTGGA TGGCTCTTAC 1860
 ATTCGATGGT GTCTAATGAC CATACTCTAG CAGACAGATG TGGCCAGGGA GTGTGTGTCA 1920
 CTGCACAGGA AGTATAGGGA CTCTTATGCT CTGAGTTCGA ATCTGATGTC AGGAAGTCA 1980
 AAGAGCTATG TAGCTTACAC CAGTCACTTA ACTGTTTAGC GATCAATTAT GCACTCTGCA 2040
 AATGGGGAT TAGAATAGA ACTCTGGGTT TAGTGTGGAG ATTAGATTA AATATATTA 2100
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 GCGCTTTGTC AACAATGG

Seq ID NO: 56 Protein Sequence
 Protein Accession #: NP_060528.1

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1 11 21 31 41 51
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 RCDCTFVDA ASAGVDDPHV HGRVADALP NEDGKDIVY GNNNGPHRY LQNHGKVR 120
 RFDIASPKFS MPSPFRTVIT ADPRDQBLE IFPHNLYAS SSANLPFVLI RREHGRPLIE 180
 ELMPDAPLEB EGRGTGGVVT DFGGKMLUL ILSHGEMHQ FLGVFTRGQS FRRHVRVTR 240
 RTYGVAFARG AKVYFTRGQS GECNCTGTT SYLCEHNEF AHPLGKPKRQ SEVETNPEQ 300
 EYFVRNVAEG ERSVLEILEY PRHEDTLDP AELETPHNAS SSFCALETS FVSVTPMERT 360
 GASPTRAVG ATSPTRMAOP ANGLSASRHA PAPPTPLLL PLRLLLLELE LPLLRSS

Seq ID NO: 57 DNA sequence
 Nucleic Acid Accession #: AJ279816.1
 Coding sequence: 1..1962

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 TGTGTGATGG TGTGTGGGCG GTACAAVSEA CCGAACCTGG TTCTGAAGTA TGAACGGGCC 240
 CAGAGCGGCG TGGTGAACAT CCGGTTCGAT GAGCGAGCTC CACCCTACTA GCGCTCTGGG 300
 GAGCGCGAGC GGAACGCCAT CAGGTTCCAC GCTGTGGACA TCGAGCGGGA GAGCGCGGAG 360
 GAGATCTACT TCTCAAGAC CAGTATAGCT TTCTCGAGGG TGGCCAGATA CAGCGACAG 420
 TTTTTCAMPT TCCGAGATCA CGGTGTGGGA TTCTACTGGA GCGATAGAGT CAGCTGTGCC 480
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 ATTTAAATGG ACCGTGAGGC CAGTAGCTCT TCCCGAGGCA TTCTGGGCTT CAGAGATAC 660
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 CTCAGAGCA TGTCTTGGGA TATCTCTCGC GACATATAGA ATGGGCTTAA CTTCCTTTTC 780
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 CGAGCTCTCT CAGGACCAAC CCGTCTTCGC GTTATCGGTA GAGAGCAGCG AGACCCCTC 1140
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 10
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 TACATCATAG GGGATGCTCT AAGGCTAGGC CCGTGTCTGG GGCATAGCT GTATATCAGG 2100
 CAGACAGGGT GCTGCGCTCT ATGGCGCTTA CATTCAGTGT GGTCTAATGA CXTATCTTTA 2220
 GGCACAGAGT GTGCCCGAGG AGGTGGTGTC ACTGCACAGG AGATATGAGG ACTTTAGTGT 2280
 CTTGAGTTCG AATCTGTAAT TGGCTCTGCG AGACACTGTC TGACTCTTCA CCGTCACTT 2340
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 TTAGTGTGGA GAGTACAGTA AATGTATGTA AGACACTTGG CACAAGACT GGCACATAGT 2460
 AAGGCTCGAA TAAAGACAGG TGGCTCTCAC TGGCGTTTGT CACACAGG

Seq ID NO: 58 Protein Sequence
 Protein Accession #: CAC08451.1

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 EYELFNTSIA FSGVATYTDK LFRFRNRWE DILSDWVWA RVASLFAGR SVACVVERKGS 180
 GRYSYLIANY AYNGVFDAL IIMDFPESDL SRGIIALIDY AIDAGVSWTT GSGVSWPDI 240
 LSGSADITFC DNBIGWPLFL RSDIGDTFVD AAASAGVDDP HQHQRVVALA DFRFRKQYDI 300
 VYGHNDPFR LYLQMGTHKQ VRFRDIASPK FSPMSFPRIV ITADFNDQBE LEIFFNRIAT 360
 RSSSANLFR VIRRRKDDPL IEEELNPDGL BPDRGTGTGT VTDFDQDML DLIILGHESSN 420
 AQLPLSVFRNI GQFNSINLRY VPRTFRQDPA RGNVYVUTR KGSULRIIDY GSGVFLCME 480
 PVAPFLQSD EASVSEVTV DQWVREBPA SSGMSVLEIL LYPFRSDTQL DPAPLBSQSG 540
 FDSQENKCHM DTNECTQFFP VCPDRKPVCV NYTVGYRCKT LKGSVGYEPD NEDGTACVGT 600
 LQSGQSPRPRT TTPTAAATATA AAAAGACATA APVVLVGDLEH LQSVVKESSC PSC

Seq ID NO: 59 DNA sequence
 Nucleic Acid Accession #: F09NEHSH
 Coding sequence: 1..4794

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 GTTCTGAAGT ATGACCGGCG CCAAGAGAGCG TCGGTGACGA TCGAGCTCGA TGAGCTCGAC 180
 TCGACCTACT AGCGGTGTC CCGAGCGGCG GGGACGCGCA TCGAGGTCA AGCTGCGAG 240
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 CACGAGCGGT CAGCGGAGGT CCGTCTCGGG TCCACAGABA ACAAGCTCTGT GTGAAAGCTT 360
 CCACTTACGA CCGCTGCGAG CCGTCTGGGT CTCTCTCCGC TCGAGCGAGC GAGCTTTCTC 420
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 TGTGCGGTGT GACTGAGACC TACCAATGAA CAGABACCAT TTCTCTCGAG ACCCAATACA 540
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 GGCATCTGCG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCGAGCAATA TACAGAGAGC 840
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Sag ID NO: 60 Protein Sequence
Protein Accession #: P0ENSH

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PFTTDAELG LPTSLRDPG SLLQAAGPD RQREVVPVC CQRIEATHE PEPPLRPHS 180
QVATYDELK EFRKNHDI LSEYVWAG VASLPAGRV ACYDRAGGR YSIYIAHYA 240
GNVPDALIE NDPEADLER GILALRDVA EGVSKYTBG FSHTASPIG EISQRTERR 300
GDPPEADRE HSGDGTSQL CBLGKDDQF KEDAAVLEE QREKAAVSP RSVRTALGT 360
SKSLADKNE PFCCTSYSC APSPAPFPA RQAPQTPYA PLYTQLTNG ELAKGLARSV 420
PIRAPAPMD KCKGHAEPQ LAEALGAW ALSTTVVPGG LRSHEBSRQ QWMSRCLR 480
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GQREVAKREI GRETAGVRP LSHLVPNPF SCLEPLRGT VPGMLPQN GMYLDHRA 600
LANNQEKREI QHLDHDEPR FLKAKAREE PPGSGSPEE LQPSGLGSG PLYVQLGLA 660
SATHCGMEF LQGRVWVCP ILSSASDIF CENEGPNPL FHRKDGTFV DAAASRRPL 720
AFVHLKVLH CDPFSLICH LASTPSSCC GRTFYSLLQA PHCHGLSMS FRTGSRPHS 780
PLTQGLASS HRETLGLQS QAPPLCLAR APCVGLSLP TAYIVLMSA IPEGLMTBT 840
SEFVSNQSV FVTIVLQSN DGLHEDNCK VDTYVSNKI PHLVQSNP HGVVPTGLA 900
GQEGDLRIE GPFPGGGQA KVTGPLMKK QKRIEDHDA RCONAQSL AKEPASALG 960
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RGLRATITT KSKQVNSL RQKNTSNH VORGLKEIT TYRKQYLOL SLPQWATYS 1080
HUYKELQLO PTTTKRQYV VQSLPHQAT GSHYKELG RPTLTTRKG YLQSLPKKE 1140
AKSHRYQEK GLRATPTTRK RGYVQSLPQ KATYSNVIR RRGGLDIEE LNPDMLEPE 1200
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Sag ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_000584.1
Coding sequence: 75..374

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AATAAAAA AAAAAA

Seq ID NO: 62 Protein Sequence
Protein Accession #: NP_000575.1

1 11 21 31 41 51
MTSLAVALL ALFLSARLC GVALPRKAL ELRCCTKTY SKPFHFKFIK ELRVESGFH 60
35 CMFTETIVKL SDRELCLDP KENWVQVVE KFLKAENS

Seq ID NO: 63 DNA sequence
Nucleic Acid Accession #: E05 sequence
Coding sequence: 52-1146

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GAGTGTGAC AACTTAAGGT TTCTTTAGC AGCTTCAAA TTAAGCTTT GCAAAATCA 1080
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GACATGACCA ATGAGAGCTC TTCTAGCC CAGAGATAT TTTGTTTTC AGTTCTCT 1260
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 AGTATGAG

Seq ID NO: 64 Protein sequence:
 Protein Accession #: NP_036338.1

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 LFWNDHVF YKQDTRFKLL GDLGRDWBL THTLATVDSB GYVLCVSHR GWFNDHRLTV 120
 SLSEVPKVT TTVIVTPTV TTVRTSTTV PTTTIVPTT VPTMSIPTT TLVPTMTVS 180
 TTTSPPTTS IPTTSPVPT TTVTFVPPH PLPRQHEPV ATERSSPQRA STHTPLTQA 240
 IREPTSPSL YSVTNDNDT VTSSDGLHIL NWQPLGLBI SLLRATGTH LYATCTSVL 300
 VLRLALVLI ARKPYFKFVE QQLSVFSLB QIKALQWAVE KKVQADNIY IBSLYATD

Seq ID NO: 65 DNA sequence
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	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 4980
60	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5040
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5100
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5160
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5220
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5280
65	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5340
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5400
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5460
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5520
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5580
70	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5640
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5700
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5760
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5820
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5880
75	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 5940
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 6000
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 6060
	CGCGCGAGC CAGTGTGCGC CCGAGAGGTA AGGCTGTGCTG AGAGAGGTA CCGAGCGCG 6120

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GAGGCGAGTT TCCGCGAGCC TGCAGTGGCT GTCTCTGAGG ATCCCTGGAG TTGCGAGTAC 6180
 CAGACATGGT GGTCTGGGCCC CGGGGGCCCC AGCTCTGCTC TTGCGAGCTG GCCGCAATAG 6200
 GGGCGCGGCC GAGGTGTCAT CTGTCTTGCT GCGCGGCTCT GAGGCGCTCG TGGCGCGTAG 6220
 TGAAGCTGAA GAGGCGAGG GAGCTCGACG GAGGAGCTCG GAGGCTTACG GTGCGCAATG 6240
 5 AAGAGCGGAA GCGAGAGGAG AAGAGAGGCC GGGCGAGGAG CTGGAAGTTC ACAGACATGG 6420
 GTGCGAATGT GTACATCTCT AGGGCGAAGG TGGAGAGGAG GTTTAGAGCT CTGACGTGTG 6480
 AAGAGCGGCA GAAAGCGCCA GTGGGGAAGG GGTGGAAGCA GCGGAGAGCT CTGGAAGAAC 6540
 CCAAGCGCCC CAAGAATCTG TTCAACTGAT TTGTGACAG GCTGAAGAGC TTCTGTCTCT 6600
 TCACTTGAGG CGGTATCTCG GCGACCGGCG TCGTGTGCTCT ACTGTGTGCT CTGACGTCCT 6660
 10 TACTCTCTCT GGTCTCTTAC ACCATCTCTG GCGAGATCAG CAGAGTCATC TTGCGTCCCC 6720
 TCGCAAGTGT ACTCTGCTG ACTTGTGACA CTCAGCCAGG GTGAGCAAGC TCTCATGCTC 6780
 GCTCTGAAAT GTCTTCTCTA CCGATGTGAG CTAGCCCGAG GTCTATGTCT TCTCTGAAAT 6840
 AAGCTATACA CAGCG

Seq ID No: 66 Protein sequence:
 Protein Accession #: B08 sequence:
 1 11 21 31 41 51
 20 MCKREWHNPR SSHQGCALFW RRRHGPPLVR SVPMGSSGSG WAWASKPRPA PLSCPRICCP 60
 SPQPCGPAY TGTVLRYLTLS FLMGDLVFE QLVYDGRREH LGEETPLVII NVTDKRPKP 120
 PFTLQALAA PRVLYLDPY GRPEOFFPL RHPNAGELT LAAPQLIED YGRLEPSVP 180
 SEVSPQLAP LVEPHSRSLR LPNVPCLVR SFRVEVLWQ LRLGRVHLL EVSQPVVLE 240
 VAGQVSEV LASYRESPIF TELVRHLTVV FKUTAPLHP QLPSPQYLQ PPLSLVIER 300
 25 RAQRHVLVG SHIVPMLRF TFGHEDPFE ESDHEBETG MFKQKQKQ SLDEPLAEG 360
 IRLGLLHNF DEREDGDDG DDQDNLINLV QETQDQIEB VKRTVEPKTA YALTKIVRS 420
 LKEEPDSEI WLVNPLYLGG QGQGGQGGGE BGSHLVGKF KOSPLYPFS EAVLSEPII 480
 SRIGPQRNPI KLLVRYVYVK ATSLAPADPM GRADPVVVS AGRRQDTKE RYIPKLNPI 540
 PGEILELIS LPARTELTVA VFEDHLVSD DLIETHIDL EHRFYSHHRA NCLGASQTEV 600
 WVOQGPQEFF

Seq ID No: 67 DNA sequence
 Nucleic Acid Accession #: NM_002449.2
 Coding sequence: 223..1026

35 1 11 21 31 41 51
 GAGGCGGGGG GCGAGCTCTT CCGGAGAGAC CAATCAGGGG CGAGCTCTCT CTCTCGGCAC 60
 GAGGCGGAG GCGAATGAGC GCGCGGCTCT TCCCACTTCC CCTCGAGAGA AAGGCTCAGC 120
 40 TCCCGGCGCG CCGCTCCCGT CTCCGAGACA AAAAGTTTGG AGTCCGCGCT GCGCGGTGAC 180
 CAGCGGAGTC GCGGTCGAGG AGCTATGATG GCGAGAGGAG CTATGAGCTT TCGCTCCAAA 240
 GCGCATGACT TGTGTTGCCC GAGCAGGAGG GCGCCAGGAG TGGTGGCGCG ACCGAGGCCG 300
 GCGCTGGGCG GCGCGCGGAG GCGCTCGAGG GAGCGCGCG TCGAGATCTC CAGCTCGGCC 360
 45 TTGACGCGSG AGGCGCTCAT GTCCGACAG AGGCGGCCCA AGAGATCGCC CGCTGTGTCT 420
 CCGGAGGCG CCGTGGCGCG GCGCCAGCTC GCGCGATCTC TCGTGTGGGG GCGACGCGCT 480
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 GGAJATTCAG AAGTGTGAGC GCGCTGATG CAGRAAGG GCGCATATG GCGTCAAGCT 600
 AAGACATAG GCGTACACAC CTGACCGCTC AGGAAACACA AGACCAATCG GAGCGCGCGC 660
 AGCGCTTTTA CCAATATCCA GCTCTCGGCG TCGGAGAGCA NGTTCCGTCA GAAACATGAC 720
 50 CTCTCATCTA CAGAGGTGCG AGAGTCTCTC AGCTCTCTGA ACCTCAGAGA GAGCCAGCTC 780
 AAAATCTGAT TCGCAAGCCG AAGCGCCAG GCGAAAGAC TCGAGAGGCG GAGTCTTAA 840
 AAGCTAGAA TGGCTTCGAA ACTATGCTTA CCGTCGAGCT CTGAGTCTCC CTTCGCACT 900
 AGCTCGCCCC TCGAGCAGC GTCCAATAC GCGAGGTCTC ACCGCTTCCA TAGACTGTG 960
 55 CTTCCATCAT CGCGCTGGGG ACTCTATGCG AGCGAGTGGG GATATGGCAT GTAGCACTG 1020
 TCGTAGAGGA GAGCCAGTCA ATAGACTCCA TGAAGTGGG TGTGTTCAA GAGTCTTAA 1080
 TCGCTCTCGT CAGAGGATTA GCGAGCGAT ACTCTGCGC TCGTAGCGCG TCGAGTTTAC 1140
 ACCGACCCG CTCTAAAGCG TACGTGACAG GCGCACCA CATACTGATA ATTTGTTTCT 1200
 GTAGGCGGAG GCGACAGGCC CTGCTTTTCT TGTGTGACCT TCGGAGTCC CCGCTTTTCT 1260
 60 CCGCTGACAA AAGACTTGAG TCTATGTTT TTTTGGATAT GATGTATAT TATATATG 1320
 AAAATATCTA CAGAGCTGAT TTATCAGCAG AGTAAAJAT TCAAAATATT TTAATAAGCA 1380
 AAGTCAATTT GTTGATATTT CTAAAGAGG AGCAAAAT GCGAGAGCG CCGTGTATTA 1440
 GTCTCGACCG TCGCTTTCAG CTGAGAGGCG CTGATATCTT ATTTGCTAAA AGTGTATTA 1500
 GCGCTGTGSG CTTCCCGAAG GCGCTCGGCG GCGCTGCGG AAAAAAGG AAAAAAGC 1560
 65 ACAATGTGAG ACCGAGAAAT TATTGATAT GAGAGATTA TGAGCATGCG TCGTGCAG 1620
 CCGAGGCGTC CCGAGAGAGG AGAGGCCCGG GCGCTGTGAG ATCAAGTGA ACCGATGA 1680
 TATTTGTGCA TTATCTTTCG ATTAAGAGAA ACTGTTTGA AGCTCTTGA AGAGCGGCTC 1740
 GGTCAATGCG GAGATCTTGA AGATGAGAG GCGTGTGATG CTACATAGTT TGTTCATCT 1800
 70 TCGCGGCCAC GCGGACACAT ATTTTTAAAG TTTTAAAGAA CCGGCGCAT ATTGCGGCG 1860
 CGAGACATAT ATAGCCGCTA CCACTGACAC CTGAGCTTTT TTAGAGATAT TTTGTAGAG 1920
 CCGATCATCT GATGTGAGAG AATCGGTGAA CCGTCTGAG CACAGATGA ATGAGAGCT 2040
 ATGCTCTCTA ATTCTCTGCA AGGCTGTGCG TAACTTGGG GCGAGATTC CTGCAAGAAC 2100
 75 AGTACCTCTC CATTGCAAG CTTCCAGAT TCTCATTTT AGATATNG AGATATTAAT 2160
 GTTAAACCT GTAGAGAGAT TTATGACCT TCTGACCTA CAGATGTGCA AGTGTCTTGT 2220
 TCTGAAATAT ACTGATGACA TGTCTCTCA CAGATGTGCA AGTGTCTTGT 2280
 TGTATATTT GTGCTTAAAG AATGATATC TTGTAGCAT TACCATATC TAAATATTT 2340
 TGAACAATTA GTGCTTAAAG AAGGAAAAAA AAATATATCT TCTCTGTGTG TGTACCTGTT 2400

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GTAATAACAG TCAATTCCCA GATTGGCTGT GATACCTCTT ATTGGACTTT TGTGAATGCT 3300
 TTTTCAATTT TGGAGAGCAT TGCACCTTAT TTGGGACATCA TTTTGGACTT TCAATGATGCT 3350
 GGAATACATG TTCTCTTTCC ACTCCGATTT GATTTTACAG GCAACAGCTT AAACGCTGCT 3400
 AGACAGCAAT ACATCTGTTT AACATACATC CTGACCTGCT CTGTGTGCTT ACTACGCGCTC 3450
 GTTGCCATCTC GATTCTCTCTC AATGACATCT TGGCCATCTCG AAGTGATATA GATCCAGAG 3500
 CATCCGACAGC GGTGTAAGGC GGAACGACAC TGGCAGACAC GACGACAGAT GTTCCGCGGC 3600
 GGGGTTCGAA CGCGGCGCTC GGGCTAGGCC TTCTGCGACC AGCGGACACTA CCGGCGACT 3650
 ATCTCCGCGC GCGGAGCATC CCGAGAGAGC CCGTCGCGCC TGTATGCCAT CCGTGGCGAT 3720
 GGCACCGCGG AGTACGCGC CACCGCGGAC AGCTGA

Seq ID NO: 70 Protein Sequence
Protein Accession #: NP_09594.1

1 11 21 31 41 51
 15
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MSTERDSETT FDEBQDNDE VVPEYDDETE DELODQGSAN EPENNVNRE ABENREFFRK 60
 ECTWQVKAND RYVHQPHFM NTKFLCKES KYANNAIKTY KYNAPTFIM HLFBOFKRAA 120
 NLYFLALLIL GHVQOISTIA WTTLVPLVL VGVPTAIKDL VDVVARHKVD KEINMRTCEV 180
 IDGRFQVAK VKEIQGVDFI ELKNDPFA DILLSSSEP HSLCVETAS LQGHNTMFK 240
 HSLBTGQL QREDPLATF GTTCSEPM ELKFTTFL WRNTEFLDA DKILLRCVI 300
 RNDFCHGLV IFAGADTKIM EISGKTRFKR TKIDVLAHYM VTTIFVLLI LSAGLAIGHA 360
 YNEAQVNSB WYLDGDDDT PSYRGLIFM GYIIVLATYV PISLYSVVEV TRLOQSHIFN 420
 NOLAQVYAEK DTPAFAKTT LMBGLAQIH IPSCGTLZL QHMYFKKCC IMQVYDHR 480
 DAQGRNKKI RQVDFSHIT ADGLAFTM HIGPCEGSH VLEQIQSK EPVQGFPL LAVCHTMWD 540
 RTDQGLAYQA ASPDEGALVN AAKRFQPAFL ARTQWTTIS ELGTERTYHV LAILOFNSDR 600
 KRMSIYRTP ENIKLVCAG ADTVIVBRLH RMPFTQSGD DALDI PANET LPTCLCLCKE 660
 IEKEFPENM KCPMAISVAS THRODALDV YSEIKDLIL LQNTLSEEL QGVPTETIK 720
 LKADIKIYV LQDQGEKSH HIGPCEGSH EPTTCVGBD DMLLRBME NQNRNGSYA 780
 KPAPVQESF FPGCNALIL ITGSMNELL LEKKTKMKI LKLFRTTEE ERMRTOGSR 840
 RLEAKBQRO KNFVLCEBC SAVICCRVPT XQKAMVDLV KRYKAITLA IGDGANDVM 900
 IKTAHGVGI SGGQBMAMM SSSYSPQGR YLQRLLLVHG RMSTRMCKP LRYTTGHTA 960
 PTLHFWYFS PDSYAGATY EDVLAHVM LSTVPLFLA GLLQAPVDSI LRLPLMI 1020
 VGGDLPLRY KFFPLWLLD VLSMILFI PLGAYLQTVS QDGEAFSDQV SFVATIASAL 1080
 VITVNPQISL FTSYMTFNA PSFSGIALY GIMPDPHSA GINVLPPSAT PQTGTASAL 1140
 ROPYVWLTII LCVAVLTVL VAIPLSMTI NPSSEDIQK HRKLKAEBO WQRQGVNFR 1200
 GVSTRSAYA FSHQGVADL ISSGRSIRKK RSLDRLVAD GTAYRTGDS

Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_138784.1
Coding sequence: 334-816

1 11 21 31 41 51
 45
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GGGGATACGG AAJACGAAT AAJACGAAT AACACGACT ATTGTATATA AGAGAAGCG 60
 GTGTAAATAT AAGTGCTCT GAAATGACTT TTTTCAAGA GAGAGAGGA GCCAATATAT 120
 CTACTCTTCT TANGAAGCTG AATTAATATT TGGATTTCTT TCTTCTCAA GCTGAGACAT 180
 GATGGCCAAA AAGGAGTTGC TGTGATTGGA GCTGGGAATTA GCGAGCTGGG GCGCATCAAG 240
 TCGTCCCTGG ATGAGATCTC GAGGACCAAC TGCTTTGAAA GAAATATGTA TATTGTGAT 300
 CTCTGGAANT TCGAAJAAA TCTCTCAGG AATATGCTA GTATCTACAA ATCTGTACCC 360
 ATGCAATCTC CCGAGAGAT ATGTGCTTTC AGTACCTTCC GTATCCCTGA TCAATTTCCC 420
 AACTCATGTC ACACTCCGAA ACTCATGACG TACTCCGGA TGTATGCCAC ACACCTTGSC 480
 CTTCTGAANT TCACTGCTTT TAAAGCTGGA GTCCAAAGTG TGAAGAACCA CCGAGTTT 540
 TCTATCAATG GACATAGGGA TGTATTGTGA GAGA CTGAG CACACAGATC CACTATACAC ACTTCAGTCC 600
 TTTGATGGG TCTTGTGTT GATGTGACAC CACACAGATC CACTATACAC ACTTCAGTCC 660
 TTCCAGGCA TTAGGAATTT TGAAGGCTGT TATTTCGATA GTCCGGAATA CAAGAFTCCC 720
 GAGGACTTTT CAGGAGAAAG AATCATATGT ATCGGCAATG GAATTCGAG AGTGERENT 780
 GCGGTGGAGC TCACTGTGTT ACCTAAACAG ATGTGCGGAG TGAAGACTA GATTCAGCT 840
 CCGCAGACTC GAGAAATPAC CACATACCA ACAATTAAT ATATTCTCTA ATTGAGTCAG 900
 CATCGACACA GTATTACAAA TATATTACAG AAAATTTGGA AGAGGGATTC TGTTTACOTT 960
 CATTTAGGCA GGAACATPAT GTGAGCAAT CAGATGTATT AAGTTTCTTA ATGTTTGTAT 1020
 CTTTGAGTTG ATGCAACACA TGAAGTGGGA GTCTATGATA GTTATATG TGBATATTC 1080
 CTTCTAANTY TAATCTCTTA TTTATATG AACCATGCT ATGTCAATGT ATTTTCTTAT 1140
 ATTTTAAAT AGTAAATCAG AAACATGTAA ACTAGTGAAT ACATTTTCTT ATTTTCTTAT 1200
 CAGAAATTTG TTGTCATAGA TCGACGCTTT ATCTGGAAT CAGTGGGACG CACTGTGTGA 1260
 GCGACAGATG GCGACCACTG TGTATATATT TACCACTCTA TCTCTTAGTG CACACACT 1320
 TAATCTGCTA TGTGTGGTG CATATGATTA AATATATC TGTAAAAA AAAAAAAA 1380
 AAAAAAAA AAA

Seq ID NO: 72 Protein sequence
Protein Accession #: NP_670139.1

1 11 21 31 41 51
 75
 80

MFSIKYKVTI NTKSENCFPS DPFVDFHFM THNSKIMDY RMVATYHGL LAYIREKTEV 60
 QPVKHFDPFS ENQGVVVVEE TEKKQETLAV DGVLCGSHH TDPILPLQSF PGIKREHCY 120
 FRESRYKPE DFKSKRIIVI GIGNGVNDIA VRLSRVAQII

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Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

5	1	11	21	31	41	51	
	ATGATGAC	TTTCTCTG	TGTGAGTG	AGGCGAGG	AGCTGAGG	GAGGATGAG	60
	CAAAAGCTT	CAATGTGG	AGATGATG	GATCTGAA	GTAAGGCTT	GAGTGTGAG	120
	GTCTGTGCA	CTGTGATG	AGAGGAGCT	ATCTTATG	AGAGTGCT	TAAATATTG	180
10	AGAGAAAG	TGAGGACCA	GATCTGCTA	CTCTGTGTA	CTGATATGA	GGCTTGAAG	240
	GAATGTGTG	CTGCTGCTG	ATCGGAGG	AATGAGGAG	ATGAGCTCG	TAAAGCTCTG	300
	GACGACCTG	CAGAGCAAT	GATCATGAA	GACGAAAT	GACGAGGAG	AGAGGAGG	360
	TAGGAACT	GGTTTGA	AGATTTCT	CGTTGAGAA	GTGAGCTGA	GATTAACATA	420
	AGAGGCTCG	GTGCGCTCG	AGATGGGTT	CAGAGGTC	ACAGAGGAC	CACCATGCG	480
15	AATGTGTGT	GTGCTCTCT	CAGCATTC	TCTGCACTC	TGACCTCTT	CGGATGGGT	540
	CTGAGCACT	CTGAGAGG	AGGCGAGCT	GTACTCTTG	AACCTGGAT	GGAGTGTGA	600
	ATGACAGCG	CTTGTGCG	GATTAACAG	AGTACGAG	GAAGTGTGG	GAAGTGTGG	660
	ACGCAAGCC	AGGCGACCA	CTGTGTCAT	AAAGGCTTG	CAAAATGAA	GGAGTGTGG	720
	GAGTTTGG	GTGAGAACAT	ATCCAACTT	CTTCTCTAG	CTGCGATAT	TTACCAACTC	780
20	ACAGAGGCA	TGAGGAGAG	CATCCATGC	CTCAGAGAG	CAGAGGAG	TCTTCACTG	840
	GTACCCATG	CTTCAAGCTC	AGGCGCGG	GTCTGTGAG	CAATCTGAG	TGAAGAGCT	900
	GACAGATGG	AGAGGCTTA	TGACCCGAG	ATCTGTGAA	TGAGAGAG	AGTCAAGCT	960
	ACGATGTGG	CCGCTGTAG	CTTCTTCTT	GTCTGTGAG	TAGTCTAGT	CGTGTAGAA	1020
	TCAAGCACT	TACATGAGG	GGCAAGTCA	GAGAGACTG	AGGAGCTGA	GAGAGTGTG	1080
25	CAGGAGCTG	AGGAGAGCT	AAACATCTC	AAACATAT	ATAGAGATT	CGAGGAGAG	1140
	CAGGAGCTG	GA					

Seq ID NO: 74 Protein Sequence
Protein Accession #: NF_003652.1

30	1	11	21	31	41	51	
	MSALFLGVGV	RAEAGARVQ	QNPVSGTGT	TDGSKLEGN	AANTWPESS	ITIEDAIKYF	60
	KEKVFQHLH	LLHAGAGAG	RAEAGARVQ	NEADLEKAL	DLHLAGMIMK	DIHMDHGGQ	120
35	TRVFLSEFE	ELKSELENDI	ELRLALAGV	QVHEKGTIA	IVYSGLEIS	SGILLVLMWG	180
	LAFFTEGSL	VILLEPGKELG	ITVALTGTS	STWDYKQKW	TQAGADHLV	KSLDKLSEVR	240
	RFLGEMISNF	LSLAGTGYOL	TROIGKDIRA	LEDRANLGS	VPMASSEPR	VYFVLSRES	300
	EQVERVIEPS	ILHSGRVELG	TVAPVSEFL	VLDVVLVPS	SKHLIDAGS	ETAEELKKVA	360
40	QELSEKLKIL	NNYKILQAG	DEL				

Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

45	1	11	21	31	41	51	
	ATGAGGAGCT	CTCGAGAGG	CAGCAGCGCC	CTCGGCTCTT	CGAGCGGCAAT	CGGCGCCGCA	60
	GCACAGGCCA	CGATGATGCG	GGGCTCCCTT	CTCGCTCTTG	GATTCCTTAG	CACACCCACA	120
	GTCTAGGCCA	AACAGAGGCG	CTCGATCTTC	ATTGAGCAAT	ACCGGCAATG	TGACCTGTCC	180
50	ACCGGCAAG	TGCTTACTGT	TGACCAAGTG	CGAGCGGAA	CGTATCTCTT	TGACCACTTG	240
	ACCAACGCA	CGCTGCGCT	CTGCGAGAT	TGCGCTGTGG	GGACCTTTAC	CGGCAATGAG	300
	ATGTCAGTAA	AGAAATGCCA	TGACTGTAGT	CAGCAGTGCC	CATGCGCAAT	GATTGAGAAA	360
	TTACCTTGTG	CTGCTGTGAC	TGACCGAGAA	TGACTGTGC	CAGCTGGCAT	GTTCGAGATG	420
55	AAAGCTACT	GTGCGGCCCA	TAGGCTGTG	CTGCTGAGT	GGGCTGTGCG	GAAGAGAGAG	480
	ACMGAGACTA	AGGATGTGCG	GTGTALACAT	CTGTCTCGG	GTACTCTCTC	AGATGTGCTT	540
	TTCTATTGTA	TGAATTCGCA	AGCATACACA	GACTGTCTGA	GTGAGAACT	GGTGTGATC	600
	AAAGCGTGGA	CCAGAGGAGC	AGACAACTC	TGTGCGCAC	TCCGCTCTCT	CTTCAGCTCT	660
	ACTGCACTT	CCGCTGAGCG	AGCCATCTT	CAACCGCTTG	AGCATATGAA	AAACCGGCA	720
	GTCTTCTCTC	CGATCTTATG	TCCGCTCTCT	CAAGCTCTGA	CGATCTCTGA	CTTCTTGCC	780
60	CTCTGTATGA	CAGAGTACT	GATGAGCTAC	CAGAGAGGCA	CACTGCTGGA	CAACCAAGAC	840
	TGACAGAGG	GGAGAGAGCA	GTGGAACAG	ACCTTCAGGT	AGTCAACAC	AGTCAACAC	900
	CAGCAGAGCG	CCGACAGGCG	ACACATCTG	AGGCTGTGCT	GTCTCATGGA	GGCTCATG	960
	CACAGAGATT	TGAGATCTCA	CTGAGAGGCG	CCGAGAGGCG	GAGCTCTGAG	ACAGAACCTA	1020
	GTCTGTGTG	TGATTTGTGT	GTGAGTATC	CGAAGAACT	GAGGAGCTCT	GAAGAGGGG	1080
65	CCGCGGAGG	ATCCGATGTC	CATTGTGGA	AAAGCAGAGC	TGAGAGAACT	CATGACTCTA	1140
	ACCGGAGGC	GGGAGAAATG	GATCTACTAT	TGCAATGAGC	ATGAGTCTCT	TGCAATGAGC	1200
	CTGTGAGCA	CCGAGAGGCG	TAGGCGAGG	AAAGTATCTT	ATAGCTTCT	TGCAATGAGC	1260
	AGTGAAGAGG	AGGTTGTGTC	TTTCTCCAT	GGTACAGAG	CCGACAGGCA	GGGCGCTTAC	1320
70	CGGCTCTGCG	AGCAGCTGAC	CATCTGAGGC	CCGAGAGGCG	CGCTGCGGCA	CGTATTGAG	1380
	CCGAGCTGCG	AGCAGCTGAC	AAACATGTTT	GTGAGAGAGG	TGTGTGTGCT	GATGAGTAC	1440
	ACGACCTGCG	TGAGATCTCA	CTGAGAGGCG	CCGAGAGGCG	GGGCGCTTAC	GATGAGTAC	1500
	ACGACCTGCG	CCAGCCGCA	CGGAGAACTT	GAGATATGCG	CTCTCTGATC	GGTGAAGCT	1560
	TGCCAGAGAG	AGGATACGCA	GGGCTCTTCT	CGAGATAGAT	CGAGGCGCTT	TCTGCTCTCT	1620
75	GATCTCTACT	CGAGGCTGTC	CTGCGGCTG	ACGAGAGAGG	GGTCTCTCTT	TACAGAGAG	1680
	AGAGAGAGCA	CGAGGCTGTC	CGAGGCTGTC	CGAGGCTGTC	GGTCTCTCTT	TACAGAGAG	1740
	GATGAGATCT	TGATCTCTCT	AAATCTGAG	GGGCTGCGG	GGTCTCTCTT	TACAGAGAG	1800
	CGTGAAGAGCA	AACTAGAGCG	GCTATTGAG	ATTATTGAG	TGAGAGAGCA	GGAGGCGG	1860
	CGTGAAGAGCA	AACTAGAGCG	GCTATTGAG	ATTATTGAG	TGAGAGAGCA	GGAGGCGG	1920

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CAGACCTCC TGGAGCTCTT TTATAGCAT CTCTCTGACC TGCTGTAG

Seq ID NO: 76 Protein Sequence
Protein Accession #: NP_055267.1

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1 11 21 31 41 51
KOTSPSSSTA LASCSEIARR ATATNIAGSL LLLGFLSTTT AOPRQKASHL IOTYRIVDRA 60
TQOVLTDCK PAGTYVSEHC TWISLKYCSS CPVGTPTRHE NOIEKCEHCS QCPCHPMIEK 120
10 LPCAALTDRE CTCPKPFQS NATCAPHTVC PVGMVREKKG TETEDVRCKQ CARGTFSQVP 180
SPWKECAVAT DCLSNLVMI KQYKEETDHW OCTLSPSSSS TSPSPQTATIP PREPHEHTRH 240
VPSSTVYPK HESTSESSA SVRPEVLSI OBGTFPVSIS SARGEDVHWK UNLQVQVNE 300
QQRHREHL KLLPHEHTAT GKSTSTPIGO FEGKPRQWIL HKHFDIHEHL PMWVILFLL 360
VLVIVVCSI REKSRITLKG PRQPSAIVE KAGLKSMPT TQREKMEYY CNKHGIDILK 420
15 LVAAQVSSQW KDIYQFLCA SREVAAPSN GTTAUHERAY AALQHWITR PRESLAQGIS 480
ALQRHREHV VEKIKELMD TQLUEIKELA LPMSPFLSE SPIPSHAKL EKSALLVEP 540
SPQDVKHTT VQESRLEAD DTSQSSSL SNKQSTYKX KUTVLQVRYE LDPCDLQIPF 600
DMLHLFLPE ELRVISEIPQ AEDKLORLFE IIGVYQREAS QTLDESVYSH LEDLL

Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: NM_003105.3
Coding sequence: 123..6767

25 1 11 21 31 41 51
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TGCGCTCGCG CTGACGATTC TCTCTGGGCG GCGGCGGCAC CTCAGATGAC GTTCCGCCGA 120
ACATGCGCAC ACCGCGAGCC AGAGAGGGAT OGGACCTCCC GTTCCATATC AGCTCATGTG 180
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WO 03/003906

PCT/US02/21338

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Seq ID NO: 78 Protein Sequence
 Protein Accession #: NP_003096.1

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Seq ID NO: 83 DNA sequence
 Nucleic Acid Accession #: NM_006012.2
 Coding sequence: 553..1095

WO 03/003906

PCT/US02/21338

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1      11      21      31      41      51
1  TCTCCGCGA  ACCTTCCCTT  CCGTCGCTCC  GTTCCGCCCC  AGCTGCTAGC  CTCCGACTCC  60
2  CTCCGCCCC  CAGGCGCGCC  CTCTGCGCTT  GCGCGAAGCA  AAGTGAGMTA  ATTACAGCGT  120
3  TCTGTGTTCT  CTGCGTACGT  TCTTCTCCCG  CTGTGGGCTT  GCGCGGCTCT  CGCTGTCTCT  180
4  CTCCGCCCC  GCGCTCTGTT  GCGCCCCCCC  CTCTTACGTT  CACTCTGTCT  CTCCACACTT  240
5  CTCTGCGCCC  CTGTATCTTT  GATACACACG  CTGACCTGAT  TCCCGATATG  TTCTTCCGCC  300
6  CCGAAAGTGA  CAGACTTGG  CCGACCTCAG  CCGDAGACGA  GCGGCTCTCT  CTGCGACAT  360
7  CAGAGCAATT  CTCCGCCCC  GCGCAAAAAA  AAAAGCATCT  CCGCGCTCT  CGCCGCTCGC  420
8  ACATTCGCCC  CCGCGAGCTC  GCGCTGCGAG  AGGATGTGTC  GCGAGGAGGG  GCGAGGAGGG  480
9  CCAAGCCGCG  CTGTTGTTT  TGACACAGCG  AGCAGGAGAG  TGCGCGCGGC  GCGTTCGAGT  540
10  TCCAGAGAC  CAGTCTGAG  CCGATCTGAG  AAGTCTAGTG  TGCTTCTCTT  CACTTCTCTT  600
11  GCGTTCGCT  GATGTCGAT  TGCTGCTTAC  GCGCCAGTGT  AGACCGCTGT  GCGGCGGAGG  660
12  CTGCTGACGA  CCGTCAAGT  GGTCTGTGGG  GACCGCGGCT  TCTACTCGAG  CAGCGCGGCA  720
13  AGCGTGTGTA  GCGCTCGCAG  CGTGGGATCT  GTTAAAGAGT  GCTGTCTCG  CAGCTGTGAC  780
14  CTGCGGCTCC  TGAGAGGATA  CTGTGCTAC  CCGCGCGAGT  CCGAGAGGAA  GCTGTCTGAC  840
15  CCGTCCGCG  TGCTTCCGGA  CAGTCTCCCC  AGATACCGCG  TGCGCAAGTT  CTTCGATAT  900
16  GACACCTGGA  AGCATCTCC  CAGAGCGCTG  CAGAGGAGCG  TGCGTCCGCT  CTGCGTGGCC  960
17  GCGCGGGGTC  AGCTGCTGCG  CAGAGAGCTC  GAGGCGTCT  GCGAGGCGCA  AGCTGACCT  1020
18  CCGCTGATTC  CTCTACCCCA  CAGACAGCTC  GCGCGAGGCG  GCGCGCGCG  AGAGATGGCT  1080
19  AGCATCTGGA  AGTGGAGAA  ACTCGTGCAA  GTGTGACGCT  GCGGCGCGAC  AGCTCGGAGC  1140
20  CTCTCTCTGA  CAGCGAGCTC  TTCCATCAGG  TTCCATCCCG  AAATCTCTCT  GCTTCAAGT  1200
21  CCGCGTGGGG  CTCTCTCTGA  CCGAGTCCCG  GTGCGCGCGC  TCCCGGAAAC  AGGCTACTCT  1260
22  CTGCGGCCCC  CTCCATCGGG  CTGAGGAAGC  ACAGACGCT  CTTCGACAT  GTACAAATC  1320
23  GATTGCGTTT  AAACGCGCTT  CACATACCTT  CCGCCC

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Seq ID No: 84 Protein Sequence
 Protein Accession #: NP_006603.1

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30     1      11      21      31      41      51
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2  RRRGIVREIC CRRSGLRSL  EYCCAPKAS  ERVSTSTPTV  LPHITPFPV  KPFYVDTWK  120
3  GSTQLRRLGL FALLRARRGH  VLAKELEAFR  BAQRHFLIA  LPTQDFAHGG  APPHMANRKL  180

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Seq ID No: 85 DNA Sequence
 Nucleic Acid Accession #: XM_092643.1
 Coding sequence: 1-8352

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3  CTGAGCATCA  TTGACAGGGA  GTAGACAAAG  AGCGACACA  CAGGCGAGCG  CTTGTGACAT  180
4  CCGAAGAGCC  TGCGCTCGGT  GATATACATG  GAGAGAGCAG  CCACTGAGCC  TTCTGTGATG  240
5  ATAAACATCT  TCATCTCGTG  CCGTGAAGTG  CCGAGAGATT  CCAACCAAGG  CAGGTCTAAC  300
6  ATTTACAACA  TCGCTCAGGA  CATCATCTAG  CAGAGAGGGG  AGCTGAGAGA  CAGATGTGTG  360
7  CAGAGGCTGG  TGCGCATGTC  CTGCAAGGAG  ATGAGAGAGA  TCCCAAGGAT  GAGGGGCTAT  420
8  ATGAAGGAGC  AGGTGGCGAG  CAGACACATG  GTGCTGTGTT  CCGGAAACCA  CTTGAGCTGT  480
9  CTGATGTAG  AGCTGAGACA  CACACTCAAG  CCGCTCAACC  TCACTGATGA  ATTTGTATCG  540
10  CAGACACTGG  CCAAGCTGAC  CAGCGGCAAT  GTGTTGATAT  TCAATGCCAT  CATGCGCATC  600
11  AGCGTGGCTA  CCAATTTTAC  CATGCTAGAG  CTTGCGAAT  AGGCGAATAT  AGCGCAAGCG  660
12  CTCTCTGTAG  ACGTGTCACT  TTTATCTAGA  GCGCTGGAG  GCGCTGGAG  720
13  GAGAGGCTGT  ACCCGTGAT  GACTGAGGAG  GAGTTTGTCC  TGAAGGTGTT  CGCCATGTAT  780
14  CCTTACTTGG  TGAACATGTG  GCTGAGGAGC  TACACACCGG  AGGTGAAGCT  GAGGCGATC  840
15  AAGTCCCTGA  AGCGCATGCT  GCGCTCTCTT  CTGCGCAAGG  ATGACTCTGG  GAGACAGTCT  900
16  TGAGACTAG  TGCCGCTCT  TACACAGGCA  GTTCTGAGCT  GTTCTGAGCT  GAGACAGTCT  960
17  ATCTCGAGAC  TTTTCACTAC  CAGCAACACC  CTGTGCGGCG  AATGTGAGCT  ACACACCAT  1020
18  TTCAACGAAC  TGCGATCTCA  GGTGTGCAAC  AAGCGCGCGG  CCGACATCAT  GTACAGCAGC  1080
19  GAGACATCTGA  GAGATGTGGT  GCACTGCTTC  GTAGCGTTTG  CTGCTCTCTA  CCGCAAGGAG  1140
20  CTGATGAGT  TCTTCTTCAG  CAGATCAAGG  AGTGAAGGCA  GATGAGACCA  GAGTGAATAT  1200
21  CTGAATCTGA  TTGAAGCTCT  AGTGAAGGCA  GATGAGACCA  GAGTGAATAT  CAGGCGCATC  1260
22  TACTTGCTTA  TGCGGCTAOT  CAGAGAACCC  ATCTCTGATA  CCGCGTCCAA  GGTGAGAGTG  1320
23  GCTATTCTCC  AATCATTTGG  GCGATGTGCT  CTCTGTGCTT  ACACAGAGAG  AATCAAMGGC  1380
24  TGCGGCGCTA  AGTACATCTG  TGTGCACTGT  ACCTTATCC  CTCTCAAGCT  GAGACATCTC  1440
25  CCGGAGAGT  TTTATCAAG  GCACTTGGAG  CAGAGATGCG  TCCACAAAGT  CAGCATGAGC  1500
26  ACTGTGAAGA  TATTAACTCT  TTCTGTCAAT  GGAATAGGCA  CCGAGTTTTG  GTGAGAGCTC  1560
27  CTGTCTGACA  TGATGGAAGC  AGACTTAOTG  CTCTCATCTG  TATCAAGCTCT  TATCAAGCTCT  1620
28  ACAGACCTGG  CAGAACACCA  GCTCATGTCG  CAGAGATGAG  ATGTGACAT  GGTGTGAGCT  1680
29  CCGAGCGAG  GCGTCTCTGG  TCACTCTGAG  AGCTCTGCT  CCGCTCTCT  GATCTGATG  1740
30  TCACTAACCT  ACAGAGGCGA  GGTGTGCGGG  ATAGCGATCG  TCAACTCTCT  GAGACAGCTCT  1800
31  AGCGAGAGCA  TGACACCTCT  CATGCGCGAC  AGTGTGAGAG  TGAGAGATTC  GCTATTGCTC  1860
32  TGCGGCGCTA  AGAACATCAT  TGAGTTCACT  TGAGTCAAGA  ATGTGCTGGA  AGACAGCTCT  1920
33  ATTCACTTTC  CCGAGAGTCA  CTTCAAGAG  ACCGCTGCT  CTGCTTGAG  CTTGCGCTCT  1980
34  AGTGAAGC  TGACAAACCA  GATTGCGAGC  TTTCAGAGCT  CTTCTCTGGA  GAGGCGCTTT  2040
35  CTGTACCGGG  CTTTGCGCTT  CACTCTTGCG  ACAGCGCTGG  AGGCGAGACA  GGTGAGAGCT  2100
36  CTGCTGTGCG  AGCTGCTGTA  CAGAGCGGAC  TACAGCAAT  ACTTTGACAG  GAGGCGGTGT  2160

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WO 03/290396

PCT/US02/21338

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ATTATGTGCT TTGGCTGTGT TGCCCGGGGCG CAGGTAAAAA CGGTGCTGAA TGGTCTTCAT 2220
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 GCTCTCACTG GCAACGCCGA GTTGTCTCTC AACCTCGTGG ACACGCCCAT GACGCTTAG 2280
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 TGACGCCCT ACCTCTCTAT TCAGAGAGCTG GATGAGATGA AGACGCTCC GAGCTTCTCT 3720
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 GACAGGCTCG CTAGGCGCAG GACTGTGCC AAGCGGCGAG GTAAACCGAG ACTCTGAC 5160
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 AACAAGCTT GA

Seq ID NO: 86 Protein sequence:
 Protein Accession #: XP_092643.1

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 GRVLATASKE KREIPEMBEY HIAVADPTV VALSRHPLG IYVEIRLEL TNYLDFBFT 180
 TLKALAKNV VEPVPFWHJ FLATIPHLR LANEAKIROA ICSAMETPCG TQYVLELW 240
 BSVYFVNTBE YGSLVLFMY RYFVTVNLHR IYVPEKGLVI KSLKMLGLL LPHDLRLEV 300
 YDIFLLELR YGSLVLFVLR ILBELVTWTF PVPFQMLRTI PFLAAQVCA KAPAGHTGSS 360
 QNLMHNVHVC VALARSVYKS LKFFFGSHG TNRKAVRVPT LLRLIRVLE DEHNSIRAV 420
 YLAKRVVNV ISTRKQVGL ALHILGQALA LCVYGRIRIG WGLKLVYQL TSLTYKLETR 480
 IRKPYQRDLR ERMVHKVMD TVKLTSSVSS GNTTEWVRL LCYIMETDV EALPICBL 540
 TMLAEHLQLG QDVSIVACK SRGVDLFPAC KLLARLAVIM SSYPYGRGRC IANMLNLT 600
 GQSIAPKMD MRELRIALV RYLRHTBFT WQKRAWEKQ IQPIRNLLE TCRHNSLL 660
 SKELNNTAS FDFSLRBEY LNALGPTLA TGLRASKVIV LLELNLNLT YSDFPGRSV 720
 INCEHLARG QKVTYLVNHL DFEREIQBSB QSWQISAWRK DHRWEETVA SALMNVSCV 780
 ASYCPQLLL NLVDSPITAK IHHVSVSCQ DICLMAHPKH GVVYVTKAIM HIDLDFBPF 840
 AKNTLTYSIT VAVIKAEPTD HLVSFVFLAL MEALSRILKLT KPIFTSRNS ELADISV 900
 ISQLPQSRM SSILHIAEM LGLRLRQMBL LGLQPLDFRG LQSNQWLEX WILKSEWER 960
 EKAVFELRL WHITVSTAV CTHLKLQGFQ TTVGLIAPCT CDNRHTPRA SSVLVSLDL 1020
 LIASTGCTSLH GFSSKQRELEK CKKDLQSTDV RKTFCASSRI AKRVVCFSC DEVLVLIQKL 1080

WO 03/003906

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CENTGASHLQ HDKASVTWIA FFLQMRKEL EDKVASILSA ILVHLPVDR PEVRLLIDQ 1140
ILLARHHQS TILTSLLQIP LPMESHIAEV KLVSEHVPE AKTNLHSLMG ELQSLSPRI 1200
SATSTADWR LAAVDEPDI CTILLIQEL DEDVDEPFI POLITILLIQ LQSSHPAA 1260
PVLVIMKWLV HTTLPPEMI LQESGRVET IKSMOLLFKR VDGRLAMLT DEQAVWDLQ 1320
DGGTFLEGV S LLAELCMHV BGHQRLEAL VLKMDSEVL SCRLSTAVC VEMHRIWNO 1380
PVLYOBLKL PAALLLEGA DQDEDEALV LSLRAGNMA LGAPKKVQY KVLIERGLQ 1440
FLREPVSRV TASBEMALT ILARLEQVQ OSSFOHMSU CRIFPKESE LLLEAFLE 1500
QLARVPMS KEIPEKIVE KNMFLMLAS DQCSNARQV RYILQPVSGS GARCSPKQV 1560
LGSAGSACNA TMRQCVHPQ WKSLESPSP SBTATDDIGT VFOTMCSIL TRKCPVLYE 1620
FLEETMAYV UNILSRIRIA CNLACIMQ MSHYLEKLD FFALENSLOE LQLDPDGPT 1680
GPEGRKLALC LHSEPIHTA DSVPRMHCA KRAKPOLPV CQGNOCQNS PGVPSSTGE 1740
CYAVQIFTRA KAFSGVVFV LFGQAKDLI SCVWESIAA KQA

Seq ID NO: 87 DNA sequence
Nucleic Acid Accession #: CAT cluster

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GGTATACAG AGCAATATG TTGCTGAAA TGGATTAAAC ATTCCTTTC AGGCTAAACA 180
AAAGCGCCTG TTACACTGT GTGACAGCA GCCAGAGAC CGAATTOTT CCTTTCCAC 240
TTGGTGTCT CTCTCACAGA CCAGGATGA GCTGTGTGT AGCTCTCTC GAGAACCACA 300
CAGCCTGGG TGGTAGTCA TCGAGACTC TTCTACTCT GTTCCGTAG GTCAAGAGC 360
CTGCAAGCA CTATCCGAC CATCCGCCC TCGAGCCCT GATVTTAAT TCACTCATG 420
CCTTTCACG CAGCGGAAA AGTATGACT TCTTGAGAC TTAACAGGT GAGTGAAC 480
CAGCGCTTT GAAGACCTA CAATCAGTC TGCCCTTGT CATCCCGAG CAGATGTGT 540
GTGATATGC TGGGACTAC TGCGAGTAC TCTGACAG AATGAAACA AGCTATAC 600
TCTATGCAA CTGCGACA GTTCTGACT AGCATCTGT CAATATGATA AAAAANAATG 660
TAAAGATG CTTCAGCTG GTTCTGACC GCATGTTTA TATAAGACT ATTGCTTCT 720
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Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..759

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GCTGCKHA TCTTAAGTA TACGCTATT CTCTTAGAA AGATGATT AACATAAC 240
ACTGATAAT CACTAAACC AGCAGGTTT CTAAACGGG ATCTATATCA AAGAGAGAG 300
CACATATGT TAGTTTAAAT TAATACAT ACAAGGTCC GACCAACT AGAAGAACT 360
GCCTTCAGA CCGACALCA CTTATAGAT GGTCTCTCC AGGTATAGA GGAAGAA 420
TACATGAG ATTCAATAT TATAGAGAA ACCTCTGTAG AATATAGGT AGAANAATG 480
CLTAATAAT GGTCTCTCTA AACATGTGG CTGTTTGCAC TACGACAACT CTTAAGAAC 540
TTACAGAAC AGAAGAGAC CATCTATAC GATCTAAGT ACAGGTTTG AGTGTCTAT 600
ACATTTGGA AATATTGAC TGACAGAT CTATTTATA GCAATGCA AGCTGATCT 660
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PSLIKYKAI LKSKDLTL TNSLNAPG LTDLYKRE HTCLVLYNH TKVFDLGET 120
PFTGQHFID GSSQVTEGR YNGYVIDBE TLVEILEGLK PMWGAQTC LFLSALAD 180
LQNGQITVT DSKYAPGVAH TFGKIWER LINSKQDLV HKELITQVLT MLQLPKETAI 240
DHVFHQKSL SF

Seq ID NO: 90 DNA sequence
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Coding sequence: 186..776

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TCTCTCAGAA GAGAGCCAG CACCCGCTC ACCTGCGAG CCGAGTGAA CGAGTGTCCC 180
CTAACATGCG GTCGCGCTCT CTGTGTCTCC CGAGAGTCTC CTGTGTGCT CTCTGCTCT 240
CGCCGCTAT CGAGGCTCT CTGAGCCGC GAGGACTCG CAGCGCGCG 300
AGACCCCTCA GAGGCTCTC CTGAGCCGC CAGCGCGCG CTGCGAGAG CGACAGAC 360
CGAGGCTCG GCGGCTCTG CTGCGAGAG GAGAGAGATA CTCTCTCGC CTGCGAGAC 420
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TCTGCTGCC TCGGCGCTGC CTGAGACAGC CCGCGGCTCT CCGGAGAGGC GGGCGTAGGA 600
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TATATAAGGT TCGAAGGT
  
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Seq ID NO: 91 Protein Sequence
Protein Accession #: NP_000747.1

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1 11 21 31 41 51
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AQAHSHRKL MEIGK
  
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Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

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1 11 21 31 41 51
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AGCAACCTCC AGGACAGGCT CTTCCGAGAA GAGCCTCTCA CCGCATCTGC ACTCTCTCTC 180
ATGACAGCTT CAGATGTCGA GAGCAAGCTT GAGCTCTGCG AGAGGTGATG GAGAGATAGC 240
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CCTCTGGGCA AAGGCAAGTT TGGAAAGTGT TACTTGGCTC GGGAGAGAGA AAGCGATTTC 360
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CTCGCGAGAG AGATAGATCT CAGCGGCCAG CTGACCATCT CAGACATCTT GGTCTCTTAC 480
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CCAGAGATGA TTGAGGGGCG CATGCACAAAT GAGAGGTGTG ATCTGTGTGT CATTGGAGTG 840
CTTTGTATAG AGCTCTGTGT GGGGAAACCA CCGTTTGAGA GTGCATGCA CAGCGAGACC 900
TATGGGCCGA TGTTCAAGGT GAGCCTTAAG CCGTCTTAGG TTCCGCTCT CTCTGCGCAG GAGCGGCG 960
GACTCATCT CCAACTGCTT CAGGTATAG CCGTCCGAGC GCGTCCGCTCT GCGCCAGGCT 1020
TGGGCCAGCT CTTGGGTCGG GCGCACTCT CCGAGGGTGC TGCTCCCTCT TCCTCTTCAA 1080
TCTGTGCTCT GATGTCCTCT GTCACTCACT CGGTGTGGTG TGTGTATATG TCTGTGTATG 1140
TATAGGGGAA AGAAGGGATC CTTAACTGTT CCGTTATCTG TTFTCTACTC CCGTCTTTGT 1200
TTAATAAAGG CTGAGGCTTT TTGT
  
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Seq ID NO: 93 Protein Sequence
Protein Accession #: NP_004208

1
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1 11 21 31 41 51
MAQKDSYFM PYGRTAFRG LSTLPQRVLK KEPVTSALV LAGESTVQPT AARGQKWMEN 60
SGSTVQLTLA HFTDLEFEG EPLQKRGKPF VYLAERKSH FVLAIVLKF SQIEKRGVHF 120
MEELACALAY CHQKVIHRD IKPEMLLGL KGELEKIDFG KSHAFSLRA KTMCGTLDL 180
PFEMIBDRHF NEKVDLNCIG VLCEYLIVGN EPPFASASHR TYERIVKVDL KPFAVPTGA 240
QDLISKLRLH NPSRLPLAQ VSAHFVWYDM SRVLPFSAL GQVA
  
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Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_007019.1
Coding sequence: 41..580

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 30
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1 11 21 31 41 51
GGCAGAGAGC AGTCTCTGTC TCTCTGCAAA GCGCGCGGCG ATCGCTTCCG AAAACCGGGA 60
CCGACGCGGC ACTAGATGCT CGGCGCGCGG TAAAGAGACT GAGCGAGGCG GGGGCGCGGC 120
CTGCGTCTCG GTGGCCAAAA GCGTACAGCA GAGCTGTATG ACCTCATGTA TGTCTGGGGA 180
TAAAGGAGTT TCTGCTCTTC CTGATACAGA CAACCTTTTC AAATGGGTAG GAGCATATCA 240
TGGAGAGCTT GAGACAGTAT ATGAGAGCTT GAGCTATAGG CTTCTCTATC ACCCCAGAGT 300
TGCTACTTAT TAGAGATGCT CAGATGTGGA GTTCTCTAGC CTTCTCTATC ACCCCAGAGT 360
GAGACAGGAG GGTAAACATAT GCGTGTGATC CTTGAGAGAA AAGTGGTATG CCGTGTATGA 420
TGTCAAGGAC ATTCTGCTCT CCGATCAGAG CTTCTTAGGA GAACCCAGCA TTGATATGTC 480
  
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CTTGAACACA CATGCTGCC AGCTCTGGAA AAAACCCACA GCTTTTAAGA AGTACTGCA 540
 AGAAACCTAC TCAAGAGGAG TCACCAAGCA GGAAGCCTGA CCAAGGCTGC CAGGCTGTC 600
 CTTGTGTGCT TTTTAAAT TTCTCTTAGA TGCTGTGCTC TTTTGTGAT TCTGTATAG 660
 GACTCTTAT CTTGAGCTGT GATAATTGAG TTGTGTATT GTCTTTTAAA TTAGLILIG 720
 GTTGAGGCTT TGTATATTA AAAATGCA TTTTGTGCT TTTTAAAAA AAAAATAAA 780
 AAA

Seq ID NO: 35 Protein Sequence
 Protein Accession #: MP_008950.1

1 11 21 31 41 51
 MASQNRDPAE TSVAARFKA EPSSGQMRP VGRHQRRLM TLMWSDKGI SAPPSEKLF 60
 KW/OTIHGA GTVIEDLEY LSEFLSGVP YNAPT/KFLT PCYHNVDTQ GNICDILKE 120
 KWSALYDVRT ILLSLQSLG EPNIDSLMT HAELNKRNP AFKYLQSTY SKQVTSQEP 179

Seq ID NO: 36 DNA sequence
 Nucleic Acid Accession #: AK053663
 Coding sequence: 30..1423

1 11 21 31 41 51
 AGAACGGCTT CCGGCGGGAG CTGTGACGT CTTATCATG GGGACAATTC ATCTCTTGG 60
 AAAACACCAA AGATCCTTT TTGCAAGTT GTTACGGGA TTTAGACTT TAGGAGCTGA 120
 CCGAAGGTCC TGGAGAGTAC TGCTCTTGG TGTACAAAG TGTATATTA CTGCTCTCT 160
 GCTTATATGG TGACATCTTA CTAATGATAT AGCTTAACT GCTTATACT ACCTGACACT 240
 TTTTGACTCT TTTAGTTTAA TGACATGTT ATAAAGTTAC TGGTAAACT TGAGGAACC 300
 TAGCCCTGTC TATTCATTT GGTPTTAAAG ATTAAGAATC TGCGCTGTAT TTGCTCCAG 360
 AGCTCTTGCA CAGTGGGAG CTCTCTTAT ATTAAGAAGA AGTCCAGAC GCTTTTGG 420
 ACCGCCAG AGTACACGAG GAGATATCAT AGTCTAAAT TTTGTGCTC TTGTGTCAA 480
 CCTGTTCAG ATC/TFTTCA TTGGAATAA ACCTTTTCCT TATGTTCTAG AAGCTGTAG 540
 TACGAGCTGG CTCGAAGAG ATGTTCGAG TCTTAGTGA AGCTTGTGTG GAATTAATCC 600
 GGGACTTAGC AGTACTTCC TTGCCCAAT GAATCAATT GTTTGTGAT ATCTTCTGG 660
 AGCACTTCT CTGTGCT CATTAAGAT AATATTTAT ACTTCCTGA TCTGCTAGA 720
 CACTGTGCT GCTAGACTA TTGCTTGAT GACATTTGG ACTATGATC CCAATGATGT 780
 GTACAGTGG AAGTCTTAC TCGAGCAAC ACCACCCCAT GTTATTGTC AGTTGACGA 840
 ACTCATCA GAAGTATCTA CTTAGATGG AGTTTAGA GTCCAAATG AACATTTTG 900
 GAGCTTAGT TTGGCTCAT TGCTGTGAT AGTGACCTA AGATATGAC GAGATGCCA 960
 TGAAGAAAT GTTGTGCTC ATGTGACCA CAGCG/ATAC ACTCTAGTGT CTACTCTAC 1020
 TGTTCAAAT TTCAAGGAT ACTGAGTAT GCGTCCCTTA TTGTCTGGGC CTUVTGAGC 1080
 CAATGTCTA AACTTTTCA ATCATCACT ATGCCCAATG CTCCTTTTAA AGGGTACTA 1140
 TGATTTGAC CAGATTACAT CACTCCAGC TAACTGAT AGTCCACTC CAGATTTTC 1200
 ATTACACT CCGGAAAL AATTGAAACC AGTTATTCT TCAACACAC AAAAGAGCC 1260
 TTATGTTTT GTTCTAAATC ATGGACAC ACCCTACAGC AGCATGTTA ATCAGGACT 1320
 TGAATTTCA GGAATTGAG CAATCAAGG ATTAGGACT GHTTTTACA ATATACAGC 1380
 TGAATATGA ACTATATA GAATTGACA ACCAGACCA TGTATGACT TACTATTAT 1440
 TTTTAAGTA TTACTCTAA ATGTTAGTA ATGATAGTCT TGTTCACAT TCATGAACC 1500
 TATGAACATA TATTTTGT AATGTATT GTAGACATGA AATCTCTATA AATTTAAAG 1560
 GCTTTAAATA GACTTCTGT AAAAAATGT TTCTTTTAA TTGTATATT GGTATTTG 1620
 GTTTGTGAT TGACTGCT GTATATGAC ATCACTTCA TAAAGCCAC TTGATGAGT 1740
 AGACTGTCA CATTACTAG ATACGATTT TCTTTTTT TCGAGACG AGTCTGCTC 1800
 TGCACTGT CCGAGCAAT ACATATTAT TAACATAAG CTGTACTTGA ATATACAGC 1860
 TGTAGTTT TGCTTTGTT GTTTTTCAG ATGAGTCTC ACTCTGCTC CCGAGCTC 1920
 ATGACTGAC ATGATGAG CTATGSCA CAGTCTGCT CTGATTTCA TACKCATTT 1980
 TGCTTCTC TCCGATGAG CTGAGATTAC AGGACCTG CACACAGCCC AGCTATTTT 2040
 TGTATTCTA GTAAGACG GGAATTTCC CAAATGTGCC AGCTGTGCT TGACTCTGT 2100
 ACCTCATGAT CCACCCCTC TAGCTTCCCA AAGTGTGG AGTACAGCA CAGACCGA 2160
 CCGAGGAGT ATTTCATTA ATGAATTTA TAAATGCT TCTGTACTA TACKCATTT 2220
 GGGAGAGGA AAAATCTCT TTCAAAAGT AAAGTCTCT TTATAGCT TTCCAACTT 2280
 AATTGCTAAA TTTTCTTGT AGTTTCTCT GAATATGTC TTACAACATA AAAACAAAA 2340
 TTTTATGAG AAATTTTGA ATACATCTA CTAGACAAA TTGAATTT TAAATATCA 2400
 GATTTTGT AAGATTCTC TCGTTTAAA ATTTAGTAC ATTTTAAT

Seq ID NO: 37 Protein Sequence
 Protein Accession #: BAB7980.1

1 11 21 31 41 51
 MGTILFRKP CRSPFKLLR RFLWADR SKWILLGVI NLICQFLIM NCSTNSIAL 60
 TATTLZLIFD LPSDWCLIS NYVILAKPS VVSFPRLEI VLAVASTVL ACGLATLIK 120
 RSARFLRDP RIKVLLIGL TPVALCPML TWLSIRNRP AVTSEASTS WLQBVADLS 180
 RSLCHILHQL SSTFLRNP FVLIDLAGP ALCTIMLIE INNYFAUTS SAIAIATPT 240
 GTVPMFVYS GKVLITTPP NVIGLDLKL RVSTLDQVL RVNRSHWTL GPGLAGSVH 300
 VLRLDANDQ NLYLNVHNL YTLVSTLVG IPRQWTRPA LLSQVANYI LNFQKRVPT 360
 MFLKLTGDL NPYVSTAEI SPPSPERSM TTKCNRPY LIATNTPYV POLNKHPTPY 420
 SMLNQLGV POLNATQER TGTNIPSY GTNRIQQR P

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Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: CAT cluster

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGAGCTTAA CCAATGCTTC ACAATATCCA AGAAAAAAT ATTTCAGTGT GATAAATATA 60
      GGAAAGTTTT TCATAAATTT TCAAAATTCOA ACTGCATPAA GAGAGAGCAT ACCGGAAAAA 120
      AGACCTTTCA AATGTTATGA ATGTGACAAA GCTTTTAAKA AGTTTTCAC CCCTACTACA 180
      CATAGAAAAA TTGATACTAG ACAGAAAACC TACAATATGT AAGATGTGG CAAAGCCTTC 240
      AACTGTGCTT CATACCTTAC TATACATAG AGAATTCATA CTGAGAGAA ACTCTACAAA 300
      TGTGAGAAT GTGGCAAGG CTTCAACTGG TCTCATACC TTACTGCATA TAAGATAACT 360
      CATACTAGAC AGAAACCTTA CAATGTGAAA GAATGTGAAA AGCCTTTAA GTACTCTGCG 420
      AACCTCACTA CACATAGAT AATTCATCT GAGAGCATCT TCTACAAGTG TGAGAGATGT 480
      GGCAAAGCCT TTAACCATGC TGAATGCTTC TTGTGCATT TGAAGATTGT A

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Seq ID NO: 99 DNA sequence
Nucleic Acid Accession #: FGBNESH predicted
Coding sequence: 1..531

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20     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGAGCTTAA CCAATGCTTC ACAATATCCA AGAAAAAAT ATTTCAGTGT GATAAATATA 60
      GGAAAGTTTT TCATAAATTT TCAAAATTCOA ACTGCATPAA GAGAGAGCAT ACCGGAAAAA 120
      AGACCTTTCA AATGTTATGA ATGTGACAAA GCTTTTAAKA AGTTTTCAC CCCTACTACA 180
      CATAGAAAAA TTGATACTAG ACAGAAAACC TACAATATGT AAGATGTGG CAAAGCCTTC 240
      AACTGTGCTT CATACCTTAC TATACATAG AGAATTCATA CTGAGAGAA ACTCTACAAA 300
      TGTGAGAAT GTGGCAAGG CTTCAACTGG TCTCATACC TTACTGCATA TAAGATAACT 360
      CATACTAGAC AGAAACCTTA CAATGTGAAA GAATGTGAAA AGCCTTTAA GTACTCTGCG 420
      AACCTCACTA CACATAGAT AATTCATCT GAGAGCATCT TCTACAAGTG TGAAGATGT 480
      GGCNAAGCCT TTAACCATGC TGAATGCTTC TTGTGCATT TGAAGATTGT A

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Seq ID NO: 100 Protein Sequence
Protein Accession #: FGBNESH predicted

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35     1      11      21      31      41      51
      |      |      |      |      |      |
      MQLTNSQIP EKYPYVNI KPTTINPQI TDIRDIREK EPKKECKGK APNKFSTLT 60
      EKIITRELE YKRCCKNAP NNSYLTIHK RHTGRILYK CEECKAFNH SEVLTAKIT 120
      HTEKPYKCE ECKAFKYSS NLTHKIIHT GRHLYKEEC GKAFNHAACE FVILKI

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Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_032589.1
Coding sequence: 147-422

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45     1      11      21      31      41      51
      |      |      |      |      |      |
      GGCACGAGGT CTTGTATGCG AAATAGGCTT CCACTTGGC AGGGGCGCTC TTGTCCACTC 60
      GTTTCGTGAA ACATGGGTGG CAAAAGAGA AGATGAGCT GGCATTTAGA ACATGCTGAA 120
      TCCACGCTTC ACTCTGCTGA GCAAATGUA AGGAGCTGG ACCGACTCT GTTACTGTGA 180
      GAAAGGCTCT TCATGTATGC AAGAGGAGAT TTGTATAGA CCTACTGCTG GAGTGCAGTG 240
      GTCAATATC GGAATCACTGC AGGCTCAGC TCCGATTTCA AGAATTTCT ATGTCTCAGC 300
      CTCCTGAGCA GCTAGAGTTA CAGACAAACC TTGGAAATCA AGAAGTGTCT GGAATATAGA 360
      AGGCTTTACT GCGCAAGCGG AAGGTGTGG CCGATATAGA GTCAATCTG TCGAGCTG 420
      GACAAATTTT TTGAGACCTC TTATTATGT TATGTTCAG ATTATGCAAT ATTATGTA 480
      TGTACATTTA ATTCCAGAGC TGTCAATAT AAAAATCTTT ATAGTACCTC ACTGCAC

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Seq ID NO: 102 Protein sequence
Protein Accession #: NP_15978.1

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      NLKPPFPVFT VKGLHSRKN APVNHILLIC DSITDHCEL HLPVORIME QPPFQLGLQT 60
      NLGNQSESN MKLPMFRFK LAQYESTQFM P

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Seq ID NO: 103 DNA sequence
Nucleic Acid Accession #: NM_024501.1
Coding sequence: 60..737

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70     1      11      21      31      41      51
      |      |      |      |      |      |
      GCGCGACGCA AGAACCGCAG AAGCGCGCGG GCGGAGATCG CCGCGCGCGG CCGCGACGCA 60
      TGAATCTCAA CGTGGAGAGC CTACCCCGCC ACATCATCGC CCGTGGTACG AAGAGAGTTA 120
      GCAACTGACG CGGACGACCA CCGAATGCGA TGAAGCTCTT TCGACACGCG GAGAGACTCA 180
      CGCACTCGCA GTCGATGCGA GAGGCGCTTC AGGCAATCCC ATATGCTGCA GGTCTTTCTC 240
      CGATGAAACT CTTCTCTGCG AAGGACTTCC CTGCTCTCCC ACCCAAGGCG TACTTCTGTA 300
      CGAAGATCTT CCACCGGACG GTGGCGCCCA ATCGCGAGAT CTGCTCTCAC GTCTCTCAGA 360
      GGCATCTGAC GCGTGGAGTG GGCATCTGAC ACCTATCTCT GACATCTGAG TGTCTCTGTA 420

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TCCACCTAA CCCGAGCTC GCACTACAG AGGAGGCGG CGCGCTGCTC TTGGAGAAT 480
 AGGAGGAGTA GCGGAGCTCG GCGGCTGTCC TCACAGAGAT CACGCGGGGC GCGCGCGGCG 540
 CCGAGCGAGG GCGCGAAGCC GGTGGCGGCC TGGCGAGTGG CACTGAGGCT TGTGCGACGG 600
 AGCTGTGAGC TCCAGCGGGC CGCGGAGGGG CTGAGGCTCC CATCGCGCAG AGCAGCATGCTG 660
 GCGAGCGGCA TAGAGAGCTG GCGCGCAGGA AAAAGACGGA CAGAGAGCGG CGCGCTGGGG 720
 CGCTGCGGCG GCTGATAGTG GCTCTCTTCC TCCTTTCACC GTGACCCCAA CTTCTCTGTT 780
 CCGCTGCTCT CAACTCTGTC TCTAGATTAT TTAATATTAT GCTGCGGCTG GCGAGGCTAC 840
 AGGCGGCACT GCGAGCTGGA TTGTTTTCAT TAAATAGT TGGAAAGCA

Seq ID NO: 104 Protein Sequence
Protein Accession #: NP_055316.1

1 11 21 31 41 51
 MNSVBIPLP IIRLVIVKEV TLTADPPGG IRVFNREGL TGLVTVIEGP SSTPYAGGLE 60
 RKMLLKGDF PAFPPKTFLL TLTITPFWVA NGEIVNWLK EDWTEGLLR NVLITIKICLL 120
 IHPNPEBAN EENGLLEEN YSEYARARL LTEINGAGG PSGRABNGRA LARSTBASST 180
 DPGAPGPGG ABSPHAGHA GERDKLAAL KKTOKRRALR ALERL

Seq ID NO: 105 DNA sequence
Nucleic Acid Accession #: NM_005101
Coding sequence: 76..573

1 11 21 31 41 51
 CGCTGAGAG CGAGCGAAT CATCTTTGCC AGTACAGAG CTGTGTCCCT GCGCCACAGC 60
 CCGACGCCCA CAGCGACTGG CTGGGAGCTG AGCGTGGAGA TCGTGGCGGG CAGCAAGATT 120
 CAGGATGCC TGAGGAGCTG CATGTGGTGA TCGAGCTGA ACGCGGAGAT CACCGCAGAG 180
 ATTGGCGTGC ACGCCCTTCA CGAGCGCTCG GCTGTCCACC CAGGCGTGTG GCGCCTGCAG 240
 GACAGCGTCC CCGTTCGCGA CGAGCGGCTG GCGCCTCGCA GCGCGCTCCT GCTGTGTGTT 300
 GACCAATGCG AGGAGACTCT GAGCATCTCG GTGAGGAGTA ACAGCGCGCG CAGGAGGAGC 360
 TACGATGCTG GCGTGGAGCC GCTCTGAGGC CAGCACTGAG ACGCATGAGG CCGCGCTGAG 420
 GGTTCGCGAG ACGACTGTTT CTGCGTGAAC TTGAGCGGGA AGCGCCTGGA GCGCCAGCTC 480
 CGCTGCGGAG AGTACGCTCT CAGCGCCCTG AGCAGCGGAT TCAATGATCT CGGCTGCGGG 540
 GAGGCGCGCA CAGAGCGCTG CGCGCGAGG TAGAGGCGCT CACCAACATC CAGCAGAGAT 600
 CAGGCGCGG AATAAAGCG TTTTGTAGG GAT

Seq ID NO: 106 Protein Sequence
Protein Accession #: NP_005092

1 11 21 31 41 51
 MNSDLTVGL AGNEFQVSLR BSMVSELKA QITQKIGVHA TQRLAVHPS GVALGRVFL 60
 ASQSLGPGST VLLVVDKDE FLHLIVEMNK GRASSTVEVL TQTVMLKGG VSLGEGVQDD 120
 LFWLTFBPG LEDQLFLGKY GLRLFTFWN NLRIRKGGTE PGGRS

Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 1..1161

1 11 21 31 41 51
 ATGAATGCG ACCACTGCA GATCACTTT CTGGAATAG ACAGAGAAGA CTGCTGTGTG 60
 TTCCGAGATG ACTCATTCG CAAGGTGTGT CGCGCGTGT TGGGCTGGA CTGTATCTTT 120
 GGGCTCTGCG GCAATGGCCT TGGCGGTGTG ATTTCCTGTT TCCACTCTAA GTTCTGGAAA 180
 TCGACCGGGA TTTTCTGTT CAGCTTGGCA GTAGCTGACT TTCTACTGAG CATCTGCTG 240
 CGCGCTGCG TCTTCATGTT TCGCATGGA ACTTCTGAGA CAGCTCTGCG CATCGCTTGC 300
 GTGCGGATG ACAGGATTT CCGGTGTGTC CATCCCGACC AGCGCTGGA CAGATCTTCC 360
 AATTGACAG CAGCATCAT CTCTTGCCTT CTGTGCGGGA TACCTTGTG CTTCAATGTC 420
 CAGCTCTGTA AGAGAGATT GCGTATCGAC AATGCGCTG CAAATGTGTC CATCAGCTTC 480
 AGCTCTGCG ATACTCTGCG GTGCGAGGA GCTATGTTC TCTGAGATT CTTCTGCCC 600
 CTGCGCATCA TCGTCTCTG CTCAGCGAGA ATTATCTGGA GCGTGGGGA GAGCAAAATG 660
 GACCGCGATC CCAAGATGTA GAGAGCATC ACTTCTATCA TGTGTGGGG CATGCTCTTT 720
 GTGATCTGCT TCTTTCGAG AGCTCTTGTG CGGATCGCA TCTTGTGCT CTTGCAACT 780
 TCGAGCGAGC AGAATTGTGA AGTGTACCG TCGGTGAGC TGGGCTTCT TATCACTTC 840
 AGCTCACTC ACCTGAACAG CATCTGTGAC CCGGTGTGTT ACTACTTCT CAGCCCATCC 900
 TTTCTCAACT TCTTCTCAC TTTGTATCAC CGCTGCTCC AGAGCAAGAT GACAGGTGAG 960
 CCGATGATTA ACCCGAGAC GAGGTCTGAG CTCACAGAGC GCGGCTCTTA TCTGGACCA 1020
 GCTCGAGG CGTTCATGCG CAGCTCTGCT GAGCATGAG TGTCAACAG AACCGATC TCTGAGGARA 1080
 ACTTCAATA ACATTTCCAA GAGCGGACAT TGTCAACAG AACCGATC TCTGAGGARA 1140
 CAGTGTGAT GTTCATGGA G

Seq ID NO: 108 Protein Sequence
Protein Accession #: NP_006099.1

1 11 21 31 41 51
 268

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| MNRHILQDHF | LEIDRKNCCV | FREDFIKVL | FVVLGLEPFI | GLGNGLALN | IFCPHLKNK
 | SSRIFLPHLA | VADFLILCL | PVNDFIVYR | SDMKFGDTFC | RVLFNFMAM | ROOSIPIIV
 | VAVDFVRFV | IPIHDLRLE | HPAALISCL | LMIITVGLV | HLLFKELGL | KSNHVCIS
 | SICHTFKKE | ANHLLLELF | LGLLPCASR | IWSLBSQRM | DRHAKIKRAI | TFMVVAIVF
 | VICFLPSVV | RIRIFWLLAT | SGTNCBYVR | SVDLAFPTIL | SFTYNSMLD | PVVYVSSFS
 | FNNFSTLIN | RCLCRKMTG | FQHRSTSVR | LTODEPNKTG | AFELKANSR | FSNVPSYIG
 | TRNHSKIGH | CHQEPASLEK | QGCCIE

Seq ID NO: 109 DNA sequence
 Nucleic Acid Accession #: NM_005030.2
 Coding sequence: 63..1874

1 11 21 31 41 51
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| GGCACAGAGG | AGCGATCCGG | AGGCTCTGCT | CGATCTCAGG | TCTCAGACCG | ACCTTCGGGA
 | GATAGAGTGC | TCCGTGACTC | CGAGGAGACG | TGGACACGGG | ACCGCGCCAC | CCTGGAGAAG
 | CGCGGGTCCC | CGAGGTGICA | GTCCTCGGAG | CTCGCGCGCG | GGCTCAACGG | CGGAAAGAGA
 | TCCCGAGGCT | CTAAGTGAGC | CCAAGCGGAG | CGCGCGCTCA | TGTGCGGGCG | CGCTTTTGTG
 | GCAAGGCGCG | GTTTCGAGAG | TGCTTCGAGA | TCTCGAGACG | GACACCAAGG | GAGGTTCCTG
 | CGGACAGAT | TGTCTTAA | TCTCTCTCG | TGAAGCGGCA | CAGAGGZGAG | AGATATCCG
 | TGGAAATATC | CATTACAGCG | AGCTCTCCCG | ACCAGCAGCT | CTAAGGATTC | CAGGCTTTT
 | TGGAGACAA | GACTCTGTG | TGGAGCTCTG | CGGCGGAGG | TCTCTCTGG | 480
 | AGCTCACAA | GAGGAGGAAA | GCGCTAGCTG | AGGCTGAGG | CGGATACTAC | CTAAGCAAA
 | TGTGCTTGG | CTGCGTAGT | CTGACAGAA | ACCGATAT | TATCTAGAG | CTAAGCTG
 | GCAACTTTT | CCGATGAA | GATCTGAGG | TGMJAATGG | GATTTTGA | CTGCAACCA
 | AAGTCAATA | TGACCGGGG | AGGAGAGA | CCTGTATGG | GACTCTAAT | TACATAGCT
 | TCACTATAC | GTTGTAGT | GCGAACCG | CTTTGAAG | TCTTGCTTA | AAGAGACT
 | ACCTCGAT | CAGAGAGAT | GATFACGTA | TCCCAACA | CATCAACCC | GTGGCGCT
 | CCTCATCCA | GAGATGCT | GAGACATC | CCACGCCC | CCTCAACT | AAGAGCTC
 | TTAATGAGA | GTTCTTACT | TCTGTATA | TCCCTGCCG | TCTCCCATC | ACTGACTGA
 | CATTACAC | AAGTTTTCG | ATGCTCCA | CGAGCTTGA | CCGACGAC | ACTGAGCT
 | TCAAGTCT | CAGAAAGG | TCGAAACG | CTTCTCTG | GCGTCCCGG | GAAAGAGG
 | ACCAGTGT | TCGAGAGCA | GGTGAGTGG | TCGACTGCA | CCTCACTAC | ATGCTGACG
 | AGCTCGCAG | TGTCAATGC | TCGAACGCT | CGAGCGTGG | GCTGTGACG | CAGAGAGAG
 | CTGAGATTC | TCGCTGATC | CCTACTTCT | GGTTCAGCA | GTGGTGAAC | TATTGAGCA
 | AGTACGCT | TGGTATCA | CTGTGTATA | AGAGCTGG | GGTCTCTC | AATGACTCA
 | CAGCTCAT | CTTCTCAAT | GATGTGACA | GCTTGCATG | CATAGAGCT | GAGCGCATG
 | AGTCTACT | CACGCTGAT | TCCATCCCA | ACTCTTAT | GAAAGAGAT | ACCCTCTTA
 | AATATTCCG | CAATTACATG | AGGAGCAT | TGTGAAAGG | AGTGTCCAG | ATCAGCGCG
 | GCGAAGTGA | TGAGCTGCC | CGCTCGCT | ACTCAACG | CTGTTCCG | ACTGAGCG
 | CATCATCT | GACTCTGCG | AGCGAGCG | TCGCATCA | CTCTTCGCG | GATCACTCA
 | AGCTCATCT | GTGCCACTG | ATGCGAGCG | TGACTACAT | CGACGAGAG | CGGAGTTC
 | GCATACCG | CTAAGTCTC | CTGAGAGAT | AGCGTACTG | CAGAGAGCT | GCGAGCTGC
 | TCGCTACCG | CGCATATG | GTGACAAAG | TGTGAGACT | AGCTCGCG | AGCACTGC
 | TCAAGCTC | CTATAGCTG | CGCTCTCT | CGGATGTG | CGCTCTGAC | TCGACCTGC
 | ATCTGGGCG | CACTACTGTT | GCGTCCGCG | GTGCTATG | TCGAGTGG | CGCCAGCG
 | CGTGGCTG | CGAGAGCTG | ATCATCTGT | CAGGTGGGG | TGTCTGTATA | AGTATTTT
 | GTACATGTC | GGTGTGGGT | TCTACGCT | TGTCCCTCT | CGCTCGAC | CGCATATG
 | AATGTACG | AATATTCTA | TGAATCTG | TACTGTCTT | TCTTGTCTT | TATGACATT
 | AATGATCT | GATATTCAA | AAAAAAAAA | AAAAAAAAA | AAAAAAAAA | A

Seq ID NO: 110 Protein Sequence
 Protein Accession #: NP_05021.2

1 11 21 31 41 51
 60
 65
 70

| KSAVTAQKL | AAPADPGKA | GYVGAAGKA | FAAAPPAKEI | FVVLVDPRR | RRYVGRFLG
 | KGGFAKCFE | SDATKEVFA | GIVFVPSLLL | KHPREKMM | EISINRSIAH | QIVVGRGFF
 | EDNDFVTVV | ELCHRSRLS | LKRSXALTE | PARYVLEGI | VLGCYLHNR | QIVVGRGFF
 | WFLNDELEV | KIGDFPLATK | VEDGSKMT | LQDFWVAP | EVLSKSHR | EDVWSIOCI
 | WTLNLCVPS | FETCLSEYI | LEIKNEVST | PEHINPVAAS | LIQMKLQDP | TARTINELL
 | NDEFSTGVI | PARLETTCT | IFFRSIAPB | SLDPSNKKVL | TVLNKLNRP | LERFRKERE
 | PVVRETVGP | DCHLSMLQG | LSHVNAKPB | KGLVKGEEA | SDPACTIPM | VSKVDSKRE
 | YGLCGVLCD | SVGVFNDSI | ELLHNKDG | LQYLEKPTK | VLYFSHSH | SLMKITLLK
 | FVRYHSHLL | LKAGANTPE | ESHVRLPFI | LTFWFETBA | IILHLSNGSY | QHNFQHTK
 | LILCLMAAV | TYDKRSDFR | TVRLSLREY | GCKCELASL | RYARTNVKL | LSSASNNEL
 | KAS

Seq ID NO: 111 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 75

| TTTCTTTCAT | GTTACGACTT | TCTATCTCT | CCAAGAAGG | CAGCAAGCT | GAGTACGAG

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CAACACGCC ACCACCAACA GCGAAAAACA AACATGATGG TGAGGGGCAT GGCATAGACC 120
 TTGCTTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCAATGTTCA AAGAGGAGCC 180
 TTTCTTTCOA CACCCGCTGG GGTAAAGACA GTGAAAGTGG CAGATATTGA GAAGAGCTCC 240
 ATAACTTACC CACTACAGCA CTGTCACGLA ATAGAGTGA TTATTTACTC GAGAGAAAT 300
 AAGGACAC GATGCTTAAA TCCCAATCCG AAGCAAGCA GCGTTATAT CAANAAGTT 360
 GAAAGAAAGA ATTITTANAA ATATCAAAAC ATATAGACT CTGAAAGGG GCATCTGAAG 420
 AACCTACAC AACCTTAACT GTGACTACTG AATAGACAG AATCTACAG TAGGAAATC 480
 AGACTTTCT ACCTTTTCT GACTTTCCAC TTCTGTCCAC TTATGTGAG GATGAAAGT 540
 GGTGTAAAG ACCAAAGCA GAATAGACT CTCTCGAAT GAATGCAAT CAGAATCCA 600
 CTGCGCAAG GACTCACCA ATTAATGGA TTCTAGAA AAGTACCTT AAGAAGCCT 660
 CTGACCATC GCACCTTACA AAGTCCCTTC ACCTTCTTAC TTGTTTAT ATACATCAT 720
 GCATTTCAG GCTAGAGAAC CTTCAGATAT TGATCTCAG AACCTTAT TTGTTTAT 780
 GACAGATT CTCTCTAG AGATTAATG TCTATTGTA TCTTANGT ATATTACTAT 840
 CTCTCTTAC AGTGGAGACA TTGACATAT TACTGGATC AAGCCTTAT AAGTCAAG 900
 CATCTATGT TGTAAAGCA TTGCTCAAAC ATTTTTTCT GCAATACAC ACTCTTTCC 960
 CCAATATCA GTAGAGCAT CAATNTGAT GMAACATC TTATGATCA TTGTTTGT 1020
 TTATATCA ATTCATAT TGTATTCAT AAATTTTCT ATGAADAA TTATAGCTA 1080
 TGGATCTG GACCAATG ACATATTCA TAACCAAT AGCAGCAGC GTCTTATTT 1140
 GATGTTTTT AACCTTTAT CATTGATG TTGGAAGCA ATTAGATAT GTGTGTTAC 1200
 TGTACTTTT GTTTTGATCT GTTTGTATTA ATGATAGCA TATCTTGAC ACATTTAAA 1260
 TACAAATGT TTTGTCTAC CAAGAAJAA TGTGAAJA TAGCAAGT TATCTAGC 1320
 AATCATTT ACTTTTGA ATTCCTGCT TMAGAAAT ACATATCTA ATCAATTCT 1380
 TTGTTCATG CTATATCTG TAAAAATTAG GTATACTGA GACTAGTTA AAGAATCAA 1440
 GTCATTTTT TCTCTATAA ACTACACAA CCTTCTTT TTAAMAAAA AAA

Seq ID NO: 112 Protein Sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 MSVKQNAL AVILCAATVVG GPFNFGRRC LCIGPGVKAV KVADIEKASI MYPSNCKDI 60
 EVIITLKENK GQRCLNFKSK QARLIKKIVE RKNF

Seq ID NO: 113 DNA sequence
 Nucleic Acid Accession #: NM_001110.1
 Coding sequence: 470..2716

1 11 21 31 41 51
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 CGCGCTCGC GTGCACTGTT GTGCGCGCGC CGTCACTGG TGAGGAGAGA CGCGGAGCT 180
 TGAGTTTCCA GCGGCGGGGG GAGAGAGAG GGAAGAGCA AGCGAGAGAA ACOCGGGAATC 240
 GGAAGAGAGA AAGAGACAG AGCGAGGAG GTCCCTTTT TGAGGAGCT AGAGAGGAT 300
 CCGCGCCCTG AAGTGGAGCG AAGCGGAGT GCTTCCCTT TATCTCTCC AGGAGAGTC 360
 CGCGCTCCG GTGAGAGCT CCGAGCAAG CCTTCAAGT TCTCCTCCG GATCATGTG 420
 CTGCTGTTAA CCGGTGAGA GCGCGCGCG GCGACAGCG CAGCGAGA GATGTTTCT 480
 GAGATGTTA ATTCGCTCC TCTCTCGCG CGCGCGGATG GAGCTCAAT TGTGATCAT 540
 TTTTATAA TATATGAGC ATTATGAGG ATATCTTAC ATGTGGAT CATTCAGC 600
 AAACACCG CTGCGAJAA GAGAGCTC CATGAGAC CAATTTTAC GTCTAGTTT 660
 CCAATCCCT AGAAGACAT TCAACTCAG ATGAGAGG GACACTCCC TTTTCAATGA 720
 TGAATTTAA GTAGAACAT CAATAAAGT ACTTATAT GATACCTCT ATTTACAC 780
 TGACATATT TATGTGAGG AAGGAGTGT TACCAATGG TCTTATTG ATGAGAGAT 840
 TGAAGATTC ATTCACATC GTGTGTGCG CATTAATG GACCGACAG AGAGATATAT 900
 TAAAGCDA ACTCTGCCAT TTCACTCTGT CATTTATC GAAGATGATA TTAATCATC 960
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 ATACAGATG ACTGTGTAG AAGAGATAC ACAGATCTC CAGAGACAG ACTCTCAG 1080
 TGCTCCAGA CTTCACAGA AAGAGATG ACTATGCT GAGAGAAATA CTTCAGCT 1140
 TTATATGAG ACTCATCAT TTCTCTTAA ATATTACGA ACAGAGAGG CTGTGATTC 1200
 CCGATATCC AGTCATGTTA AAGGATGGA TACATATT CAGACACAG ACTTCCCG 1260
 AATCGTAC ATCATCTCA TGTGAGACG CATAGAGTC AATACACTG CTGTAGAGA 1320
 GGACCTTACA ATCTCTTCC GTTCCGAAA TATGTGTG GAGAGATTCT TGGATTTGA 1380
 TTCTACAGC AATCGTATG ACTACTGTT GCGTATGTC TACAGACCC GAGATTTGA 1440
 TCAATGCTA CTTCCTCTGG CTGCGTGTG AGCACTTCA GMAAGCTCG GAGGATATG 1500
 TCAAAAGAT AAATCTTAT CAGAATGTA GAGAGATCC TTPAACCTG GAATATTAC 1560
 TCTTCAGAC TATCGCTCT ATGACTCTC AGAGATGCA TATGATCT TGTCTCAGA 1620
 ACTCTCAT ACTTGTAT CCTCACTGA TCTTGAGCA CATGTGCAC CAGGAGATCT 1680
 TAAATATTG COTCAAAAG AAATAGCAA TTACATCAG TATGCAAG CACATCTGG 1740
 GGACAAATC AACACAATA ATTTCTACT CTGATGAT AGAATATAA GCGCATTTCT 1800
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 TACAGACAT AGAGACATC GTTTTGTGA ACTGACGA CTATTTCT GATAGAGAT 2040
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 TCCCATGCA AATCAAGAC GTATGTTG CTATGAGC CAGTATAG AATGATGCT 2160
 TCCCATGCA AATCAAGAC GTATGTTG CTATGAGC CAGTATAG AATGATGCT 2220
 TCCCATGCA AATCAAGAC GTATGTTG CTATGAGC CAGTATAG AATGATGCT 2280

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5 ATCAACTTGT GCCATACAG GCTCTGTGCA GTGAGATAGG CACTTCAAGT GTCGACCAT 2340
 CACCCTGCCAA CTCGATACAG CTTCGACAGG TTTTAGAGGT TACTGTGAGT TTTTCATGCG 2400
 GTGCGATTAA GTTAGAGTCTG ATGTGCTCTT AGCTAGAGGT AAAAAAGCA TTTTTPATCC 2450
 AGAGCTCTAT GAAGACATCT CTAATAGGAT TGTGCTCAT TGTGGGCGAG TACTACTAT 2520
 GGGATATGCT CFCATCATCG TAATGCTGCG ATTTATTAAG ATATGCAAGT TTCATACTCC 2580
 AAGTAGTAAT CCMAAGTTGC CTCTCTCTAA ACCACTTCCA GGCACCTTAA AGAGAGGAG 2640
 ACCTCCACAG CCATTTCCAG AACCCGACCG TCMGCGCCCG CGAGAGAGTT ATCAATAGGG 2700
 AGACATGAA CCGTAACTCG ACCTTTTGCG TTAGCTCTTC CTATGCTCTA CAATGEEAA 2760
 ACTTCACTCC AAGAGAGAAC CTATTAGATC ATCATCTCCA AACTTAAACC TCAGAGTAA 2820
 CAGTGAAGA AAAAAATGCA TCGCATGATA TCTCCAGACC AGGTGGAATT ACTTAAATT 2880
 TAAACCTGGA AAMTTCNAAT TGGGGGGTGG AGAGTGGAA AGAACCTGAA TTTTCTTATG 2940
 AACGAGATAT TTTACTTTAA TGGCAGAGAG TGTGCTTCTC CTATGCTCTA CAATGEEAA 3000
 CTCTTCTTC GTTGTGCTG TTTCTTCACT TCGACGCCAA CTTGCGCTCC AATAAACTTT 3060
 TACCACAAAT TGAATAAAT ATATTTTTTT CAACTGCCAA TCAAGGCTAG GAGGCTGAC 3120
 CACCTCACCA TTGGAGACAT CACTTCCGCA TCTATACATC TGTATTATGT CAGACATATA 3180
 TCTTTTATT ATAAATATT TCGACTTTTA ATAAAAAT ACTGTTTAT TACACATGCT 3240
 AGGATAACAG AGAATGTGCG TATTCACTCG TCCAAGATC TGTATTGCTT TACACAGCA 3300
 GTTTTGAAT GAAATCAAT TAAACCATG GTACCCGAGT CTGAGATTC 3360

Seq ID NO: 114 Protein Sequence
 Protein Accession #: NP_001101.1

25 1 11 21 31 41 51
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 RLDPHANRRH PHLRKGDDTS LYSDEPKVET SNKVLDTVTS HLYTHIYGE BQSPHSGVFI 120
 DRDFRFOFOT RGDTTVPVPA RYKIDKDTLP PHSVLYRED IYPIKGTGP KCSGASVFE 180
 RMKYTGOTG EBNHLYPQHE KCTTGADELLA KCTTGADELLA LPTFVYDTH LPTFVYDTH 240
 30 AVLQATSRV KADITVYDTH DPSGINTSIF MKYRIRINT ADEKDFNFP EFNINQVSKF 300
 LELNSRQND DCLYAVFTD RFDPDGVGLG AMVGPSPGSS GQICEKSELY SDQKSKLNT 360
 GIITVQNYGS RVPVPSBHIT FAREHVHNG SPHDSGTCT PHSRSLGQK EBNHLYHAR 420
 ATSDKDLNHS RFELCSIRH SVQSEKHSR CPVSPGQIC KPSHSGQES KCSGASVFE 480
 35 DRCPGAMG RERKELCAL KESGSRQDC CTAQCAFKSK SEKSRDSDSD ARBGTCHQPT 540
 ALCPABDFPK NPTDCNHTG VCINGQCAHS ICNKYGLBEC TCASDDSDSD KBLGCVCMK 600
 KMDPSTCAST GSVQSKRHSR GRITITLQBS PCNDPRGYCD VPMRCLWDA DPLASLKKA 660
 IFSPELYENI ABMVAHWHA VLLMGIALIN LMAAGFIKIS VHTPSNIFEL PPHPLFSTGL 720
 KRKRPPQPIQ QPQRPRRES YONGEHR

Seq ID NO: 115 DNA sequence
 Nucleic Acid Accession #: NM_000577.2
 Coding sequence: 41..529

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 CGGACCCCTCT GGGAGAAAT CCAAGCAAGT GCAAGCCCTC AGAATCTGG ATGTTAAACA 120
 GAGACGCTTC TATCTGAGGA ACAACCAACT AGTTGCGGGA TACTTGCAG GACCAAAATG 180
 50 CAATTATAGA GAAGAGATAG ATGTGTATAC CATTTAGGCT CAGCTCTGT TCTTGCGAAT 240
 CCATGAGAGG AAGATGTGC TGTCTGTGT CATCTGTGT ATGATAGCA GATCTCCAGT 300
 GGAGCCAGTT ACATCACTGT ACCTGAGGGA GAACAGAAAG CAGACGACAG CTCTGCGCTT 360
 CATCCGCTCT GACATGTGCG CCACACACCG TTTTGAATCT CGCCCTGTGC CGGTTGGT 420
 CCTCTGACGA GCGATGGAG GTACACACCG GGTGAGGCT ACCAATATG CTGACAGAG 480
 55 GTCATGTGCT ACCAAATCTT ACTCTGCGGA GACAGCAATG TACCTGGG GGTGCTGTCT 540
 TCCGATTTCT GATGCGAAG GACTGAGAGG ACATGCGACT CCCTGTGCC AGGGCTCCCG 600
 GCTATGGGGG CACTGAGACG CAGCCATTGA GGGTGTGACC CTCGAAAGCG GTCAACACAA 660
 CCGTGTACGA GATCTGTGCG TCTCTTCTGA CTGACAGCG TCGATCTGCT TCTGAGATAT 720
 CTCTCAFTCA GATCTGATCT AGGACAGCG AGCCGCTCA CAGACGCTT CAGCTGTCT 780
 60 CTCTCCCTCT CATTCAGCT TCCCATGCGG TGGATCCATC AGGCCACTPT ATGACCCCGA 840
 ACCAATGCG TCCCAACCG TTTTTCATCA AAAAGAAAG ACCAATCAT GTGGCGGCTT 900
 TTTTAAAGTT TGTGGAATAT GAAATTAAG ATTTGAGAT TTTTCTTTT CAGTCCGCT 960
 GAGAGAGAG CTTCTTTTGG GAGATATAT TCTTTGGGG AGAGGCTGAG GACTTAAAT 1020
 ATCTGTGAT TTTGTGAATG ATGTGTGAAG TAACTGTGAT CTTTTCCTT CTPTTTCTCT 1080
 65 TTTTCTATG ATGCCCAAC TGTGAAATAT TAAAGATAT GGTATATGT TAGCCCATTA 1140
 GCTTTTCTAT TCTTTTAAA ACCTTCTCAT AATCTGAGCT TTTTCTTTT CAGTCCGCT 1200
 CCGAGCTCTC AAGTCAAGC TCACATCTCA ATTTTTCAG GCTGCTGCG GATCTTAC 1260
 TCTATAGAG ATCTTCTAG CTCCCAAGCG TCTGAGACAA TGTGCTCTCT GGGTGTCTT 1320
 TCTCTCTCG CTGAGAGAT AAATGTCTCT TTGACATTTT AGAGCTCTG GACTTGTAG 1380
 70 ACTGTATGA AAGATGGTG TGTCTCTGCT TGTCTCCCG ACCAGAGCTC GACTCTGCA 1440
 GAGCGGAAA CATGAGCTGT AATATCTTCA GAGCGCTCA GGGTCAAGCA GACTACTCG 1500
 CTTTGGCG GTATCTGAG AATGATGCT GTATATATGT GGTGCAAAAT TCCATCTCT 1560
 CTGTCACTC AGCTCTGTT TACAATAAAA TCTTGAATAT GCTTAAAAA AAAAAAAA 1620
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 116 Protein Sequence
 Protein Accession #: NP_000568.1

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	1	11	21	31	41	51	
	MALETICPES	GRSSSKOPAT	RINDVHOKIT	TURNINGLVAQ	VLOSHNVLE	BRIDVVIEEP	60
	HALFLCHHQ	KMLKCHQK	DETHULURV	HTLSEBHW	QDKRFAPIRS	DSQPTTSES	120
5	AACHGWFLCT	AMBADEQVSD	THMPDQVWV	TKFYQDEE			

Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
	GCACITTAGC	TCAGTGATG	ATTTTAAGAA	GSATTACACC	TGTGCGCTGT	GCTCTUACTC	60
	CAGGCACTGG	GCTCAGGTAC	TTCTGCTCCA	GGTAAGCTTT	ATGAATTGCT	CTACAGCAT	120
	CATCAATGTT	TCCTTTCTGT	CGCTTGGCTT	TATTCATGAG	GCTCAGGTGG	GGGAAAGACT	180
15	GATGCTCCAC	TGTGACACGA	AGACAGATAA	TGCAAAATCS	GATTTCTATC	GGTGAGTCC	240
	AGSPACAGA	CTCCGACG	CGGATAAGCA	GATGGAAGC	TTTATCGTTC	TTTCACTAAG	300
	ANGICTGGTT	ATAGAAAGCC	CTGCTTTTGA	GGATGCTGGA	GTTGATCTCT	GTATGCGAAT	360
	GAATAAGCAA	GGCCTGTTAA	ATGAAATGCT	GGAGCTGACA	ATAAATGTGA	GCAATTTCCG	420
20	TGTAAACAGA	TGCCATGCTC	ATGAGGAGCT	TACACAGACT	TTTACCACTC	TTCTGCTTCT	480
	CTTGCGCAT	ATGCTTTTGT	TACTTTGTGA	CGCTATCTCT	ACTGCACTCC	CTGCAAGTGG	540
	TAAAGCCGAG	AGACAGAAJA	ATATGCTACA	CCAAAGCAAT	GCCATTCAT	GCAATTCAG	600
	TCCTGCGCCC	GACTAGTATG	CGTCCGCTGA	TGAAAGGAGG	GCAAGTGCAG	GTAAGAAGAT	660
25	GGTGTTTTTG	AGACCCCTGA	AGATACTCTG	AGCAAGGCGAG	AGCGGGAAAG	TCAGACTCTT	720
	TCCCAACGAG	CGAGGTATG	CTAAGGCTAT	CGAAAGGTGC	ACGAGGGGGA	ATCTGTACTC	780
	AGATTCACTG	AATTCAGTGT	TTTCTGACAG	ACCTTTTGTG	GGTTCACATT	AA	

Seq ID NO: 118 DNA sequence
Nucleic Acid Accession #: AB032989.1
coding sequence: 1..1316

	1	11	21	31	41	51	
	CCCATTCGTT	CGCCAGTTAC	AGAGCACTAC	TGGACCTGAG	TCCACACACAC	CTAGCGCGCC	60
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	ACACCTGGAA	CTTCATCTCC	CTGAGGCGCT	TTTCCCGCGT	ACCCAACTGT	GGCTACGTTG	180
	ACCTCTCTCT	CAACGACGTT	CGTACACTGT	ATGAGTTTCT	GTTCGATGAC	CTGCAATGAC	240
	TGGAGGTGCT	GCTCTCTAC	AAATACACCA	CGATCTGCTT	CGACCTCTGC	CGCTTCGATG	300
	ACATGGCCCA	GCTCGACAAA	CTCTACTCTGA	CCGAGAACCA	GATCTCTCCT	TTCCCTCTGG	360
40	AACGTGTCCA	GGAAGGAGGC	AMGCTACCCA	AACTAAAGCT	CGTGGATCTC	TTTTTAAGCA	420
	AGCTGAAGAA	CTTGCGATTG	CGTGAAGCTG	AGAGGCTGCC	GGCTCGGACT	AGAGTAAGGC	480
	TGTACTTACA	TAAAGACCC	CTGAAGCTGT	ACTGTGACT	CTACAGCTGT	TTTTCAACT	540
	CGCAATATCG	CGACCTGAGC	TCCGTGATGG	ACCTTCAGAA	GGATCTGTAC	CTGATGAACT	600
	CGAAGAGCT	CGCAATGTC	TTCAACTCTA	GTTTCTCTAA	CTGTGGGAG	TACAGAGAGC	660
45	GTGCTGTGGA	GGCCCACTGT	GGTGAACGCT	TGATGATCAA	GTGTGACACC	AAGCAGAGAG	720
	GGATGACCAA	GGTGTGGGTC	ACACCAAGTA	ATGACGCGT	CGTGAATGAG	GTGACCAATG	780
	CGACGTGCG	TGTCTTAAG	GATGCACTC	TTCTTTTCCA	CGAGGTGCG	GTGAGGAGCG	840
	GTGTGTGTGA	TACCTGCTAT	GGCATGGGAG	AGACTTTCAA	TGAGACACTG	TCTGTGGAA	900
	TGAAAGTGCA	CAATTTCAAC	TTGACGGGAC	ACCATGACAC	CTTCAACACA	CGTATACCA	960
	CCCATATGGG	CTGTATCTTT	ATGTGTGCTC	TGCTCTGAT	ATACATATAC	CTCAACCTTT	1020
50	CGCTGTGCTG	GTGCGCGGCT	GTGAGAGAGC	CTTCGAGCCA	TGAGAGAGAC	AGCTCTAGCT	1080
	CTTCCATGCT	TAGTACACCA	CCCAACCATG	ATCCTATGCG	TGTTGGGAGC	AAGATGATG	1140
	GTTTTGACCG	GGGGTGCTCT	TTCTCTGACAC	CTGCTGAGCC	TGGCAGCGGT	CGACGAGGAG	1200
	AGCTCAAGCG	AGGCACACCC	CTGCGGCTGC	CTGAGAGCAC	AGCCAGAGCG	CAAGGAGGAG	1260
55	TGTCGAGCTC	AGACATGCTC	AGCTCTGCTT	TTCTCTGATC	CGCCATCTGT	GTGTGAGCAG	1320
	GATGGCTTGG	TGGGAGAGTT	TTGCGCCAGG	AGAGGTAAAT	CAATCGTGA	GGATATGAGG	1380
	GGATGAGAGA	GAAGCGTGCG	TGCCCAAGGA	AATGGATTCC	TGCTACAGAG	AGAGGAAATG	1440
	GTCCGAGTGA	CACACAGAGG	CAGAGGCCCA	AGAGGAGGAG	CTGTGCCAGC	ATTTTCAAT	1500
	GGGGGTATAT	TAACTGATCT	CGAAATGCTA	CGAGCTTACC	CAAGGCCCTC	CGAATTTCTA	1560
	GTGTGTGAGA	GGAGAGAGAG	CATGTGAGTC	TTGGATGGGA	ATGAGAGAGG	AGTGAGGGGA	1620
60	AGACACGATT	CCCTAAACTT	TGATGAGCTC	ATCCCTAGCT	CGTTAAGAGA	AAACATTTTA	1680
	GAAAGAAATA	TTTTTTCTAT	CTGTGCCGAC	CCACACCTGT	GATGTGTGTG	GTGTGGGAGT	1740
	AGCTTCACAG	GGAGCGAGAG	TGGGAGAAAG	CTGTGATATC	TTTCTTTTAT	ACGATGATCT	1800
	CAATCGACGC	TGGGAGAGTT	GAAACCTTT	GGAAGATGAG	TGAGAAAGG	GCTGAGACTC	1860
	CAATCGGTAA	CAATTCGCCA	AGCTGTGTTG	AGAGCTTTCC	ATTAAAGCCT	TTTCTTTTCC	1920
65	TGATGTGCCC	TGGTGGATGG	GATCTTTGCA	GGAGCTTGCG	CTGCTGCTCT	TGATGTACAA	1980
	CAGCATATGT	GGATGTGATTA	GTGCTGCTCT	AGCTGCGAGC	CAATCTACGA	GAGGTGTATA	2040
	CGATGATGCT	AGGCTGCAAT	GTACAGCACT	AGTGCGCAGC	AGGAACTGTC	TGATGCGGGG	2100
	GTGAATTTCA	GATAGGCTTAA	TTTCCCTGGT	GGTGAAGGCT	TTGGTTAGTA	TTTGATTTCC	2160
70	AGCATCTGTG	TGTCAAGGCA	GAGTGCGGCG	TGCTAAAGGC	AGAGCTGTAT	TGATGCTGCT	2220
	CCAGAGAGCT	GGTACATGCG	CCCTATCTAC	GAGAGAGAGA	TGAGGTGATA	TGACCTCTTA	2280
	TTATGTAGCA	CTGATCTGGA	CTTAACTGAT	TGCAATATTA	TGCTCATCTT	TAATCCACTG	2340
	TCCTTATCAA	GCTCAGGTGG	GATTTCTGAT	TTTCCCTTAT	ATGCTGTCTCT	GTAAGCGGAG	2400
	GATTCGAGGA	AGAGCTGGCC	CGAGCTGGCT	TAGAGTAGGC	TTGGGATAGG	TGAATATCCA	2460
75	GTATATATCT	CGTCTGTGTC	GAGAGAGGTT	CTTGTCTCTC	CTAGAGAGCT	CAAGCTTTTC	2520
	CGAAGATGCA	AGGCTGGGAG	TTTGAATCTC	AGAGAGGTTG	GAATGTGGTG	GTCTTACACC	2580
	CAGATATGCA	ATTTTGGAGT	CAGCTTGAG	TTCTGCGCTC	TGCACAGATT	CAGGCAATTC	2640
	CTAAGGAGCA	GATATCAATG	ATACTTAAGC	TTTCAAGAGG	GGAGTTTCTC	CACCCCATTC	2700

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CTCATCGAG AGGTGTTTC AGTTGTGGT GTGAGCCAG AGCACTTAA GAACATGAG 2760
 CTCACATTC CATTCATCC AGGTTGCGG ATACTCTGA GTATGAGAT GACCATGCC 2820
 TTBACTTT CCTTTGAG ATACAGGAG CATTGTGAT GGTTCCTTG AGCTTTGGG 2880
 GGGATGAG AGGTTGAGG TGAATAATG TCTGATGTT GOTTTTCTT AGTGTCTCT 2940
 5 CTCCTCAAG TTCTAGTCC ATTGAGAGT CTCAGATCC CTGAGATTC TGACCTCTTT 3000
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 CTCTCTATT AGTGTGAGG AGGAGGACT AACACTGTC CTTGTCTGG TCTTGAGAG 3120
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 10 CACTTGACT ATGACAGGA CAGTGAACT GTAGTCCCA TTAATGATC TCTGAGATG 3300
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 15 AGAAAGTTC CTGAGAGCT ATATATAGA GGAATATAG AGCAATTAG ATGAGATAGA 3600
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 TOTTAAGCT CCGCAGGGA GAAGATTGT CTGATTAT TCAGAGAGT CCGTGAATT 3720
 TTGTTATGG AGCTATAGA ACTAGGACT CCTCTCGA CTCATCAGA AATCTGGAA 3780
 AATCTCAT CTCTCTGCA GTCTCCGCG TTGAGACAT TAGGGCTCT GAGATCTTT 3840
 20 GTCATGAG GATCTGAG GAGGCTCT GGGGCTGT GAGTGGGCT CTGAGAGCT 3900
 GAGAGGCT TTCTTCTA ATTCTACCG AGTTTAGGA ATGAGAAAG GCGCTGTGG 3960
 TCTTAAGCT CCGTACTATA TCACTAGT TGGCTTGG TTGAGACAC CTGTAGATG 4020
 TACTGCGTG CCTACAGAG AGATTGAT TTCTCTTC GGTGTTTCA GGTGATAGA 4080
 25 CCGAGAGTA GCTTTTAT TGGAGATTG ATATACAGC ATATGAAAG GACTGAGAG 4140
 CCTGTGTGA AAATCCGAG GTGTGGTAT AGGAAAGGC CGAGAGATCA CCACTCTCT 4200
 TTACCTTAC CCAACCCAT AAACACAGA TGTCTCCAG GAGACAGTG TCGCTGAGA 4260
 CAGGATAGA CAGGCTCTA CAATCTGGT AATTATTAT ATTATTATA TTTGTATT 4320
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 30 GGTCTGCT TTCTGTGT TCTATCTCT GTACTCTCT GTAGCTCTG TGACAAACA 4440
 AGCAGGCTC CCGTGTCAA GACCCATTC CTCGACTTG TTACACCTA GGTGTGCAA 4500
 TCTTGAGGC TCTGGCTCT GAJAACTAG CATGTGAT TAAACTGAG TGTGTTCT 4560
 GTTCTGC

Seq ID NO: 119 Protein Sequence
 Protein Accession #: BAA96477.1

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 LVKSAKPK TFLDLSVKK LKLPFLPLG KLPKHNKGL YLRNPLACD CFTQLFSPW 180
 QYQLSSVMD FQDLVQMS KELINVFVLE FLNGBYKER AWEHGLDYL IIKCDTKQG 240
 MKVHVFPN SRVLDVHTG TVSVSKDGL LFQGVQVED GYVCTYAME TPNELLEVEL 300
 RVINDFLRH HDLNTAYTT LVGCLSVLV VLYLYLTFP KWCGRVIER SHSGDSELS 360
 50 SMSTTPHSD PHAGIGKGGD FDRVAFLEP ASPPQQNGK LKPNLPLPV EATGKQRHM 420
 SDPSVSVSF SDPIIVV

Seq ID NO: 120 DNA sequence
 Nucleic Acid Accession #: NM_005071
 Coding sequence: 9..1703

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 GCGTCCGCT CGAGACCAT AGCTCTGAG AGCTGTGG CTCTCTGGC GAAACGCTCT 180
 TCAATCTGT AGGCTCAGC GCGCTGGTCA TTGGGTTGAG CTTGGCTCTT GCGCTCGC 240
 60 CATATCAT CTACTCAT GAGTCAAGT ACTCTCTT TCGAGAGAG CTTCTGATGA 300
 GATGCTGCA GATGCTGGT TTACTCTCA TTCTCTCCG CCGTGTACA GGTATGAGAT 360
 70 GATGACAA CAGAGCGAC GGGCGGATCG GATCGGAGC AGCTGTGTAC TACATGTGTA 420
 CCAACATAT GGGGTCTTC ATGCGATCT TATGTTCTT CATATCATCT CCGGAGATG 480
 GCTGAGGA GGGCTTGGC CCGAGGAGCG GATCGAGC CATATCAGC GAGTCAAGCT 540
 80 TATGAGACT GATCAAAAT ATGTTTCCAC CAAACTCTT GAGAGGCTGC TTCAACAAGT 600
 TGAAGAGCA GTACACAGC AGGTTGTAT CAGAGAGAT GTGAGAGCA GAGAACGGGT 660
 65 GCGAGCGGG TGCTTCAGT CTTCTCTCAT TCTCATGGA GAGAGAGACC AGGCTCTGAT 720
 AATATCTAT TGGCTGCT AGGAGAGCT CCAATCTAT GATCCACAC GAGTCTGAT 780
 CTTGCTTGG CTCCGCGAG GGCATCAAG CCGTGGGCT CTGGTCTCT TCTGTGGCT 840
 TTGGCTGGT CATTTGTGG AGGAAACACA AGGCGAGAT CTTCAAGGAC TTCTTGACA 900
 90 GCTCAATGA GCTTATTAT AGGCTGTGG CTGATCAT CTGTATGTA CTTGTGGCA 960
 TCTGCTGCT GAGAGAGCT CCGTCTTGT AGATGTGTA AGATGTGTA CTGCGGCTC 1020
 AGTGTGAG GTACACCTG AGCTCATCT TGCGCTCTT CTTCTCATCG GCGATGTCTC 1080
 TCTCCCTCAT CTACTCTCT GTCACTCAC GAAACGCTT CCGCTCAT CTGGGAGTCC 1140
 TACAAGCCT CATCACGCT ATGGGCACT CTTCAAGCT GCGAACGCT CCAATCACT 1200
 100 TCTGCTGCT GAGAGAGCT CCGTCTTGT AGATGTGTA AGATGTGTA CTGCGGCTC 1260
 TGGGCTCAT GTTCAACAT GAGCTCAAG TGGGCTGAT CACAACCAT AGCATCAAG 1320
 75 TGGCTGAT TACAACAT GAGCTCAAG TGGGCTGAT CACAACCAT AGCATCAAG 1380
 CCACAGAGC CAGTGTGG GGTGTGCGA TCCCCAGC GGTCTGCTC ACATGTGTA 1440
 TTGTGCTAC GTGCTGCGC TTGCGACG AGAGCTGAC GCTCATCTC GCGTGGACT 1500

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GCTTCCTTGA CCGCTCTCC ACAAACACCA AGCTACTGGG GCACTCAATT CGAGCGGCGG 1560
TCTCGGACCA CTCTCTCAG CCGGAGCTGG AGCTTCAGGA AGCTGAGCCT ACCCTCCCCA 1620
GCTCGGAGAA ACCCTACAG TCCCTCATCG CACACAGAA GCGGGCATCC CGGCGACCGG 1680
GAGGACAGCA GAGCTCATG TGGGCGGCT CCGCTCTG

Seq ID NO: 121 Protein Sequence
Protein Accession #: NP_005962

1 11 21 31 41 51
MSHGNLSPL RESQRLGRV GWLRLRBSL QORALERLR LQNTMLEHLV RFLRNAPIL 60
LVNVAIVIG BLAPLRFPO LTROIKFTS FFSLELLRGL QWVLEIVLS ELYNCHASL 120
NRTGQWBE AJYFVVTI AWFGILAW TITNFGSKS BGLRRRERIE TITPDAMPD 180
LIRNMFPHL VEAFCQFRT QSTRVVTI MVRTENGSEP GAKMPPFPVS ENKTSFLENV 240
TRALGTLOEM LSEETVPVP QGANGINALV LVVPSVAPOL VIOGMHKGK VLRFDFSLN 300
BALRMLVGII IVYAFVLLI LIASIKLEME DMALVSGGLG NYTLTVIVGL FMRHIVLPL 360
TFLVTHNP FFDIDQLG LITMGTGSS GATLTYFIC LREGLQVBR ITFVULVQA 420
TVNMGTALV DALAAIFIA VNNYELNAGL ITTISITATA ASVGAAGIPL AGLVTHMIVL 480
TSVGLTFDI TLIIAVDWFL DRLRMTNVL GDSIGAAVIE HLGQRELEQL BASLFLSLG 540
KPYSLMAQE KGAORGRON ESMH

Seq ID NO: 122 DNA sequence
Nucleic Acid Accession #: NM_031966.1
Coding sequence: 178..1479

1 11 21 31 41 51
ACGACAGCG CATAAGAGG GAGCAGTGC GGGTTTAAA TCTGAGGCTA GGTCTGCTCT 60
TCTCGGCTTO CTGCGAGCGA AGCAGCTTGT GTTCTCTGT GTTCTAGCT CTGTGCTGT 120
CGGCTCTCG GTTCTCTGT TCTCCGCTCT GAGCTCTGCG CTGCTGAGGA GAAAGCCATG 180
GGCTCTCGAG TCACCAAGAA AATGCTGAA ATAGCGGAA GATCAACATG 240
AGAGCAGCTA AGCCTGCTC TACGCGCCCT GCTGCAACCT CCAAGCCGCG ACTGAGGCCA 300
AGACAGCTCT TTGGGACAT TGTAAACAAA GTCACTGAC ACCTGCGCG CAATAGCTT 360
ATGAGAGCG ACGAAACAT CTAGGCTCT GGAAGATCA TGTATAAAA ACTACAAAA 420
CCTCTGAAA AGCTACCTAT CTGTGTGCA GTGCACTGT TGGAGCAAG GCGACAGCA 480
GAACTGAGC CAGACAGCA GCTTGTAAA GAGAAAAAC TTTGCTCTGA GCTATTPTG 540
GTGATGATG CTTCTCGAG CCAATGGA ACATCTGAT GTGCTCTGAG AGAAGAAAC 600
CTGTCTCAG CTTCTCTGA TGTATTCTT GCTGAAATG ATCTGAGC AGAATAGGA 660
GCTGATCAA ACCTTTGAT TGAATATGT AAGATATTT ATGCTATCT GAGCAACTT 720
GAGGAGAGC AAGCGTACG ACCAAAATAC CTACTGGTC GGAAGTCAC TGAACATG 780
AGAGCATCC TAATTGACTG GCTAGTACG GTTCAATGA AATTCAGTT GTGCGAGG 840
ACCATGTACA TGACTCTCT CATATTAAG CCGTCTATC AGATTAATG TGTGCTCAG 900
AAGATCTGC AGCTGTGAG TGTCACTGCG ATGTTATTG CAAGCAATA TGAAGAAATG 960
TACCTCCAG AATTTGTTGA CTTTCTTTT GTGACTGACA ACATCTATAC TAGCACCAG 1020
ATCAGACAGA TGAATAGAA GATTCATAAG GCTTAAACT TTGCTCTGG TGGCTCTTA 1080
CCTTCTGACT TCTCTCGAG AGCATTAAG ATGCGAGAG TGTGTTGCA GCAACTACT 1140
TTGACCAAT ACTGATGCA ACTAACTAG TTGACTATG ACATGTGCA CTTTCTCTCT 1200
TCTCAATGT CAGCAGAGC TTTTGTCTA GCACTGAAA TCTGATATA TGTGATGAG 1260
ACACCACTC TACAACATTA CTTGTATAT ACTGAGAAAT CTTCTCTCT AGTATAGAG 1320
CAGCTGCTTA AGATGTAGT CTTGTAAAT CAGAGCTTA CAGAGCACT GACTGTGAG 1380
ACCAATGTA CCAATGAA CAGTCTAAG ATCAGCACT TACCACAGCT GAATTCGCA 1440
CTAGTTCAAG ATTAGACAA GCTGTGCGA AAGGTGTAAC TTGTAAACT GATTTGGAT 1500
ACTATATTA CAAATAAAT TGGCACCAG TGCATCTGT AAAAAAANA AAAAAAANA 1560
AAAAAANA AAAAAA

Seq ID NO: 123 Protein Sequence
Protein Accession #: NP_114172.1

1 11 21 31 41 51
MALRVTRNG INAENIAKIN MAGAKRVPTA PAATSKPLR PRALQDIGN KVSQQLQAM 60
PMKKBKPSA TGTIDIKPL KPLKRVHMLV PVPSPVPV PEPEPEPEV KEELSEPEI 120
LVSTAQSPM ESDCAQAE DCAQSPQV LAMCVQAD GAMPKCSY VIDIVALEQ 180
LREKAVRPE YLGRGVTON BRAILIDMLV QVQKFRLLQ STNMIVSII DEPMKNCVF 240
KRMGLVGVT AMPIASKYSE MYPPGIDFA PVTINVTIKI QIRQMBKIL RALMFQGRF 300
LPLHFLERAS KIGRVVDEH TLAKYIMELV MLDYNNVHF PQSLAQATF LAKLILNBE 360
WFTLQHTLS YTESLLPMM QILAKNVWV NGDYTKMVF KRYATSKIA KISTLPQAS 420
ALYDLAKAV AKV

Seq ID NO: 124 DNA sequence
Nucleic Acid Accession #: E05 sequence
Coding sequence: 13-1424

1 11 21 31 41 51
TAGAAGTTA GATGAGATT TCTCTTAATA CTGCTCTGCG AGGCCACTGC TTCTGAGCT 60
CTTCCCTGTA ACAGCTCTAC AAGCTCTGGA AAAAATAATG TGCTATTTCG TGAAGATAC 120

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TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACCTTA TGAGAGAAAA AATCCAGAGA ATCAGACACT TCTTGGGTCT GAAATGCACC 240
 GGCGACTCTG AGACATCTAT CCTTGAGAGT ATCAGACACAC CTGCAATGTG AGTCCCGGAT 300
 GTCCATCAT TCGAGAAAT GCCAGGGGAG CCCTPATGGA GGAACATTA TATCATTAC 360
 5 AGAATCAATA ATTACACACC TGACATGACG CTGAGGATG TTGACTACCG AATCCCGMAA 420
 GCTTCCCAAG TATGAGATAA TGTTAACCCC TTGAATATCA CAGAAATTAA CACAGGCATG 480
 GCTGACATTI TCGTGGTTT TTGCGCTGGA GCTCATGAG ACTTCCATCG TTTTGATGAG 540
 AAAGGTGAAA TCGTATAGCA TGCTTTTGGT CCGGAGCTG GATATGAGG GATATGACAT 600
 TTGATGAGG AGAATCTCT GATTAACAT TCAAGAGACA CAAACTTCT CTTCACTGCT 660
 GTTCAAGAGA TTGGCAATTC CTGAGTCTT GCGCACTCTA GTGATCCAAA GCGCTTAATG 720
 TTCCCACTCT ACAAATATCT TGACATCAAC ACATTTGCGC TCCTGCTGTA TACATACAGT 780
 GGCATCTCAT GCGTGTATG AGACCCMAA GAGACCAAC GCTTGCAAGT TCTTGAGAT 840
 TCGAGCCAG CTCTGTGTA CCGATATGTA AGTTTGTG CTCTCACTAC CTGCGAATA 900
 NAGATCTTTT TCTTCAAGA CAGGTTCTTC TGCGTGAAG TTTCCTGAG ACCAAGAGCC 960
 15 AGTGTAAIT TAATTTCTTC CTATGAGCA ACCTTGCCAT CTGCGATTGA AGCTGCTTAT 1020
 GAAATGTGAG CCAGAAATCA AGTTTTCCT TTGAAGNTG ACAAATAGT GTTAATTAAC 1080
 AATTATGAC CAGAGAGCA TTATCCAGAG ATGATACAT TTCTTGTTT TCTTAATCT 1140
 GTGAAAAAAA TTGATGACAG TGTTTTAAAC CCGAGTTTT ATAGAGCTTA CTCTTGTGA 1200
 GATAACCAAT ATTGAGGATA TGATGAAGG AGACAGATGA TGGACCTGTG TTATCCGAAA 1260
 20 CTGATTACCA AGAATTCGA AGGAATGCG CCGAAMTGG ATGAGCTCTT CTATCTTAA 1320
 AACAACTACT ACTATTCTT CAGAGATCT AAGCAATTG AATATGCTT CCGATCCAA 1380
 CGATTACCA AACACTGAA AAGCAATAG TGCTTGCTT GTTGAATAA GTGTATTAA 1440
 TGGTTTTTGT TAGTCACTT CAGCTTATA AGATTTTAT GCAATTTTG TATCTGCTCA 1500
 GTGTACACT ACTTAGAGT ATGTATCTA AAAATAAAT CCGTAACCA TAGTATATG 1560
 25 TTATATAAAA TTTTCAATT TTTCAATT CTGAAGCTCT TGTATGCTT TCTTGCTGA 1620
 CTCTATCTT AGTGTGAAA ATAGTATGCT TCAAGCCAG ATAACTTAT TTGAGAGCT 1680
 CTCTGTAGT TGCTTCTGAA CATCTCTGA CTGAGAAAT ATACTACTT CTGCGATAAC 1740
 TAAATTAGT TATATATAT TTGCTCAAA TAAATTTG

Seq ID NO: 125 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 35 MKFLILLILLO ATAGALFLN SSTLSKXNV LPGRYLEKF YGLEINKLPV TRMKYSGNLM 60
 KBKIQGQHF LGLKVTGLD STSLNEMAP RGVFDVHIF RMFGPQVWR KHYITRIHN 120
 YTDNRBBDV DYAIRAFQV WSNVPLATP KHTGADLL VYFARGAGG HAFDGRGDI 180
 LABAPQSSQ IGDARFDD EPYTHWQST MFLTAVHEI QHLLGLRSH DPLVWPFY 240
 40 KYVDINFLP SADDIRGDS LYGGPKEMR LPNFDSEPA LCPHLSPDA VTVGNKIFP 300
 FDRFPKLEK SERPKSTNL ISSHLFTLP GIEAYEIEA RNOVFLKDD KYWLINLAP 360
 EPNYFKIHS GPFNPVKKI DAAVNPREFI RTYFFWQVQ NYDESRQHM DPGVPLKLT 420
 NFGSLGPKID AVFYSGKNFY YFGSQSQPE YDLQLRITK TLKSNHSPG

Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 272..742

1 11 21 31 41 51
 | | | | |
 50 CCGCACTCTG GCGCACTCA GGTGTCCAC ATCCGTAAAG TGCTCGAGAT TAATAGACAG 60
 TCTCTCGAG ACTGCTCAC GGCCTCCCTT TGCTTGGAAA GATGACCGAG TCCCTCCAGA 120
 GGATTGAGG GACAGGGTGG GAGCGGGCTC TTCCCGCAGC ACCCGAGAGA GAAGAAGAGA 180
 GGGCTGAGT GTACACAGAG GGTGGGGGCG ACCGCTTGGC CTGCGGGCTT CGGGAGAAGG 240
 55 GAGAGACAG CAGCGGGCGG CGGGAGACAG CATGAGGCC CGCGGGGAGA GACACATAGA 300
 GCTCTGAGT GACTGCTGCG CAGAGGCGCT GCGCGGGGPT CGGCTGAGAG AAGTTCGAGC 360
 GCTCTGAGG GCGGGGGGCG TGCCCAACGC ACCGATAGT TAAGTTCGGA GCGCGATCCA 420
 GACTGATGAT ATGCGACGCG CCCAGATGCG GAGCTGCTGT CTGCTCCAGC GCGCGAGCC 480
 CAACTGAGCG GAGCGCGACA CTCTCAACCG ACCGCTGAC GACCTGCTCC GAGAGAGCTT 540
 60 CCGTACACG CTGTGTGTC TGACCGGCGC GAGAGAGGAG GAGCTGCTCT GAGATGCTCT 600
 GCGCTCTCTG CCGCTGAGAC TGCTGTAGGA GCTGGGCGAT CGGATATCTG CAGGTFACCT 660
 GCGCGGGCTC GCGGGGGGCA CAGAGGGGAG TAACCATGCC CGCATAGATG CGCGGAGAG 720
 TCCCTCCAGC ATCCCGATT GAAGAGACGA GAGGAGCTCT GAGAGAGCTC GCGAAACTTA 780
 GACTGTAGT GACTGAGAT CCGTACGCGC CAGACTCTCC GAGAGAGCTC GCGAGCGG 840
 65 TTGTAGAT TTCAATTAGA AAATAGACT TTGAAAAAT TCGTGGCTT TAACTAGAT 900
 ATATGCTCC CCGCACTAGC GTAAATGTCC ATTATATCA TTTTITATAT ATTCTTATA 960
 AAATGTAAA AAGAAAAACA CGCTTCTGCT CTCTTCACTG TGTGAGGATT TTCTGAGTG 1020
 AGCACTCAGC CCTTAAGGCG ACATCTAGT GGCATCTCT TGACTAGAGG AACTCCAGCG GGGTACTG 1080
 GAATCTCTG ACTCATAGC AAGCACTTTG TGACTAGAGG AACTCCAGCG GGGTACTG 1140
 70 CTCTCTCTGA GTCACACTCG TAGCAATGCG GAGACCCAAA GCTCAATAAA AATAAATAA 1200
 ATTTTCATTC ATTACCTC

Seq ID NO: 127 Protein sequence:
Protein Accession #: NP_000068.1

1 11 21 31 41 51
 | | | | |
 75 MEPAAGSKSE PSADHLATA ARGEYSEVA LLEAGALPNA PNYGSRPIQ VYMGGAARVA 60
 ELLLLAGAEF NCADFATLIE FVHDAARESF LDTLVVLHRA GARLDVRDAN GELPVLAE 120

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LGRDVARYL RAAAGGTRGS NHARIDARBG PSDIPD

Seq ID NO: 128 DNA sequence

Nucleic Acid Accession #: NM_058196.1

Coding sequence: 104...421

5
1 11 21 31 41 51
| | | | |
TGTGTGGGG TCTGCTTGGC GTGAGGGGG CTCACACAA GCTTCTTTC GTTCATGCGG 60
GCCGCCACC TGGCTCTGAC CATTTCTGTC TCTCTGGGAG GTATATATGA TGGGCAAGGC 120
CGATGTGGC GAGCTGTCTG TGTCTCAACG GCGCGAGCCC AACTGGCCGC ACCCGCCAC 180
TCTCAACCA CCGGTGCAGC AGCTGTCCGC GAAAGGCTCT CTGACACAGC TGGTGTGTCT 240
GCGCGGCTC GCGGCGGCTC TGGAGCTGGC CGATGCTCTG GCGCTCTCTC CCGTGTGACT 300
GCGTGAAGG CTGGGCAATC GCGATGTGCG ACGTACCTC CGCGCGCTC GCGGCGGCGAC 360
CGAGGCGAGT AACCATGGCC GCATAGATGC CGCGGAAGGT CCGTCAGACA TCCCCGATG 420
AAGAAGCAAG AGAGGCTCTG AGAAACCTGC GAAACCTTAG ATCTCATCTC ACCGAGAGTC 480
CTACAGGCC ACACATGCCC CGCGCGACAC CGACCCGCTT TTGTGTATTT TCATTATGAA 540
AATAGAGCTT TTAAAAATGT CCGTCCCTTT AACTGAGATA TAGCGCTTCC CCGCATACCG 600
TAAATGTCCA TTATATCAT TTTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
CGCTTGTGCC TTTTCACTGT GTTGGAGATT TCTGAGTGA GACTACACGC CTTAAGCGCA 720
CATTCATGTC GCGATTCTTT GCGAGCTGCG GAGCTCCGCG AAGCTGTGCG CTTCAAGACA 780
AGCATTTTGT GAACATAGGA AGCTCAGGGG GGTACTGCGC TTCTCTGGAG TCACACTGCT 840
AGCAATGGC AGAACCAAG CTCAAAATAA AATAAAATAA TTTTCAITCA TTCACCTC

Seq ID NO: 129 Protein Sequence

Protein Accession #: NP_478103.1

30
1 11 21 31 41 51
| | | | |
MMGSGARVAE LLLHGGEPN CADPATLTPH VDAAREGFL DTLVLRHAG ARLDVRDANG 60
RLPVDLAEEL GHRDVARLYR RAAAGGTRGSN NHARIDARBP SDIPD

Seq ID NO: 130 DNA sequence

Nucleic Acid Accession #: NM_058197.1

Coding sequence: 272...646

35
1 11 21 31 41 51
| | | | |
CCCAACCTGG GCGGACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGAGT TAATAGCACC 60
TCTTCCAGAC ACTGCTGCAC GCGGTCCGCT TGCTCGGAAA GATACCCGCG TCCCTCCAGA 120
GGATTGAGG GACAGGGTGC GAGGCGGCTC TTCCGCCAGC ACCCGAGGAA GAAAGAGGAG 180
GGCTGTGCT GTACACAGG GGTGGGGCGG ACCCGCGGCT CTGGCGGCTC GCGGAGAGGG 240
GAGAGCCAGC CAGCGGGCGC GCGGAGCAGC CATGAGAGCG CGCGCGGJGA GCAGCATGGA 300
GCGCGGGCGG GGGAGCAGCA TGGAGCCTTC GGTCTGACTCG CTGGCCAGCG CGCGGGCCCG 360
GGGTGCGGTA GAGGAGGTGC GCGCGCTGCT GAGGCGCGGG CGGCTGCCA AGCAGCCAAA 420
TATTAGAGT CCGAGGCCA TCCAGGTGGG TGAAGGJCTC GCGAGCGAG CAGGAGATGG 480
CGGAGATCTC TGGAGACAGA AGTTTGCAGG GGAATTGGAA TCAGTGAAGC CTTCAATTCT 540
CCGGAAGAA GGGAGGCTTC CTGGGAGATT TTCAGAGGCG GTTGTATAC ACAGAGCTCC 600
TCTCGGACAC GCGCTGGGGG CTGGGGAAC CAGGAGAGAG GATGAGAGG CCAGCGCGCT 660
ACAGATCTCT CGATGCTGA GAGATCTGA AAGCGGAGAC ATATTGTAT TGAATGAGAG 720
TCATATGAT GGGCAGGCCG CGAGTGGCGG AGCTGCTGCT GTCTCACGCG CGGAGGCCCA 780
ACTGCGGJGA CCCCGCCACT CTCACCGGAC CGGTGCAGJA CGTCCGCCCG GAGGCGTTCG 840
TGAACAGCT GTGTGTGCTG CACCGGCGCG GCGCGCGACT GAGCTGTGCG GATGCTGGGG 900
GCGCTTGGC CTGGAGCTG GCTGAGGAGG TGGCGCATCG CGATGTGCGA CGTCACTGCG 960
GCGGCGTCT GGGGCGGCTC AGAGGCGATA ACATATCCCG CATGATGCTC GCGGAGGCTC 1020
CATCAGCAT CCGGATTTGA AAGAGCCAGA GAGGCTCTGA GAAACTCCG GAACTTAGAT 1080
CATCATGAC CGAGGTCTCT ACAGGCGCAC AACTGCCCCC CGCACACCCC ACCCGGCTCT 1140
CGATGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGCTC TGCTTTTAA CTTATATATA 1200
TCTTCTCCG CATCAGCTGA AATGTGCTAT TATATCATTT TTATATATAT CTTATATAAA 1260
TGTAAAAAAG AAAAGACAGC CTTCGTGCTT TTCACTGTGT TGGAGTTTTC TGGAGTGAAC 1320
ACTCAAGCCC TAAGGOCACA TCTATGTGGG CATTTCTTGC GAGCTCCGCA GCTCCGAGAA 1380
GCTGTGACTC TCAATGAGAC CATTTTGTGA ACTAGGAGAG CTCAGCGGGG TTACTGTGCT 1440
CTCTTATGTC ACATGCTAGC CNAATGGGAG AACCGAGACT CNAATATAAA TAAATATATT 1500
TTCATTGAT CACTC

Seq ID NO: 131 Protein Sequence

Protein Accession #: NP_478104.1

70
1 11 21 31 41 51
| | | | |
NEPAAGSSSE PAAGSSNEPS ADPLATAAAR GVEEVRALL EAGALNAPM SYGRNPQVQ 60
RSGMAGAGCG GRANRTFKAG ELSSGASATL EKKKRLPGHF SGVCHRRFP FQMLGAMET 120
KEEE

Seq ID NO: 132 DNA sequence

Nucleic Acid Accession #: NM_058195.1

Coding sequence: 163...684

75
1 11 21 31 41 51
| | | | |

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1      11      21      31      41      51
|      |      |      |      |      |
CTCTCCCTACG GGGGCTCTCG GCGAGCTTTC CCGCTGCGCG AGGCTCTAGA GCTCTTCCGA 60
GATCTTGGAG GTGCGGTGGG GACTCGGGGT GGGGTGGGGG TGGGGTACGA GTCGAGGGG 120
5 GAGCGCGGCTC AGGAGAGGCG GTGTCGCGCC TGCGGGGCGG AGATGGGCGG GGGGCGGTGC 180
GTGGGTCCCA GTCTCGAGTT AAGGGGGGAG GAGTGGGCGT GCTCACTCTG GTGGCCAAAG 240
GGGCGCGGACG CGGCTGCCGA GCTCGGGCCT GGAAGGGGCG AGACATGCGT GCGCAGCTTC 300
TTGTGCGACCC TCGGATTCGCT GCGCGCGTGG GCGCGCGGCC GAGTGGAGGT TTCTCGTGTT 360
10 GCACTCTCTCG GCTCTGAGGG GGGGTGGGGA GCTCTAGAGG GCGTCCGCGC TGTGCGCCCTC 420
GTGCTGATGC TACTGAGGAG CCGAGCTCTA GGGCAGCAGC CCGTCTCTAG AGAGCCAGGT 480
CATGATGATG GCGAGCGGCC GAGTGGCGGA CTCTCTCTGT CTCGAGCGCG GAGAGGCCAA 540
CTGCGCGGACG CCGCGGACTC TCACCGGAGC CTGCGACGAG GCTGCGCGGG AGGCGCTTCT 600
GGAGGACGCTG GTGCTGCTGC ACTGGGGCGG GCGGCGGCTG GAGTCTGGTG ATCTTGGGG 660
15 CGGCTGCGCC GTGAGACGTG CTGAGGAGCT GCGCCATCGC GATGTCCGAC GTACCTCGCC 720
CGGCGCTGGG GGGGGGACGA GAGGCGATAA CGATGCCCGC ATAGATCCCG CGGAGAGTCC 780
CTCAGACATC CCGGAGTTGA AGAACCGAG AGGCTCTGAG AAGCTCTGG AAACTTAGAT 840
CATGCTGAC CGAGAGCTCT AGAGGGCGAC AACTGCGCCG GCGCAAGCGC ACCGCTCTT 900
CGTAGTTTTC ATTAGAAGA TAGAGCTTTT AAAATGTGTC TGCTTTTAA CGTAGATAA 960
TGCTTTCCCC CACTACGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1020
20 TGTAAAJAG AAAAGACGC CTCTGCTCTT TCACTGTGT TGGAGTTTTC TGGAGTGAGC 1080
ACTGAGGCCG TAAAGCGACA TTCTGTGGG CATTCTTTCG GAGCTCGGCA GCTTCGGA 1140
GCTGTGACT CATGACAG CATTTTGTGA ACTAGGAGAG CTCAGCGGGG TTACTGCTCT 1200
CTCTTGAGTC ACATGCTAG CAATGGGCG AACCAAGCTC CAAATAAAA TAAATAATT 1260
TTCATTGATT CACTC

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Seq ID NO: 133 Protein Sequence
 Protein Accession #: NP_478102.1

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30      1      11      21      31      41      51
|      |      |      |      |      |
MGRGRGVGPG LQLRGNRRC SPINPKQGA AARLPGQGG NNVRRFLVTL RIRRCQPPR 60
VRVPPVHIPR LTGNGAAGA PAAVALVLM LRORLQOQP LPRPQHDDG QRPSSGAAA 120
PRRGAQLRRP RSHHPTRARR CPGULFQAG GAAPGRGAG RARCLGFSAR GPG

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Seq ID NO: 134 DNA sequence
 Nucleic Acid Accession #: NM_023915
 Coding sequence: 1..1077

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40      1      11      21      31      41      51
|      |      |      |      |      |
ATGGGGTTCA ACTTGAOCT TGCAAAATTA CCAATAACG AGCTGACGG CCGAGAGAT 60
GACATTCAG CGAGAGAGG CGACGGGCCA GGAAGAAACA CCACCTCTCA CAGAGATT 120
GACACAATTG TCTGCGCGG GCTTATCTC ATTATATTG TGGCAAGCAT CTCTCGAAT 180
GTTTAGCAG TGTGATCTT CTCCACATT AGGAATAAAA CGAGCTTCAT ATTCTATCTC 240
AAAAACATAG TGGTGGAGA CCTCATATG AGCTGACAT TTCCATTTC AATAGTCGAT 300
GATGGAGGAT TGTTGACGT GACTCTGAG TTATCTCTC GAGATACCA TTGATTTG 360
TTEATGCAA ACGTATATC TTCCATCTG TTCTTGCGG TGATAAGCAT TGATGCGTAT 420
CTGAAGGTGG TCAAGCAATT TGCGGACTC CGATATACA GATAAGCTT CACGAGGTT 480
TTATCTGTTT GTTGTGGGT GATCATGGT GTTTTCTCT TGCCAAACAT CATCTTAACA 540
AGTGTGCGC CAGCAGGAG CATTATCAT GCTGCTGCA AACTATAAAG TCTTTGGG 600
GTCAANGGC ATAGCGGCT CAGTATGTG AACAGCTGCT TGTTTGGC GTCTGCGG 660
ATTCTGATCG GATGTTAGT AGCCATATCC AGGTACATCC ACAATACGAG CAGGCAATTC 720
ATAAGTCAGT CAGCGCGAAA GCGAAACAT AACCAAGACA TCGAGGTTGT TGTGGCTGTG 780
TTTTTAACT GCTCTGACG AATGCACTG TGCAGATTTC CTTTAGCTT TATGTACTA 840
GACAGGCTTT TGGATATC TCACAGAAA ACCCTATT ACTCGACAG AATTACGCT 900
TCTCTGTCTG GGTGTAAGT TTGCGTGGAT CGATAATT ACTTTTTCAT GTGTAGGTCA 960
TTTTCAAGAA GCGCTTTTCA AAATCAAT AATCAAGACA GAGTGAAGA CATCAGATCA 1020
CTGCAAGGTG TGGAGAGAT GGAAGTTCG ATATATTATG ATTACAGTGA TGTGTA

```

Seq ID NO: 135 Protein Sequence
 Protein Accession #: NP_076404

```

65      1      11      21      31      41      51
|      |      |      |      |      |
MGPNLTIAKL PNNRHHQES HNGNRSDGP GNTTLINRF DTIVLVLYL IIPVASILLN 60
GLAVWIPFHI NKTSFIPYL KNIVVADGIM TLTFPFRIVH DAGPGWYFK PFLCRITSVL 120
FIRHWYSIV FGLIDIRYI LAGVFPFDS HNGISFFPKV LQVCHYDA VLEPHILE 180
NCPPIEDNH DSKRLSPGL VKHATVTVV NSCLFVAVLV ILIGYIALS RYHKSSRF 240
IQSSSRKRKH MGRIRVVAV FTTCLEPHYL CRIPPTFSHL DRLDLSAQK LLYCKEYLL 300
70 FLGACNVCLD PIYFPMGNS PSRLFKKGN ITRBSGIRS LQSVRSSEVR IYDYDTDV

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Seq ID NO: 136 DNA sequence
 Nucleic Acid Accession #: NM_005329.1
 Coding sequence: 1..1662

```

75      1      11      21      31      41      51
|      |      |      |      |      |

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PCT/US02/21338

Seq ID NO: 140 DNA Sequence
Nucleic Acid Accession #: Eos sequence

WO 00/003906

PCT/US02/21338

Coding sequence: 53..459

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      CTTCTGCGCC CCGTGAACCTC TCTCTGAGAG CCGGGCAGAG GCTCCGAGGC CATGACAGGCC 60
      GAAGGCCAAG GACAGAGGGG TTCGAGCGCC GATGCTGATG GCCGAGGAG GCCGTGCATT 120
      CTGATGAGCC CAGAGGGGCA TCTCTGCGCC CACGAGAGAG CAGGTGCCAC GGGCGCCAGA 180
      GTCCCGGGG GCGCAAGGAG AGCAAGAGCC TCTGCTCGAG GAAGAGAGCC CTTCTGCGAT 240
      CCGCATGGCC GTCCGCTTC TCCGACGAT GAGAGCTGCC CCGCGGGGC CAGAGGCGCC 300
      GACAGGCGCC TGCTTCAGTT CCGACTGACT GTGCGAGACC ACCGCAACT CGAGCTCTCC 360
      ATGAGTCTCT GTCTCCAGCA GCTTTGCTGT TTGATGTGGA TGAGCAATG CTTCTGCGCC 420
      GTGTTTTG GTGACGCTG CCGAGGGGAG AGGCGCTAGG CCGAGCTGAG GCTCTCTCC 480
      TGGTCACTG CTCTCCCTCC AGGGAATGTT CCGACACAGA GTGCGCAATT CATTGTGCG 540
      GCGTATTGT TTGTCCCTGG AGGAGGACGG CTTACATGTT TTTTCTGTA GAAATAAAG 600
      CTGAGCTA

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Seq ID NO: 141 Protein Sequence
 Protein Accession #: Bos sequence

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20     1      11      21      31      41      51
      |      |      |      |      |      |
      MQABEQGTQG STEDACDFPG PIFPDGPGN AGSPGEAGT GGRPPRGAG ARASGPRGA 60
      PRPHHGAAS AGDGRCPDA RPDPSRLQF RLTAADHRL QLSISLQQL USLHWNITQC 120
      FLVPFLAQAP SUGRR

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Seq ID NO: 142 DNA Sequence
 Nucleic Acid Accession #: NM_130467.2
 Coding sequence: 246..638

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      AGCAGAGCT CTCACAGGAG AGTGTGTGTC TTGTGTTCTT CCGCATCTT GGTCTTTCC 60
      AACACTTGG TTCTTTCTCA CTGACCGAGA CTCAGCCGAT AGGCTCGAG AGTGCTCTTC 120
      CTGTGTAATT AGTTGTGAAT GAATGTGTGG AGGAGCCGAG GGGCTTAGA CAGTGTCTGT 180
      GGCGACATCC GTGCGTTTGA GGGAAAGGG CCTCGCGGTG GTCTCCGACC TTCCCCAGG 240
      TCTGTATGCA GCGGCCATGG GCGGTAAAT GTGCGTGGC TGAGAGAGG GAGATATGA 300
      GAGATATGAG TTAGCATGTA ACAGATCCG AATCTCCAG AAGAGGAAT GACCAAGAT 360
      CTTCCGAGCC AGTTGAAGCT GTGATTGTCC AGCAGCCGAC TGAGGAAAA COTCAAGAG 420
      AGGAGCAGCC AACTGATAAT CAGGTATTG CACCTAGTGG GAGATCAAA AATGAAGAG 480
      CAGCTCTGTT TCAAGAGACT GATTGTGGAG CTTTTCACG GAACTGCTCT CTCTTFAAG 540
      TTAGGATGAC AACTGGAAT GTCTCTGAT TCAAGAGAG GACTCTGCC ACTTTGATC 600
      CCACTAAGT GCTGAAGACA GTGAAAGGC AACTATAGT TTAACCCAG ACAATGAAG 660
      ACTGAACCA AGAATATTGT TCTTATGCTG GAAATTTGAC TACTACATT CTCTTAATA 720
      AGTTTACAG TTTTC

```

Seq ID NO: 143 Protein Sequence
 Protein Accession #: NP_569734

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50     1      11      21      31      41      51
      |      |      |      |      |      |
      MSHIVTRSG SERGNQDES QPVGVPIVQG PTEKKRQEBE PPDNQGIAP GRIKNDGAP 60
      AVQCTGVRAF QBELALLKIE DAPDGDPEVR RUTLPFDPT KYLEAGBQGL

```

Seq ID NO: 144 DNA Sequence
 Nucleic Acid Accession #: NM_001467.1
 Coding sequence: 82..435

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      CCGAGGAGC TTGAGGCAZ TGTGTGTGG TTCTGCGGTT CCGGACTCTT TTTCTCTAC 60
      TGTATTGAT CTGTGTGAA TGTGAATGG CAGGAGAGAT GAGACTATTA TTGCTTAGA 120
      CAGAGGCTCT ATGACAGCC TCTGAAATG ATTGAGCCTA TGCGGCGCCA GCAATCTAT 180
      GATGATGCG AACCAAGCA ACCTGAAGAA GGGAGCCGAG CAATCAAGC TCAAGATCT 240
      GCACTGCTC AGGAGGAGA GATGAGGGA CACTCTCGAG GTCAAGGGCC GAGAGCTGA 300
      GCTGATAGCC AGGAGCAGG TCACCCACAG ACTGAGTGTG AGTGTAGAA TGTCTGAT 360
      GGGGAGAGG TGAAGCTCC AATCCAGAG GAGGTAAAG CCGTCAAGA AGTGAAGAG 420
      CAATGACAT GTTAAAGAA GACACTTGA AATGATGAG CCGTCTCCTA TGTGGAAT 480
      TTTGTATTA AATTCTGCC AATAAGCTT TACAGCCTTC TGCAAAA

```

Seq ID NO: 145 Protein Sequence
 Protein Accession #: NP_001467.1

```

75     1      11      21      31      41      51
      |      |      |      |      |      |
      MSHRSESTY WPRPRRYVQF PEVIGPMRPE QFSDEVEPAT PESDEPATQ GPAAACGEG 60
      DSGAAGQGF KPRADSRQRC HPQTGCBCEG PGDGKVDVDF NPREVKTPER GEKQSQC

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WO 03/003906

PCT/US02/21338

Seq ID NO: 146 DNA Sequence
 Nucleic Acid Accession #: NM_005562
 Coding sequence: 50...3671

5
 1 11 21 31 41 51
 10 ACAGCGGAGC GAGAGTGAAG AACACCCAAC CAGGCGCCG GACAGCGACC CCGGAGGCG
 AGACAGAGAG TGAGCGGCCG GCGACCGGCC TCGCTCGCCT CTGGCTGGGC TGTGCTCTCT
 CGCTTCTGCT GCTCTCGGCC GCGACCGGCC GCGACCTCCG GAGGAGAGAT TGTGATTTGA
 ATGAGAGTTC CAGGAGGTGT ATCTTTGATC GAGAGTTTCA CAGGCAACCT GGTATGTGAT
 TCGCTGCTCT CACTCGAAT CACACACACT GTACCGATTA CTGCGAGAGG TGGAGAAATG
 CGCTTTACCG GCGACAGAGG AAGGACCGCT GTTGGCCCTG CAATTGTGAC TCCAAAGGTT
 15 CTCTAGTGGC TGAGTGTGAC AACTCTGAGC AGTTCAGCTG TAAACCGGTT GTACAGAGAG
 CCGAGTGGGA CCGATGTCTG CAGCGCTTCC ACATCTCCAC GAGTGGGCG TCGACCGAG
 ACCAGAGACT CTGAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG
 ACGCGCGCCG CTGTCTGTGC AAGCCAGCTG TTACTGGAGA ACGTGTGAT AAGTGTCCAT
 20 CAGTGTACTA TAATCTGAGT GCGCGGAGCC CTGAGGCTCG TACCAGATGT TCTGTGATG
 GCGATCTGAC GAGCTGCGCG AGCTCTCGAG ATAGAGGTAT CCGATGATCT ACGTGTACTC
 TTATCAGAGA TGTTAATGCG TGGAGGCTG TCCACAJAA TGGGTCTCTC CGAAGCTCTC
 AATGTTGACA CGCCCATGAA GATGTGTTTA GCTCAGCCCA AGACACTAGC CTGTCTATT
 TTGTGCTCTC TGCAGATTT CTGCGAATC ACAGAGTGAG CTATGGGCAA AGCTCTCTCT
 TTACTACGCG TGTGACAGGA GAGACAGAGC ACCATCTCTC CCGATGTG ATTCGTGAG
 25 GTCTCTCTCT ACGGATCACA GCTCCCTTGA TCGCATCTG CAGACACTG CTTTGTGGG
 TCACCAAGAC TTACCACTTC AAGTTAAATG AGCATCCAG CAAATAATGG AGCCCCAGC
 TGAATTAATT TGATATMGCA AAGTTACTGC GGAATCTCAC AGCCCTCGC ATCCAGATTA
 CATATGGAGA ATACATTAAT GGTATCATG ACATATGAGC CCGTATTTCA GCGCGCCCTG
 30 TCTGTGCTCC CCGACCTTCC TGGGTGAGC TGGTTATG TCTTGTGG TACAAGGGCC
 AATTTCTGCA GATTTGTGCT TCTGGCTACA AAGAGAGTTC AGCGAGACT TGGCTTTTG
 CGACCTGTAT TCGTTTAACT TGTCAAAGGG GAGCGGCCG TGTACGAC CACAGAGGAT
 GTTATTGAG GAGTGGAGAT TGTGACATG AGTGTACTGA CTGCCAATTT GGTTCATCAA
 35 AGCTTCGCA GAGCGCTTCC ATCTGACAGC AGTGTGAGG TGTGACTCTT TGTGACTCT
 CAGTGATGCC GAGACCGAGG GAGTGTGTGT GGAATACTG CCGTCCCGCG GTCAACCGTG
 CGCGCTGTGA GCTCTGTGCT GATGGTACT TTGGGACCC CTTTGTGGA CATGCCCGG
 TGGGCGCTTG TCGGCTGTGT CAGTCAACAA ACATGTGGA CCGGATGCC TCTGGGATTT
 GTGACCGCTG GAGTGGAGAG TGTGTGAGT AGTGTGAGT CAGACAGG CAGCAAGTTC
 40 ACATGTGCAA AGCAGCTCAC TTGCGGAGCC CATTTGCTCC GACCCGACA GAGCAAGTTC
 GAGCTTGCAG CTGTAAACCC ATGGGCTGAG AGCTGTAGG ATGTGGAGT GATGCCACT
 GTTGTGTGCA GCGAGATTT GGTGGCCGCA AGTGTGAGCA TGGAGGATC AGCTTCCAG
 CTGTCTATA TGAAGTAGG ATTCAGAGG ATGATTTAT CCGACCTACT CAGGATAGG
 AGGCTCTGAT TTCAAAGCTC CAGGTTGTGT ATGAGTATG ACCTGATACA GAGCTGGAG
 45 CGAGATGCA CAGGCTGAG CAGCGCCCTC AGCACATCT GAGAGATGCC CAGATTCAG
 AAGTGTCTAG CAGATCCCTT GGTCTCGMT TGGCCAGGT GAGAGAGCAA GAGACAGCT
 ACCGAGGCC CTGTGTGAC CTGAGATGA CTGTGAGAG AGTTGCGCT CTGGAGATC
 ATACAGGAA CCGAGTTTCC CATACTACA GCGCTACAC TCGATGAG CAGAGCTGG
 50 CAGAAATGA AGCTTCTGT GAAACACATA ACATCTCTCG CTGAGAGCAG TACGTGGGCG
 CAATGTGCTT TAAAGTCTG CCGCAGAGG CCAAGAGATT AGCAGAAAGC CAGCTTGAT
 ACGCATATA CATGAGGGA CTGACAGAGG AATCTGAGG CATTCCGAA CAGGCTCTT
 CATCTGTGCG CAGCGCCCTG CATGAGAG CAGGAGCGG AAGCTGTAG CCGAGCGTT
 55 CTGTGTGCA AGGCGTTGT GAAAAATTG AGAAAAACCA GTCCCTGCC CAGCATTTGA
 CAGGAGAGGC CACTCAAGCG GAATTGAGG CACATAGCTC TTATCAGCAC TGTCTCGCC
 TCGTGGATC AGTGTGAGCG CTTGAGGAG TGAATGATCA GTCTTTGAG GTGAGAGAG
 CAGAGAGAT CAGCAAGAA GCGATTTCA CTTCAACCTC GTTACCGG CTATGATG
 60 AGTTCAAGCG TACAGAAAG AATCTGGGA ACTGGAAAG AGAGACAGAG CAGCTCTTAC
 AGATAGGAAA AAGTGAGAGA GAGAAATAG ATCAGCTGCT TTCCCTGCC AATCTTGCTA
 AAGCAGAGC ACAGAGAGCA CTGATATGG GAGATGCCC TTATTATGAA GTTGAAGCA
 TCTTAAAA CTCTCAGAG TTGTGCTCTG AGTGTGAGCA CAGAAAGCA CAGACTGAG
 65 AAGCATGAA CAGACCTCT TACTATGACC AGAAGTTTC AGATGCCAT CAGAGAGCC
 AGCAGCGGA AAGGCGCCCT GGGAGCGCTG CTGTCTATGC ACAGAGGCCA AGAATAGG
 CGCGGAGAGC CCGTGAATTC TCGATGATG TACGACAGA GATTGCCAT GTAACTTGG
 AGCTCTCAG AGCTAGTGA GAGGCGCTG CTGTATGGA AGTGTGAG CCGTCTGAG
 70 GTAGATGAG GAGATGGA GAGCAGCTG AAGGAGGA GCTGGAGTTT GACAGGATA
 TGAATGAGT ACAGATGAGT ATTACAGAGG CCGAGAGGT TCAATACGGA CCGAGAAAG
 CTGGGTATAC AATCCAGAGC ACATCAACA CATTAAGCG CCGCTGCA CTATGAGAC
 AGCTCTCAG TCTGATGGA GAGTGGGTT GATCGGAG GATCGGAGT TCCGAGGAT
 75 AGACAGAT CAGACCGCA CTGCGGCCCA TCAATCAGA GCTGAGAGG AGCCAGCTC
 AGCAGAGG CGACCTCAT TTGCTGGAGA CAGCATAGA TGGATTTCT GCTCATGTA
 AGAATTTGGA AGCATTTAGG GACACCTCC CCGCAGGTE CTACATACC CAGCTCTGT
 AGCAGAGGT AAGTCCCAT AAATATTTCT CACCTGAGGT TCTTGGGATA CAGACTCG
 GATTTGGAG CTATCTCAT TGGTGGGTG GATCGGAG ATTTGAGAT GTTAAATGG
 80 TATCTCAG TCACTGACC TACCCCATCT CATTGATCCA TGGCAGGT GTTGTCTTAT
 TGCACCATC TCGTGTCTG CTGATGCTG GAGTATGAGC ACATAGACT GGGTGTGACA
 ATGATCAGG ATTCAGGCC CAGAGAGAT ATCTGATGT TCAAGAGT CAGCAGGAG
 85 ATTTTTCAG CATATGATC GTATGTGGG TCTTGAAAT TCAAGAGT CTTTGGAT
 ATGATCACT TATCTTTTGA GTATGTGAC TAAAGAGAAA AACTTTGACT TTGCCAGGC
 ATGAAATCT TCGTATGCT AGAACAGAT GCACCCAGT CACATCTGG CAGTAAAT
 ACTATGCT CATATTGCT TCTGCAAGCT TCTGTGTAAT CAGATCTCT CACTACTACA

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PCT/US02/21338

ACCCAAGGTG TGAACATGTT CTCATTTC AGCTGGAAG AAGTGAGCAG TTTTGGAGTG 4260
 AGAGACTGTA AGGCAGGCC ATTCAGAGCT ATGDTGCTTG CTGDTGCTG CACACTTCAG 4320
 GTTCGAGACG TGCTGATGAC ATCTTTCTTG TTATGATGCG CATGCGACCT TAGACATTCG 4380
 ATTTTATTAT AGCACTTTTC TACCAAGCAA GCAAAATGTT GGAAGATATT TACTTTTCCG 4440
 GTTCAAGATG GATAGAAAAG TGTGGCTTGG GATTGGAAG AGGTAAATTT CTCTGATTTT 4500
 ATGTTAGCTCA ATTCATCTCT ACTTTTTCGA CACCAAAATG GATCGCGATC AATGATTAATT 4560
 ATCTTATTTT CTCAATCTCC TCTCTCTTTC CTCCACCAT AATAGAGAGA TTTCTCTACT 4620
 CACACTTCAG CTGCTGTGCA TCATCTCTTC CATCTGCTCT TCATCTCTATC TTTCATCTCA 4680
 TTACTCTCAT CCATCTCTCC ALCATATATT TATGAGTATC CTACTGTGTG CAGCGGCTCT 4740
 TGTGGACAGT GGTGTACATAG TCTCTGCCCT CATAGATTTG ATTGTCTAGT GAAGGAGAGA 4800
 AGCACTTTTA AAAAAATAAT TTAATCTTAC AAGCTTTGTT TGTACAGAGT GGTGTTTATT 4860
 GCATTAACCC CTGATCTGAG AGCTCTCTTC CTCAGAGAGA CATATGTGTC AAGACCTTTC 4920
 CATGCGGGCA CTGAGTTT TTGCAAGGCTG ACAGAGCTCT GDTTGTGTCA CATTCTCTTC 4980
 CATTCCAGCT GTCACTCTGT GATTCTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
 TACACCAAGT GGAATTTGCT GAGGAGACCA GAGGCACTGC CACTCTGCTG GGAAGACATA 5100
 TGSTGCGCC TTGCTCTGCT ATTCTCTGG ATTTCCTGGA AAGTGTTTTT AAAAAGAAA 5160
 CAATTGTAG ATGCC

Seq ID NO: 147 Protein Sequence
 Protein Accession #: MF_005553

1 11 21 31 41 51
 NPALVLCCL CPALLPAAR ATSPREVCK NKSSTQCI FD RLLHPOTMG FRLGCHDNT 60
 25 DGIRCEKCKG QFYRRERDR CLPCHNSHG SLRSCDNBS RCCKPQVTG ARCDCLPQF 120
 HMLTDAGCTQ DQRLDSEKD CPAGIAGTFC DAGRCVCKPA VTERGCDRCR GQYTNLDQGN 180
 PHGCTCFCTY GHSASCRSSA EYSVHKITST PQQDVNDGHA VORNGSPAKL QHSORHGVF 240
 SBAQGLDPVY PVAPKPLQW QWSTQGSLS FQYEVDSGR HPASADVILE GAGLRITATP 300
 30 HPLGLTCLG LHTVITGAG AGGDRHSPG LFTVETPRL PHLTALEIDA TVRACCTTCA 360
 DNVTLSIRAP VSGAPAPWVE QCI CPVYSG QFQDCASGY KQDSARLGGF GTCTPCNQG 420
 GGACDPDTGG CTSDENPDI ECADCPGIFY NQPHDPRSCK PCPCRNQFSC SVHPETSEVV 480
 GSNCPFGVTV ARCELADGY PQDFPQHHF VRPQCPQCN HNPVPSASG CRLTDECLK 540
 CLIRVAYIC DQCSQATCT FQAPWRKAC EKHVQVDEL EKVTLQAGQ TREATQIE 600
 NCEBAGFSCP ACYVQWIKQ DQFMQGLPK BALISQAQGS DQVVFTELE GPMQARQAL 660
 35 QDILEDQIS EDSARSLEQL LAKVRSENS YQSLRDLLIM TVERVRLGS QVQRVDRTH 720
 RLITQMLSL ASSASRLHT NIFASDIYV PMGFZELAQE ATRLASRIVE SASMQLTR 780
 ETEYSEKAL SILVRALES VSGSGSPD AVVQGLVEL EKVTLQAGQ TREATQIE 840
 ADRSYQSLR LLDSPVSLQG VDSQSPQVE AKRI KQKADS LSTLVTEHD EFKRTQKHLG 900
 40 NNIKEAQQLL QMGKSGREKS DQLLSRANLA XSRAGQALSM GNATPYEVBS LKHLREPLD 960
 QVMDKABAE EAHKRLSYIS QKVSASDRT QCARALGSA ADAQARHNG ABGAELISSE 1020
 TEGSIOBLML EMTVADALP AMEGLASLE SEMEVRSEL ERHLEEDTH HGVQVITTE 1080
 AKQVTRAMN ADVTIGDTLM TLEGLILMD OPLSVDESL VLEGLKLSRA KTOINQLRP 1140
 MNSELEERAR QORQHHLLE TSDIOLADV KNLNIRDM LPPGNTQAL EQQ

Seq ID NO: 148 DNA Sequence
 Nucleic Acid Accession #: MF_021046.2
 Coding sequence: 327..1436

1 11 21 31 41 51
 GGCAAGAGG AGAAGAGAGG TTCTCTTCT GAGGAGACAG CTGAGATCG GCTGAAGAGA 60
 GCAGGCCAGG GCTCTGTGAG GAGGCAAGGG AGGTGAGAAC CTGCTCTCA GAGGTGAGCT 120
 55 CAGTCAACA CAGGAGACCC CTCTTTTCT CAGACACAGT GGTGTGAGAG ATCTACAGAG 180
 AGTCTAGCTT CTCTGATGAG AGAGCTCAG AGCTTGTGGA CACACAGAG 240
 CACACTGMA GAGAGAGACC TGCTCTTGGG TCCCATCGCG CAGTGTCTGG CCACACTCTC 300
 CACTGCTAC CTGATGAGA GTCATCATCG CTGAGCTCC AAGGTGTGAG GCTGTGATCG 360
 CTGAGAGAGA TCTTCAATCC CAGATGAGA CAGAGGCTCT CGAGGRTGCA CAGGCTCCCC 420
 TGCTGTGGA GAGATGAGT CAGCTGAGT TCTCCGACAG CTGCTCTTCT CAGCTCTCT 480
 TTCTCTCCCT CTCTCTTCT TCTCTCTCT CCTGCTATCC TCTAATCCA AGCACCCGAG 540
 60 AGAGGTTC TGCTGATAGT GAGACAACA ATCTCTCCCA GATGTCTCAG ATAGCTGAGT 600
 OCTCTCCCTG GGTGTTGAGT TCTCTCTTCT TATGATGAGT TATGAGGCT TCAGACAGCT 660
 AAAAGAGGA GAGTCAAGC AGCTCAAGG ACTCTCAAGT CATGAGGCT TTAACCAAAA 720
 GTGAGTAGA TGAAGAAGCT ACTAATTGG TCGAATTTCT GCTCTTCAAG TATGAAATGA 780
 65 AGAGCCGAT CACAAAAGCA GAATACTG AGAGTGTCT AAAAAATTAT GAGGACACT 840
 TCCCTTATTT GTTATGAGA GCTCCAGGT GCATGCTACT GTCTTTTGGC ATGATGTAA 900
 ATGAGTAGA TCCGCTGCG CACTCTTTC TCTGTTTCT CTCTCTGAGC CTACACTTA 960
 ATGAGTCTT CAGTATATCT CAGAGCTGCT CAGAGCTGCT CATCTCTA CTATCTCTTA 1020
 70 GCATATCTT CATGAGGCG TACTGCAACC CTGAGAGAT CTCTCTGAGA GCACTGAATA 1080
 TGATGGGCT GTATGATGG ATGAGGACCT TCATTATAG GAGGCCAGG AGACTGCTCA 1140
 CCAAGATTT GTTCAGAGAA AACTACCTG ATACCAAGC CTGCTCTGAGC ATGTGCTCG 1200
 CAGCTATGA GTTCTGTGG GTTCAAGGG CTCACTGCTG AATTAGAGG ATGCTGCTC 1260
 TGAATTTT GGCCTAGTA ATGTGAGATG ATCCAGATC CTCTCCACTG TGATATGAG 1320
 75 AGGCTTTGAA AGATAGAGA GAGAGACCC AGGACAGAT TCCCAACCA CATGATPACT 1380
 CTCCATGCG CAGTCAAGT TCTAGGCTCA CAGGTAGCTT CTCTTACTT GAATPAGTA 1440
 AAGAGAGCT TTTTAAAGG AGGTCAAAT CAGCATGATT TTATCTCAT 1500
 GTGATATCTA AAAAAAATA AAAAAAAA

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PCT/US02/21338

Seq ID NO: 149 Protein Sequence
Protein Accession #: NP_066386.1

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5      1      11      21      31      41      51
|      |      |      |      |      |
MPKAPKQRKC MPEEDLQDGS ETQGLEQAQA PLAVEEDASS STSTSSSTPS SPFSSSSSSS 60
SSCYPLIPST PEVSADDET PHPPQDAQIA CSPPQVVASL PLQDSISGSS SOKRESPTLT 120
QWLPBSESLP RSEIDSEKVTQ LYGKILFKVQ MKETPYKAE LSVHYVEDY HFFLLPGRAS 180
ECNMLVFGID VKKEDVPTGHS FVLVTSGLIT YDMLSDVQGS MPKTOILLIL LGLIFISQYC 240
TPEEVIDEAL RMGLKIDGME HLIVSPEPKL LTQMLVQBNY LEYRQVPGSD PARYETLWGP 300
RAFAEIRKHS LLKLTAKVNG SDPSFPLMY SEALEDEBER AQRIATITDO TNMAASASSS 360
ATGSPSYPE

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Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: NM_003695
Coding sequence: 12..398

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20      1      11      21      31      41      51
|      |      |      |      |      |
CUCATACGGA GATGAGACCA GCATTGCTGC TCTTTCAGCG CTTGGCTGTG CTACACGGGC 60
CAGCCCTTAC CTTGGGCTGC CAGGTGTGCA CCGAGCTCCG CAATGCAAGC CATTTTGTGG 120
TCTGCCCGAC CAGCTCTGCG TTCTGCAGAA CACCAACACG AGTGAAGCCT CTGAGGGGGA 180
TTCAGTGGAA GAGGAGCTCT GCGAGTCTCT GCACACCCAG CTACACCTGT CAGAGCCAGG 240
TCAGCAGCGG CACGAGCTCC ACCGAGTCTT GCAGGAGAGA CTTGTGCAAT GAGAGAGTCC 300
ACACACCTGC ACCACCCGCG ACCGCTCTCG GCGAGAGTGC CTTGAGCTCT GGGCTGCCCC 360
TGAGCTCCTCT GCGCCTCATC TTAGCCGCCA GCGTGTGAGC TTCCCCGACG GGAAGGCCCC 420
TCTAGCCTTT CTTCTCCCTTT CTCTGGGGAT TCACACCTCT TCTTCCCCAG CCGGCAACGG 480
GGGTGCCAGG AGCCCGCAGG TGAGGCTTTC CCGCAAAATC TGGAACCAAG TCGAGGTGGG 540
CATGTGATGC TGTGATCTTG CAGTACGCTC ACAGAGATCC ACAGCAATCT GAACCAACCG 600
ACAGGAGATG CAGCCCTCCG CTGCAATGAA GTGTGAGGAC AGAAGCCCTG TGGATCCCCG 660
GATTTGACAC TCTTTCTCTT TTGTGTCCGT TTATTTTATA CTCAATCTCT TACATGAGAA 720
TAAATGATTT AAACC

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Seq ID NO: 151 Protein Sequence
Protein Accession #: NP_003686

```

40      1      11      21      31      41      51
|      |      |      |      |      |
MRTALLLLAA LAVATGPALT LRCHVCTSSS MCHGSVVCFA SERPCKTNT VEPLRGNLVK 60
KDCASRCTPS YTLGQGVSSG TSTGTCCQSD LQNEKLHNAA PRTALAHSA LSLGLALSLL 120
AVILAPSL

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Seq ID NO: 152 DNA Sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

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50      1      11      21      31      41      51
|      |      |      |      |      |
GGCCCTCTGT CTGACAGATG GGTCTCCCAT GCTTCTGAGC TGTGTGTGCA TGTCCGTCTC 60
GAGGATGTGG ATTATATAGC CTTTGGTCTT AACCTCATGT GACGCTGGA AAAATGTAAA 120
GAACTATCTC GGTCTAAGAC CAAAGTTCTT GTGACGAGAC AGGTTCTTTT GCTGGCTCTC 180
AAGATCTTAA AGCCACGGAG AAGCTCTCCA TCTTATGGCA TTGACAAAGA GAAGCAATCT 240
CAGCTTACCC TGAAGATGSG GAAGCCCAAT GATGAGGAGC TGCCTCTTCT TGTGTGTGAG 300
TCAGATATAG AGCCAAAGAG GCACTCTCTC CAGTGCCTGA GGTGCMCTCT AGTGGACAAA 360
GTGAAGACAA TGATCGAGAC TAAGACCGGT ATATCCCTGT AGACCCAGAT TGTGACTTGC 420
AATGGAAGAA GACTGGAAGA TGGGAGATG ATGGCAATT ACGCATGAC AAAAGGCAAC 480
TTACTCTTCC TGGCACTTTA TTATATTGGA GGGTGACAC CTTGGGATGT GGTGTGTGAC 540
AGGGGTGAAA AAGCTATATC CTTTATATCT CTACTCAAC GAAACATCT TCTGATGATT 600
TCCCAATATT AATGAGATAG AGATGAGTAG AATAAGATT GGTGTGGATG GTGATGATGA 660
AGTATATTGC CCAACTCTAT GTTCTTTTGA TTCTAACACA ATTAATTAGT TGACATGATT 720
TTTACTATGT TATTACTAGC ACTATAAAT AAATTTTTRA GCGAAATAG AGCATTC

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Seq ID NO: 153 Protein Sequence
Protein Accession #: NP_006389.1

```

65      1      11      21      31      41      51
|      |      |      |      |      |
MAPHASCCLV HVSEBMDMLT TFDANPYDSV KKIKHHVRSK TKVPVQDVL LLSGHLKPR 60
RELSSYIDIK EKTHLLTLKV VKPDBELPL FLVBSGDRAK RELLOVERSS SVAOVKMLIE 120
TCTGHIIPETQ IVTCHQKLE DGRMMADYGI EKONLLFLAS YCIQGG

```

Seq ID NO: 154 DNA Sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74..2788

```

75      1      11      21      31      41      51
|      |      |      |      |      |
GTGGGTTCAG TGAACCACTT TTGCGCGGAA ACTTGTTTGT TGTGTATGTG GCGAGAGGAA 60

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WO 03/003906

PCT/US02/21338

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 10
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 20
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 30
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 40
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 50
 55

TGTGTGTACT GCTATGCGGG AATCATCGGA ATCTCTCACG ATGCGATCCA GCCCGGCCCA 120
 GCATCGGGGA GGCAGATGATC CTCTCACTCT CAGCGCTGCG CGAGCTCTCC GGGCTACTGA 140
 TGGCTCTCAC TGGCGCGGTG GCGGTGACCT TCCACCATTT GAGTATAGTT CGAGAGGGCT 160
 CTTAGACACA GAGGGGCCCT TGGAGGAGA AGAGATGATG AGAGAGCTCA TTGGATGTGT 180
 CATTGAAAGG GACTCAAGGA CCAATCCGGA CTCTGACGCT TATGGAGCTT AGGACTCGCC 200
 TCTGATGATG GAGGACGGTAG AGGAGCTGAC GCGCAATCGA AGGAGAGTAG CGAGCGGGCC 220
 CATGCGGACG GGTGACCGGG AGGCTGGCGG GGGCTGTGGC CCGATCGGCC GTGGGCTCTCT 240
 GTATGAGCAG GATGAGAGGG ACAGAGAGCG GCGTCCCGCC AAGCGGCCCG AAGTGGAGCG 260
 GTCACGGAGG GACGCGGAGG AGGA GAGAGA GATATGCGT AGTGTGAGG ACCTGTGAGG 280
 TCTCAAAGCG CACTCTGTGC GCGAGTGGGT GAGCATGCGG GCGCCCGCGC TGGAGATCCA 300
 CCACGCGCTC AAGAACCTTC TGGCGACTCA CPTGCGAGCG CAGCGCCACA AGCTCTTCAA 320
 GAGGCGCATC AGCGACATGT GCAAGAGAGA CCGTGGAGCG CTGGTGTGTA ACTATGAGGA 340
 CTTCGAGGCG AAGAGGAGG TCTCTGGCTT GAGCGGCTCA CGGAGCTCTT 360
 CGAGATCTTT GATGAGCGCTG CCTGGAAGGT GTACTGCGCT ATGTACCCCA AGTACAGCGC 380
 CATCACCAAC CACATCCATG TCCCGATCTCT CCACTGTGCT CTGTGTGAGG AGCTGGGCTC 400
 GCTGAGGCGA CTGACTCTGA ACCAGCTGAT CCGCAGCGGT GGGTGTGGTA CAGCTGAGCA 420
 TGGCTCTCTG CCGCCCTGCA GATAGGTGAA GTACACTGCT AACAGATGCA ATTTCTGTCT 440
 GAGTCTTCTT TGGCACTCTC AGAACCAAGA GGTGAAACCA GCTCTGTCTC CTGAGTGGCA 460
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 TARGAAGTG TCCAGCCGAG CCAATCTTAC CACTGCGCAG GGGCTGTGCG CTGTGGGCTC 1740
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 Protein Accession #: AAB17490.1

60
 65
 70
 75

1 11 21 31 41 51
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 DEBAGGAGLR REHGLLYDSD ESDERPARK ROVERATED GSEDERWMS THMSDLRGR 180
 SVRNVYAGG PLEITHREPK HTVETVDSH GHWFEKIEE DCKMERYSL VHYELAR 240
 EHTLAFLEP AHEGLQTD EALVEYLVN YPKYELITH HVRVLSHLEP VHSRLSGL 300
 HMLQLETSR VSTSCGTGLP QLSNVKXCN KCHFVLGPPC QRQNGVKPG SCPECGSAGP 360
 PYNMERTIY YGSLRIEIQ SPKGVANGL PRSDALLA DLVDSCKPG EBLTVIYRN 420
 NYDSLMTAT GPFFVATVL AMNVAKORH VAGVETUSD VMKITSLSH QIQGKITAG 480
 IAPSLVGRD IREGLALPL GQSPNPKX FVPRDHWL LQCEVTPAKS QFYATIEYS 540
 SLPIITFGG ASAVGLTAV QHPVSRNT LEAGALVLD RGVLIDLEPD MNDQORTSI 600
 HEAMEQSSIS ISKAGITVSL QARCTVAAA SPLOGRDEPS LTPSBVDLT EPLISRFLL 660
 CVYBTVDVY QPKLARFV GHVSNPHN KREGLIAMS AKSPAMPT OVPLKQVLD 720
 KRTIIVYR HRLKANDG DVALMGRSL KREKATGSI FTVREISM IEMASAGL 780
 HLEDVIEDH VSMLEVLE SPIDTKFSV MRSMRT7AR YLSFEDRNNE LLPLIKQLV 840
 ABQTVQRNR PMAQDTIN PIRKILVFKAR QIMHKLSPF YLSFEDRNK ZHSLDKRMI 900

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PCT/US02/21338

LQQP

Seq ID NO: 156 DNA Sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

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10  GTTCTCTGTC CTCGGAAGCTC GCACCTTGTC GGCACAACTCG GGTGGAGACG GCGGACTCTG
      GCGACTGGCC GCGCATGCTC TCCCAGGCTC AGGACTATGA AGTGTGTAC AACTCGTGCA
      CAGGCTCTCA GCGCCAGCTC CAGAGATCTC GAGAGGAGCG TGAATGCCAG ATATTATGTT
      GGAAGAGATC TGATGATCTC TCGATGACG AGCTGATCG ACAGATCTT GTTCTTCGAG
      TGAATTGCTC TCGTAGACTG AAGACTCCAA ACATCGTTCC TACTATCAT CGATATTATG
15  ACCGACCCAA TACACACTCG TACATTGTAA TGAATATTG TGAAGAGGCG GATCTGCTTA
      GTGTATTATC AAGGAGAACG AAGGAAAGGC AATACTTATA TGAGAGTTT GTTCTTCGAG
      AATCAGATCA CTGTGATGTG GCTCGCTGTC TGTATGATTT ATGTCCATTA ATGCTTCGAT
      CGCTATGCTA TCGGATCTTT AAACGAGCTA ATGTTTCTCT GAGTGGCAGG CAAMAACCTCA
      AGCTTGAGAA CTTTGGGCTA CCTAGAAATAT TAAACCATGA CAGAGATTTT GCAAAACAT
20  TTGTTTGAGC ACCTTATTAC ATGTCTCTCT AACAATAGAA TCGCTGTCTC TACAATTAGA
      AATCAGATCA CTGTGATGTG GCTCGCTGTC TGTATGATTT ATGTCCATTA ATGCTTCGAT
      TTACAGCTTT TAGCCAGAAA GAATCGCTC GAAATACAG AGAGGCGAAA TTCGGGCGAA
      TTCCATACCG TTACTCTGAT GAATTGAATC AATATTATAC GAGGTGTGTA AACTTAAAGG
25  ATTACCATCG ACCTTCTGTT GAAGAAATCT TTGAGAACCC TTTAATAGCA GATTGTGTTG
      CAGACAGAGA AAGAGAAATC CTTGAGAGAA GAGGCGACCA ATTGAGAGAG CAGAAAAAT
      CCGAGATCTC GCGCCTGTTA TTGATGAGC TGAACCTGAA GAAATATCAG TACAGGAGAC
      GAGAGGAGCG TCTCAAGCCA AGAGAGAAA GATTGAGCA GAAAGAACAG GAGCTTGTG
      TCTGTAGAGC ACTAGCAGAG GACAACTCTG CTAGAGAGCA AAATCTGTGT AAGACATACA
30  GCTTCTAAAG GAACAGAGAG TCTCTCTCTC TCGCAATGTA TCGCAATGTA CTGATCTCTC
      CATCTCTCTA AATTAATGCT AAGGTCTATC TCAATGAGCA AAGTAAAGAG AACTCATGTA
      GAGTAGAGAA TTCTGAGAGT CAGCTCACTC CTAAGTCCAA GTCCAGAGCG CTGAGAAAAG
      GCGTTCAGCG TCCGCAAGCT GCGGCTCAAG CCGCTGACGA TATTGAGAAA AATTACCAAC
35  TGAAGAGACG ACGATCTGCT GCGCTGCGCT ACCGAGGTAG AGAGCACAGC AGCTGTATAC
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      GCGCCCACTA TCGTCTGCTT TCTGTATGTA AACACAGATA TTTGCGAATT GGTTTTACTG
      TCTTTCAGCA ACTATTGAC AAAATGTTCA CATTATATTT TCTTCTCTC TTTTAAAGAC
      ATATTATARA AAGATACTTT TCTGTGTGCG GCTTTTAATC CTGTGTGTGA TACTAGTAG
40  GAGCTAGAGA TGTGACATCT TAACCTGTG GAGGAAAAAT AATATTATGA AAAAATATT
      TATGCGAGAA GAATGACACT CACTGATATG TTTTAAATGA CTGATGTGTA TGCTTCAAT
      TGTCACTGCT AGATTAAAT TTTAATGCTG AGATTTTAAA TGTTTTGA GCTTGAAGAAC
      CCGATGATAG GCAATTGTGT CATTAATACC ATACACTCTT GCTATATAAT ATTCCATTCG
      TCTGTAGCTC AATCTGTGTA GCTTGTGAA AATTCACAC TGTATGATTT GTATCTTTT
      TTTTCTCTG TTACACAGAA TATGAGCTGT CTGTCACTTA CTAATCTCTT TCCACTTAAA
45  TAAAGAAATT CTTCAGTTA

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Seq ID NO: 157 Protein Sequence
Protein Accession #: NP_002488.1

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      ELKHPNIVRY YDRIDIMNTT TLYIVMEYCE GQDLASVTHK GTKEGYLDE EFLVRLMTQL
      TLALKECHER SGGHTVLHR DLKPNVFLD GQNVKLGDF GLARLHEDT SPKATVGTPT
55  YNPSFQPNH NYNVEDSHL SGLCLLTCL ALMPPTAPS QKELAGTIRE GFRRLPFYV
      SEELNLTTR MATAVYRP SVSELEHFL LADLVADRP RMLERLRQK GFEKRGDSB
      RFLSLAKRE TQLSERIAL KARERLSEK EQLCVRLER AELKARERL LKMYSLKE
      RFLGLALSDP ELLNLPSVI KKKVFSRSE XENIMRSNS ESQTSKSKC KILKKLLIAA
      QLRALQALSD ESNYQLSRQ ILDMR

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Seq ID NO: 158 DNA Sequence
Protein Accession #: Bos sequence

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      ATTGTGCAAC CTGGTGGGCG AACTGATAC TGGCNCNTAA TCGATAGAG GCGATATAGC
      TGTCAACATC CTGAGAGAGC TCTGAGAGCA CCGCCACACA AGGATATXV CAGTACCCAA
      ATGTCAGATA CAGTCTGTTT GAGAAACCT ACCCGAGAT CTACTGTGSC TTCTATGTTA
70  AGCTTGCTTT TGTTCTGCTC TCTGTAGATA TATAAAATAA AGACATGCG CAGTCCCTCC
      CTCAACATCC GAGACAGAGG CTCAGAGGCA TTCGAAATAC AGTGAATGA ACCTGAATTA
      TTGATTTCAA AATCTCAGCA ACTGAGAGAA TGACACACCA TCTCTGTTC CCTGGAGATC
      TCTCATTTT ACATATGAAA GTTTCAGGTT CCGAGAAAC CCGAGAGCTC GAGCTGCTGG
      TCCACCTAGC AGCTGAGGGA CTTTCAATTA CAGAATGAT CTCTGTGAC TGAAGATGAA
75  TATACTTTAA TTGTAAACAT GTGAAAGACT CTACTAAGAC CTATCGAGC CTGTTCTGTC
      TCCAGCCACA TTTCATATTA GTACAGATCT TTCTACACAG ATACAGATCT TCTACACTT
      TCGAGGCTCT GTATAAATC AGCTTTTACC TATTTTAAA ATATACAGAA ATATGATAAAA
      CTGAGATTA CCGAGATTC GGTATTTTC AATTTCCTG GAGACTTGA GAGACAGAA
      ATAAAGAT TATTTCAACA TCAATATAT GCTATTGTT ACATATGAG ATACACACAT

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ATATGTATATA ATTCAACCTT ACFTTTIAGC AATCACTATAA AATCCAAACAG AAAAAATAG 900
CATTTACTAT

Seq ID NO: 159 DNA Sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 264..782

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	TCTATCGGCG	ACTATTATTC	CTTAAATTTT	AGACTTGCAC	AATTAAGACT	TCNACTGACC	120
	TTCTCTGACG	TGAGAACTGT	TTCCAGTATA	TACATCAAGT	CACTGAGTAC	TCGACGACCC	180
	TCCGCGTGCG	ACTATGAGA	GCGAGGTGCG	CAGTGTGTGT	CTGAAAGTGC	CTGAGACCTC	240
	AACTTATGAC	CAGAGAGCTC	ATCATCTGCA	CAGAAGTCAT	GGAGGTCTGC	CATGCGTTAG	300
15	TGATGCGGGT	GGTGTCCCTC	TTCTGCGAGG	CCTGCTCTCT	CACCGCCATC	AACTACCTGC	360
	TCGACAGGCA	CATGCGCCAC	AAGAGTGAAC	AGATACTGAA	AGCGGCCAGT	CTCCAGCTTC	420
	CCAGCGCGCG	CCCTGCGTAC	CATCATCCAC	CTCTCTGTGA	AGATGTAGAG	GGTCTCTAGA	480
	CAGACGAGA	CATCCCAATG	TCTGATTCCT	CTTACAGGCA	TGACAGGAC	ACACCTCCAG	540
	ATAGCTTGGA	TAGCTCTGCG	AGTTCCGCTC	CTGCTTGCCA	GGCCACAGAG	GATGTGAGAT	600
20	ACACACAAGT	GGCTTTTCTT	GAACCTGGAG	AACTAAAGAA	TGCTCCCTCC	CTGGACTATG	660
	AGAAACATAA	GAGAACTACA	GATTATGTCA	ATGTCAATCC	AGAAAGACAC	AGCGGCAATT	720
	TCTGGATTTT	TGCAACCTCT	CCTCTGTCTG	AGCCAGCGGA	ATATGATCAA	GTGCGCATGT	780
	GAATGCCAAA	TATTTTAAAT	GGGATCCAGT	TCTCTATGGA	TTCTTACATT	TAATTTGTAG	840
	GGAATGCCAA	TTTTTCCCCC	TTAAACAAGG	CATGGGGCTC	ACAACTCTAT	GGAGCAACCC	900
25	CAAAAGAAAT	GTGAGAGGAA	AAACTGTATA	AGTACAGAGG	GGTCTCTAGA	CCCATGCACT	960
	CCTGTCTGTT	ACCAAAGAAA	CGTTTCTGTT	CTCTCAAAAC	AAAAACAGG	CTTGGCTGAG	1020
	AAACAGGCGC	AATGCGCCCG	CAGAAAAGGT	TGACATCAGA	TGTTAGGAG	ACCTTTCAAG	1080
	TAAAGTATGA	GAATCATGGA	GTCCATCAGC	AGAGTATGTA	GTGAGTCTCT	TCGCCAGGGA	1140
	AAATTTTAAA	AAGGTTGAAT	CAGCTGTTGT	AGATTCTCAT	TTGGCAATCT	CATGTGTAAT	1200
30	TGACTTCGCA	TTGAGCTCTT	TAAATTATGG	CATATACACA	CTCTCTTAAA	AGTTTAAAT	1260
	AAATAGCAAA	CCACCCACA					

Seq ID NO: 160 Protein Sequence
Protein Accession #: Bos sequence

	1	11	21	31	41	51	
40	NLTVEVNEVH	GLVIAVVSFL	LQACFLTAIN	YLLSEHMAHK	SEQLKAAEL	QVPRSPGH	60
	HPFAVKEMKE	QTERDIFNS	DELYRHESDT	PESELDSSCS	SPFAQATED	VDYTVVSD	120
	PGLKNSDFSL	DYENIKEITD	YVNVNFERIK	PEFWYFNPA	LSEPAETDGV	AM	

Seq ID NO: 161 DNA Sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

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	GGACACAAAG	TTGTATATGT	TTGTGTGTGT	GGAGGTTTTT	TCTACCTGTT	CATTTTTTTT	180
	TCTAAATCTC	TGATCATGCG	GGCATGTGAT	AAAAACAGAA	AATTTCAATT	CCCTTCTTAC	240
	TACCTGTTGG	CTAATTATAG	TGCTGCCGAT	TTCTTCGCTG	GAATTGCTTA	TGATTCCTGT	300
55	ATGTTTAMCA	CAGGCCAAGT	TTCAAAAATC	TTGACTGTCA	ACCGCTGAGT	TCTCCGTGAG	360
	GGGACTCTGG	AGGTAGATTT	GACTGCTTCC	CTTCCAACTC	TGCTGGTATC	CCCGGTGAG	420
	AGGCACATGT	CAATCATGAG	GGTGCGGTTC	CATAGCAACC	TGACCAAAA	AGAGGTGAAC	480
	CTGCTCATTT	TGCTTCTGTG	GGCATGTGCC	ATTTTATGAG	GGGCGTCCCC	CACACTGGGC	540
	TGGAATTGCC	CTGCAACAT	CTCTTACTCG	CTTCTCTGAG	CCCCCATTTA	CACAGAGAGT	600
	TACCTGTTTT	TGTGAGATGT	GTCCGACCTC	CTTCCAACTC	TGCTGGTATC	CCCGGTGAG	660
	CTGCGGATCT	ACGTGTACGT	CAGAGGGAAA	ACCAACGTCT	TGTCTCCGCA	TACAGTGGG	720
60	TCCATCAGCC	CGCGAGGAC	ACCATGGAAG	CTATGGAAGA	CGGTATGAC	TGCTTAGGG	780
	GGTTTGTGG	TATGCTGAGC	CCCGGGCTTG	GTGCTCTGCG	TCTCTACAGG	CTGTAATCTG	840
	AGGCACTGTC	GGCTGACGCA	TGCTTAAAGG	TGCTTCTGCG	TGCGTGGGCT	CTGCACTGCG	900
	CTCTGAAACC	CCATCATCTA	CTCTCAACAG	GACAGAGACA	TATATGACAC	CATAGAGAGC	960
65	ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GGAGAGGCTC	CCTCTGCACT	CCCTCCACA	1020
	GTCTCATGCA	CAAGTGACAC	AGCAGCGCAC	TACATAGAGG	ATATGATTAG	CCAGAGTGTCA	1080
	GTCTGCAATA	AAAGCMCTTC	CTAAACTCTG	GATGCGCTCT	GGCCACACCA	GATGATGACT	1140
	GTCTTAGG						

Seq ID NO: 162 Protein Sequence
Protein Accession #: NP_036284

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	FFFTFYLLA	NEAAGTFAG	IAYFLMFTN	GVSKTLTVN	ENFLQGLLD	SSLSATSLNL	120
	LVIIVERRHS	IMMRGESHNL	TKRRVTLLEL	LWMAIAIFNG	AVPTLGNRLC	CHIASACSLA	180
	FYSRSYLTVF	IVVSNLMAPL	IMVVVILRLY	VYVKKRTNVL	SPITSGSISR	RRTPRMLNKT	240

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	VMTVLGAFVV	QWTFGLVVL	LDGLMCRQG	QVHVKNFLI	LALLSNVNP	IYSTRKEDM	300
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	GCTTACAGCA	CTTATATATG	AGGTATATAT	CTTATGATGC	TTTGTCTTGA	TCCTCTCTGC	180
	TGCGAAGAGA	TCTGGGCTGA	CTATGAGAGA	GAGAACCTTA	TGCTTATCTG	TGCTGTCTCTC	240
15	CACAGGCTTC	CGGCTGCAC	CGAACCTCTA	GGCCAGAGCC	TTTACGTTTT	ATCATGTCTC	300
	AGATGTGGAT	ACCACTCAAG	AATCTGTAT	TGCAACTGTG	GCTAAAGACA	TGTGGAGGTC	360
	TGCAATGAC	GUTTATATG	GTACACTCTT	TGCAATATGA	CAGACTGGCT	CAGGAGAGAC	420
	ATTCTATGT	ATGAGACCAT	CTGAATCTGA	TAAATTTTTCT	CATACCTGTA	GAGAGGTAA	480
	CCGAGAGAT	TTTGAAATTT	TGTTTCTCTT	AATTGATCTG	GAAAGAGAA	AGGCTGAGCC	540
20	TGGAAAGAT	TTCTCTTCTA	AGTTCTCTCT	TATGGAATCT	TAGACGAGAC	AGATATATGA	600
	CTTACTAGAC	TCTCATATCG	CTGACCTGTA	CTTAAAGGAG	GATATCAAGA	AGGAGGTCTT	660
	TGTTTGTGT	GGGAGTGAAG	AGGTGTGATC	TGAGTCTGCT	GAGACTTATC	AGGTGTCTCT	720
	TGGAGATGAG	AGGAATAGAC	GTGTGGCATC	AGCATCAATG	AACAGAGAA	CGTCTAGGTC	780
	TCATGCGCTC	TTTCAATTTA	CAATPAGGTC	AATGAGAGAA	AGTATGAGAA	TTGTGAATAT	840
25	ACGGKCTCTC	CTACTCAACT	TGCTGTATTT	AACGAGGATCT	GAAGAGAGAT	AGAGTACCCA	900
	TGCGAAGAG	ATGATATCTA	AGGAGGAGAG	TACATTAAT	CGATCTATGA	CGTCTCTGAG	960
	CCAGGTGAT	CACGACTGTG	TGAGCTGTGG	TATGAGAAA	CAGA.GACATG	TTTGCTACAG	1020
	AGACTCCAAA	CTTACTCTCT	TACTACGGGA	TTCCCTTGGG	GTAATGCGCA	AAA.CAGCCAT	1080
30	AATTTGAAAT	GTTCATCTGT	GATCAAGGTG	TTTGTGGGAA	AGCTATCAAA	CACCTTAACCT	1140
	TGCTCTCAA	CGGAGAGGCT	TAGATAGACA	AGCTAGTATG	ATGAGAGACA	CCCAAGGAAA	1200
	TGTGAGCAG	CTCCAGGCTG	AGTGAAGAG	GCTCAAGAGA	CAGCTGCGGG	AGCTGTGCTC	1260
	AGGACAGACA	CGACCAAGAA	GCTTCTGAG	CAGAGACAAA	AGAGAGACTA	ACTATATGGA	1320
	GTATTCTCAG	GAGCAATGTT	TTATTTCTTA	GAATATCTGA	CAGAGAAAAG	AGTCTCTGAT	1380
35	AGAAAGATT	ACCAATATGG	AGATAGATGC	CTTACAAAG	AGAAATTTTA	TTTATGTATGA	1440
	TAAATGATT	TGCAAAATCC	GAGAGGATCA	AATATACGCC	TGGAAAAGC	TCCACAGAGA	1500
	ATCCCGGGGA	GTTTTTCTGC	CTGAGGAGCA	GGATCTGTTT	CTCTCAGAA	TAAAGAAATGA	1560
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	AAATCTCTCT	CTGACGGAGC	AGATAGATGC	ATGAGAGGTA	TGAGAGGCTG	TGAAGAGAGC	1680
	TCAAGAAATG	GATGCCAGCA	CCATTGCMA	ACTAGAGAAA	CGTTTCTCTG	AAATAAGTGG	1740
40	CATGGAGAAA	AGTGCAGAAA	ATCGCAGAG	ATTTTCACT	AAAGCTCAGA	AGAGGCCATG	1800
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	TAAATGAAG	CAGATATATG	AGATATCTGA	AGACATTTCT	AGGAAAAGCC	AGCTAGAAAT	1920
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	TAGATATTAT	ACTACACCCA	CGAAGGCTCA	CGAAGCTCAT	TCCCGACGAC	TACCAAAAT	2100
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	TGAGAGGCTT	AGACAGTCTC	AGGACCAAA	GAGTCTCTCT	CAGGCCAAAC	TGATGAAAGA	2280
	AGAGCAATAA	AACCTTAAAC	TTGACAGCA	TGTTGACAAA	CTGGAACATC	ATTTCTACCA	2340
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55	TGAGAGACAC	ATGACGTGAC	AGCTGTAAT	AGATATCTC	AGGTTAGAAA	ACGAAAAGCT	2640
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	ATCATGATCTG	AATAAATTTGA	TGAGAGTCTCT	TGAGCGCAGA	AAAGAACGCA	ATACGAATCT	2820
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	CGCTTATCT	CGAGAGGATCT	TGCTTGAGCG	CGATGATCTG	CGATGATCTG	CGAGAGAGAT	2940
60	ACGAAACTCA	GAGAGAGGCT	TGCTTGCTAC	TGAAAAGTGT	ATGACTTCCC	TGGAAGAGTC	3000
	TAGAGATTCT	GATAGAGAAAG	TTGTAGCTGA	CCTCATGAAC	CAGATCCAGG	AGCTAAGAAC	3060
	ATGAGTGTGT	GAGAAAACAG	AAACTATAGA	CACCTCTGAA	CAGAGACTGA	AGGACATPAA	3120
	TTGCAATAC	AAGCTCTCTT	TGCTTGAGCG	AGAGTGTGTA	AGAGTGTGTA	TGAGAGAGCA	3180
	GGAGTGTGAT	ATTCTGAGTC	TGAGAGAAAC	CTTATGAGAG	AGATATCTTT	CTGAGGACTT	3240
65	AGAGAGGAGT	ATTGCTCTGTG	AGGACCTGCG	TCATGCCACT	GAGCAGCTGA	ACATGCTCAC	3300
	AGAGGCTCTA	AAAAAACACT	CGGCGTCTCT	CGAGTCTGCG	CAGAGAGAAC	TGACAGAGAA	3360
	GAGAGGCTCT	ATTACAGAAC	TTGACAGACA	CGATTAACCA	AGAGAAAGAG	AAATGAGACA	3420
	GAGAGAGAT	GATATTAATC	TGCAATATGG	GCACATGAGA	CGTGTGTATG	ATTATCTCTG	3480
	TCAGAGTCCC	CAGAGTCTCA	AGACACGACC	TCATCTTCAA	ACACATTTGG	CAAACTCTCT	3540
70	CGAACACACA	GAACAGAGAGA	TAGAGAGATG	AGAGGCTCTCT	AAAGCTTTCT	TGGAACACCT	3600
	TGTACAGAG	CTAATAGTAG	ACAGAGAAAT	CAAAATCTCT	GAATCTTCTA	GATGAGAGGA	3660
	CGAGTGTCT	GAAATGAAA	AGCTGCGCTC	GGAGATCTGA	AGATTAATGA	AGAAATCTCT	3720
	CGCTCTGACA	GTTGACTGTG	ATGATATTAA	AGACAAAGAG	GAACACAGTG	ATCGAGATCT	3780
	TCAGATATAT	CACAGCTGTA	AGATTAAGCA	AGAGAAAGAT	ATCAAGAGAA	GACTTGCAAA	3840
	AGTAAATATA	TTTGAAGAAA	TGCTTAAGAT	GAAGCAGAC	CTGAGAGAGG	TCCAGAGTGC	3900
	CGTTTACACA	CAGAGAGAGG	AAATCTCTGA	AGATCTCTGA	CGACACACCA	GAAGAGAGAC	3960
	TTTGTGTGCT	AAAGACTTCC	AGGAAAGAAA	ACAACGTAGA	TGAAAGATCT	GAAGATATCT	4020
	TGAAGAAAGA	CAGAGAACAT	CCGACAGAT	GGAATATGTTA	AGAGAGCAGG	TGAGATGTCT	4080

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TGCTGAGGAA AATGGAAAGT TGGTAGTCA CCAAAATTG CATCGAAGA TTCACTAAGT 4140
 AGTGCACACT AAGAAGAGAA ATGTGAGCT TCTCTGAGG ACAGAAAATG TGCTGTGCGA 4200
 AATGTATTAT TTAAGAAGAA ACAAAGAGG TGAATCTTGA GATCTCGGT CAGCTACTCA 4260
 GSKATCACT TGTGTGAGA TGTCTCTCT CTTTAGAAG TAAAGACTAC TCTCGGCAC 4320
 5 TTAGGAGAGC TGAATTTATG GACCTTAATT ATTAAGTGT TATAGGTGG TGTAAACAC 4380
 CTCAGATTTC TGATGAJCAT TCTGCATCCA TATACACCT GTGACGTGA CAGCTCTGCT 4440
 ATTAATGTGC CTACTTCAGG GCTTTGAATC AACTTAAGGG AAAACCTTTT GTCTTTGTAA 4500
 AATAAAGC CTGTGATCA GCTTACAGT GGAATATAGC CAGATCAATT TCTTCTTAGA 4560
 10 TATGCGATA ATCTCCTTTG ATTCCTATGC AAGTCTTAAC AATATATGTT GTTCCACAA 4620
 CCTGAGTGA GTTATCTTAC TGACTTAGTA GCAAGTACAA GAAGCAACT GTTATAATA 4680
 GATTATTATT GTATTCTTAC TTAGTATTAT TTACTTGAGC ATTTTCAGT ACTGTAATA 4740
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Seq ID NO: 164 Protein Sequence
Protein Accession #: NP_064627

1 11 21 31 41 51
 MAPGCKTELK SVTNQSNQNP SNBQDAIKVF VHIRPAPRR GSADGBQNLK LSVLSSTSLR 60
 LSNVPEKPTV TFDHADVDT TQESVATVA KSVESGMBG INCTTPAYGQ TQSGCTPTTM 120
 QPESSEFHS NLRGVPRSP EULSLIDRE KESAGAKSV LCKSCSTIYI NEQIYDALDS 180
 ASAGLVREH IKKGVFVGA VEQVVTAAE AYQVLGQWR NRRVASTSMN RESSRSHAVP 240
 TTTESMEKS NEIVNIRSL LNLVDLAGE RKQTHABGM RLKEAGNIRN SLSCLOQVIT 300
 ALADVQRIQG RHVCTRDEK TELRRLSLQJ NAKTALIAN HIGSRFCGET LSTIAFATGA 360
 KLIJHNVNTP EDPOQVQGL GAEPRLLKQJ LASELAGTTP PESPTRDCK KTYNNEFQJ 420
 AMLFFKSEQE EKSLIEKYT QLEDLLKKE KFIQENQMI KPEDDIIRL EKLMKESRG 480
 FLPESDRLLL SELRNEITVL RQIEKHPRV AKYAMENHSL REENRLRLL EPVIRACEMD 540
 AGTTALEBA FSEIIGMEKS DMQGGQFPR AKQEPCLFAM TELKLAQLQJ IQTELMSHQA 600
 30 FTEFKEFTR KQELIEBIE DLRGKQHLN DILLATATCA KQGVPRQAK HANFLIIT 660
 TPTKALQHS RVPVLLSFEM GSGSLYQTN SSIENLDILN EFPVPEQNEQ AFEAISELR 720
 TVQBGHALQ AKLDEEBHN LKLQGVDLK EHNSTQWEL FSSERIDWTK QQBELLSQIM 780
 VLEKQLQGTQ TQNDPLKSEV DLRGVLIHA DEKLSVYLE YSFPRTNQEK EPNKLSEIRM 840
 35 HVQLQDLNR LDEHMLQ QELMVEDL LRMFLGNFK EMTSLAKK 900
 NLMLELEAK ERNKLRLQF EEDKENSKE ILKVLAVRG EKQKETAREC QMAKVQKLE 960
 ESSLATEKI SLEKSRDSD KKVVDLMQJ IQELRTVCE XTSTIDTLKQ EDKINCYNV 1020
 SALVREERB VLKIKQVDI DDLKELRLR ILSEIDRDM LCEPLAIATE QLMPTFASK 1080
 KESBLLSQA BELTETTTA ACATACAAH DPTACGATG TYPVBAQGHG VQGBALBDQ 1140
 PRUPPHUTV HMLLETOE GEIDGRASK TSEELVTKL NDRREVKNAB ILRMEQLRE 1200
 40 MENLRLESQ LIEKHNLQJ QLDIDKQKE NSDQHPFMD QLMNEQESI KERLAKSKI 1260
 EBMLOKADL EVQSALYHK EMECLMYTE VERTQYLEK AFQEKBLRS KLEENYERE 1320
 RTSGSEENLR KQVECLAENH GKLVGRQNLH QKTQVVRLL KDFVRLAEST EKLRAENVPL 1380
 KKKKSES

Seq ID NO: 165 DNA Sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TTTTITTTTT TTTTITCACA TGTGATGTT GCTGCCGATG ATTTCAAGC CTGCGCTTGA 60
 GATGCTGGGA GTAGCTTGA ATATATGAA ATTCCGAAT CAATATCTAC TTATTCTTAC 120
 50 TTAATGCTAT TGTATTCTCT AATTCTGAGC TTACATGAT AAGAAGTAC TTTCGTGAG 180
 GGTCTTAATT GAAAGTGTGG CTGCGATGA CTGCGCAGA ATTAATCTC TGGAGAGCT 240
 CTGAGCTCTT TTAATAATCA TCMACAGCG AAATCTCTTA TCAATAGCTA TGGGGATG 300
 GATAGGTAC AGATATTATA ACATACAAH DPTACGATG TYPVBAQGHG VQGBALBDQ 360
 55 TAAATATAA GGAATATGA TGTCTTAAG TTATTATTAA TCMGACGTA TGACTOIAAT 420
 TGAATAATG AGACAAATA GATTATAATA GNAACACCA GTAACATG GTATGCGAT 480
 AATCTGAGG GTAACTTGT GATACATTA ATCTAATAA GTCACTTACC ATCAAAATAT 540
 TACTGATCC TACTATTTC TGTCCAGCT TTAAGATG TTTTACATG GGGGATCTAT 600
 60 TTTCTTCCG TCTTCCAGG AATTATCCAG CGAGTCCAA TACGGCTTTT CAATAATGT 660
 AATTAACCT TTAGAGTGA ATCCGAGCT GTTCCAGAA AATACCTTT TATAAGTGT 720
 AGTCTCCCT GTAACTGGT TTTCCCGGA ATCCGGGAG GCAATGTGT TTTTATTG 780
 GCAATTTTG TGTGCTCTT TTTGTTTGT TGTGCTGTG GTTCTTCTT CCAAGGCT 840
 GAGAAATTT TGTGCTGCT AGGCATCTT ACCGGTTTA GAGAAAGAC ACACCTTTCC 900
 CGCAATGTC GCTTTGGAT GACACATGA

Seq ID NO: 166 DNA Sequence
Nucleic Acid Accession #: NM_06953.1
Coding sequence: 33..896

1 11 21 31 41 51
 CTCTTCCGGC CTCGCGGCGC TCTCCGCGG CGATGCTGCC GCTCTCGGCC CTGCTGCGCC 60
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 75 TGCACACAA CAGCCGCCA CTACACAGT TGGCTTGA AAAGCTCTC TCACTTTTG 180
 AAGACAGAA GCGCTCATC GATACAGCA AGTCTCAT GTATGCGCTG GTCACAG 240
 CCAATTCCG GATATGCTCA GTGACAGCA GCACACACAC CCGACGCGGC TCAAGCTTC 300
 TACAAACGA GGGTGGCAG ACGATGCTCT ACAAAGTGT GCTCTTGAC GTATGCTCT 360
 CGATGACTCT GCCAGCGCT GATCGATTG GAGATGTGTC CAAAGCCTCA CAGATCTCA 420

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 10
 ATGCTTACCT GGTCAAGGTG GTTCTGACAG GGAAGTGTGCT GTGGATATCC AACTTCCAGG 480
 GCTCTGTGTA GCGACCCCTG TGCGACGCCA CGAGGTACAG GTTCAAGTAT GTCTGTGTCA 540
 ATATATCCAC GGGCTGTGTA GAGGACACGA CCGTGTGGTC GAGACCATCT CGACACCAAC 600
 AGCTCAACCC ATACTACGAG ATGCAACAGT GGCACGCGCT GCGAGGACGA GCGATATGTC 660
 TCTACACTTC GATCTCGAGC TCCCTGCGCT TCTTCTACT TGTGGTITTT GCTGCGGCCA 720
 TTGCGCTCAG CCGTGTGGAG ATGGGGAGTT CTGATGGAGA AAGACTACAC GACTCCCAAA 780
 TCACTCAGGA GCGCTTTCCC AAGTGTGCTG GGGCTTCGGA GTCTTCTTAC ACCTCCGTGA 840
 CCGCGGACCC GCGACGTGAG AGGCTCTGAG TGTATTCCG CAGCTCTCCA GACTGAGCC 900
 AGGCAACGCT CTGGACGAZA GGAATCTACT CTCTGCTCT GCGCCAGGCC CTGACACAGT 960
 GGTTCGACA CCGTGACTTC AGGGAGGTG AAAACAGGCT TGTCCCTCCA ACTGACGAA 1020
 AAGCCTTAAT AATAATCTCT GATGAGTTCT AAAAAAAA

Seq ID NO: 167 Protein Sequence
Protein Accession #: NP_008884.1

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 NPLMLALLAL GCLRFQGSVAL LQPGASVTF ATNMFPLITV ALEKPLCFMD SKEALTGTHE 60
 VYLVLVDSA ISRNASVQDS TTFLGSTFL GTGGRTOPY KAVAFDLIPC SLDPLSLDAIG 120
 DVSKASQLIN AYLVVRVQAG TGLMDHIFQG LCHAPLSAAT EYRFKVLVIN MSTGLVEDQT 180
 LMSDFLTRQG TVEYSITIDW FGRSQQHIV ITSLIGSLTF FLVLVSPALAI ALSLVDHSS 240
 DGETHDSQI TQEAVPKSLG ASSESYTSYN RGFPLDAREV YSSKLQD

25
 Seq ID NO: 168 DNA Sequence
Nucleic Acid Accession #: NM_005672.1
Coding sequence: 18..389

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 AGGGAAGGCG AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GCGTGTGCCC 60
 TGCGACGAGG CACTGCCCCT CTGTGCTACT CCTGCAAGCG CCAAGTGAGC AAGCAGGACT 120
 GCGTGTGGCT GGAAGACTCG AGGACGCTGG GGGAGCAGTG CTGACCGCGC CGCATCTCGG 180
 CAGTGTGGCT CTGATCGAAG AGGCTGAGCT GATGTGAGCT GAGCTGCTGG GAGTCACTAT 240
 AGGACTACTA CTGTGGCGAG AAGAACATCA CAGCAGTTGG TGCAACGCCA 300
 CGGGGGGCCA TGCCCTGCGG CGGGCTGGCG CCATCCTTTC GCTGCTCCCT GCACTCGGCC 360
 TGCTTGCTGT GGGAGCCGCG CAGCTATAGG CTCTGGGGGG CCGCGCTGCA GCCACACATG 420
 GGTGTGTGCG CCGAGGCTTT TGTCCACATC CTACAGAGAC CTGGCCGAGT GGGAGCTCTT 480
 CCTGTGTTCT GAGGACATCT CTAACCCAGG TTGACCAATG TATGTTTGCA CCGCTTTTCC 540
 CGNAACTGT ACCTTCCTAT GGGCTTTTC CAGGATTCGN ACCGGCGAGA TCAGTTTTAG 600
 TGANACNAT CCGGTGTCAG ATGGCCCTTC CAGACNTTTH TGTGTGTTGT TCAATGACC 660
 AGCATTTTCC ACCCTTAACC CTGTGTGTAG GATCTTHTTC CCGAGGAGAG CTTCTCCGCG 720
 CCACCCCTTT TATGAAATGA GCCAGGTTTG GTCCGTGGTG TCCGCCGAGC CAGCAGGAGG 780
 ACAGGCMATC AGGAGGGGCC ATAAAGGCT GAGATGAAGT GGACTTGAGTA GAACTGGAGG 840
 ACAAGAGTTG ACCTGATGTC CTGGGAGTTT CCAGAGATGG GCGCTGGAGG CCTGAGAGGA 900
 GGGCGCGGCC CTCACATTTG TGGGSHCTCC GAAATGCGAC CTAGACGACAG CTTAGGCGCT 960
 TAATAACAC CTGTGGGATA ACCCAAAA

50
 Seq ID NO: 169 Protein Sequence
Protein Accession #: NP_005663.1

55
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 HXVALLALLM AGALAQPTTA LLYSCAGV SHRECLQVEN CTGLGRQCTT ARIRAVLLLT 60
 VLSVQSLMIC VDSGGDYVVG KNIITCCDFD LNAAGGHAL QPAAITALL PALCLLLHGF 120
 QGL

60
 Seq ID NO: 170 DNA Sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

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 AATCCCGACA ATGCGGAAAG ACAACTCAAC TGTTGGTTGC TTCCAGGGCC TGCTGATTTT 60
 TCGAAATGTA TCAATTGGTT GTTGCGGCAAT TGCCCTGACT GCGAGGTGCA TCTTCTTTCT 120
 ATCTGACAGA CAGACGCTCT ACCGACCTCT TGAAGCCACC GACAGAGGAG ACATCATATG 180
 GCTCTGCGTG ATGCGACTAT TTGTGSGGAT GAGCTCTCTG TCCCTGCTG TCTTAGAGAT 240
 TTTAGGATCT ATGAGACTCG CAGAGAAAT TCTCTGCGG TATTCTATC TGATTTTATC 300
 ACTATATGCC TTGAGTGG GATCTGTGAT CACAGACAGA ACACAGAGAG ACTTTTTCAC 360
 ACCCAACCTC TTCTGTAGAG AGATGCTAGA GAGGTACCPA AACACAGGCC CTGCAACAGA 420
 TGTATAGGAG TGGAAAACCA ATGAGTCCAC CAAACCTTGG GAGAGGCTCA TGCTGACGGA 480
 CAACTGCTGT GGGTAAATG GTCATATCGA CTGCGAAGAA TACACATCTC TCTCTCCGAC 540
 TGAGATTAAT GATGCTGACT ATCCCTGGCC TCTTCAATCG TGTGTTATGA ACAATCTTAA 600
 AGAAGCTCTC AACCTGAGAG CTTGTAAACT AGGCTGAGCT GOTTTFATTC ACAATCAGGG 660
 CTGCTATGAA CTATGATCTG GTTCAATGAA CCGACAGGCC TGGAGGGGTT CTTGTTTATG 720
 ATTTCGAT CTGCTGCGGA TTTTGTGGT TCTCTGGGCT ACCAGTTCT ACTGSGMAG 780
 ATTGAATAT TAAAGA

WO 00/03906

PCT/US02/21338

Seq ID NO: 171 Protein Sequence
 Protein Accession #: NP_068883.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MAKINSTVRC PQGLLIPGVN IIGCCGIALY ABCI PFVSQD HSLYPLLEAT DNDIDYGAAM 60
      IGI PVGICLF CLSLVGIYGI MGSERKILLA YPILMFIVYA FEVASCITAA TQRDPFTFNL 120
      PLKQPLERIQ NRPFPNEDQ MWRGVPYKYM DRLMLQDWCC GWNSGSDWCK ITSAPFTSRN 180
      DEDYFHPKCC CWNHLLSEI HLEACKLQVP GPYINQDCTE LRSQPMWRIA WDAWMPQPAI 240
10    LCMTFHVILG TMPYMSRIEY
  
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Seq ID NO: 172 DNA Sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 1..672

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15      1      11      21      31      41      51
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      ATGAGGCTCC AAAGACCCCG ACAGGCCCGG CGGGGTGGGA GGCAGCCGCC CCGGGGCGGG 60
      CGGGGCTCCC CTTACGGGCC AGACCGCGGG AGAGCGGCCG GGAAGCTGCC AAGGTTCCAG 120
      AAGGGCGGGG AGGGGGCCCG CGGGGCTGAC CTTCCCTGGG CACCGCTGGG GAGCATGGCG 180
      CTCTCTGCGT TGCTCTGGT GTGAGCCCTA CCGCGGGTGT GAGCAGAGCC CAACTGACAT 240
      GCGAGACACR GAGATCCAGA GACATCCCGG CGAACCGACG AGGGTGACAA TAGAGTGTGG 300
      TGT CATGTTT GTGAGGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360
      ACAGAGCCAT ACTGAGTTAT AGCAGCGGTG AAAATATTTT CAGCTTTTIT CATGTTGTGG 420
      AAGCGTGTCT CCCTGTGGT TGCGGCGMGT GMRAGACCCA AGCGGAGAGA GAGAGCGTTT 480
      CTCTCGAGAG AGGCCATCTA CTTCTCTGCT CTGAGCTGTT GTAAATATCG CTACTGCAAT 540
      TTGAGGGGCG CACCTATCAA CTCATCAGTG TTCAAGCAAT ATGCTGGAG CATGGGTGAG 600
      AGCTGTGGTG GGCTGTGGCT GGCCATCTCT CTGCTGCTGG CTTCAATTC AGCGGGCTCT 660
      AGCTTCTCTT GA
  
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Seq ID NO: 173 Protein Sequence
 Protein Accession #: Bos sequence

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35      1      11      21      31      41      51
      |      |      |      |      |      |
      MRLQRPRQAP AGERRAPRGG RGSYPKPDGP RGARRLRRTQ KGGGAPRAD PFWA PLOTVA 60
      LLALLLVVAL FRWTTDANLT ARQSDPDSQD TDECDNRVW CHVCEBNTF BQGNPRRCNW 120
      TEPVCTIAV KIPFPRFWA KCGAGCAAM ERPKSEEFY LLEKPMFFY LKCCNRYCN 180
40    LEGFPINISV FKEYAGSMGE SCQDLMLAIL LLASIAAGL SLG
  
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Seq ID NO: 174 DNA Sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

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45      1      11      21      31      41      51
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      CGGAGCGGAG CAGAGGCTG ACCAGCTTCC TCTCTCTGCT CTCTCTCGGC TCCAGCTCCG 120
      CAGCTCGCGG CAGCGGGGAG CAGTCCGACC CAGAGCGCCC GCGCGCTCCC CGAGCGGCTT 180
      CGCGCGCTCT CTCTCTGCTC TTCTCTTGCA CTCTCGCGCG CGGTGAGCGC CTTCTGAGAT 240
      CCCAGAGGGG AAGCAAAAGG GCGAGCTCCG CAGAGGGGAG GTGGTGACC TGTATAATGG 300
      AATGTGCTTA CAGGGGCCAG CAGAGTGGCC TGCTCGAGAG GGGAGCGCTG GGGCCNATGG 360
      CATTCTGGGT ACAGCTGGGA TCCGAGTCCG GATGTGATTC AAAGGAGAAA AGGGGGGAGT 420
      TCTGAGGAAA AGCTGTGGAG AGTCTCGGAC ACCCACTAC AAGCACTGT CATGGGTCTC 480
      ATTGAATAT GCATAGATC TTGGGAAJAT TCGGAGTGT ACATTACAA AGATGCTTTC 540
      AATATGTGCT CTAGAGTTT TGTTCAGTGG CTCACCTCG CTAAATGCA GAAATGCATG 600
      CTGTGAGGCT TGATATTCA CATTCATGG AGCTGAATGT TCAGAGCTTC TCCCATTTGA 660
      ACCTATATAT TATTGGGAC AAGAGAGCCG TGLAATGLAN TCACACATA ATATTCTCG 720
      CACTCTTCTT GTGGAGGAC TTGTGTGAAG AATTGTGCTG GGATTAGTGT ATGTTGCTAT 780
      CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
      TTCTCGGACT ATTAATTGAG AACTACCAAA ATAAAGCTGT TAATTTTCAT TTGCTACTCT 900
      TTTTATTAT ATGCTGTGGA TGCTGTGCTC TAAAGGAGAT TTATAAGAG TTATATGTGA 960
      CATCTGAAAT AAAGCAAGC CTAATATGTT TTAACAGACA AAGTGTGATT TCACTGCTT 1020
      TTTAACTCTA GCATTATCTA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTITATG 1080
      TGATTAGAA ATCTTTCTCA TAGTCAATT CTCTCAACT ATAATTGGA ATATTGTTGT 1140
      GGTCTTGTGT TTTTCTCTCT AGTATAGAT TTATAAAAAA ATATAAAAA TACCATCTT 1200
      TCAACATTT GTAAATCTTA AGATTTTITT TTTATCTGTT TAAATAAAAA TTAATTTCAA 1260
      CACCTTAAA AAAAAAAA AAAA
  
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Seq ID NO: 175 Protein Sequence
 Protein Accession #: XP_057014

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75      1      11      21      31      41      51
      |      |      |      |      |      |
      MRPQGPASP QRLRLLLLL LLQLPAPSSA SEIPKQKQA QLRGQEVVDL WQMCCLQGA 60
      GVPGRDGSFG ANGIPTGFI PGDGFKGEK GECLESFEE SNTPNYKQS WSLIAYGYDL 120
      GKABCTFTFK MRSNSALRVL FSGSLKLECR NACCGHYFT FNGACSGEL PIRAITLYLQ 180
  
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WO 03/003906

PCT/US02/21338

GSFEMNSTIN IHRSTSVDEL CBGIGAGLVD VAINVGTCSB YPKDASTGN NSVSRILIEE 240
LPK |

Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 1..2268

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	CTTCATGAGC	TAAAGGAGC	NGCTTTCCCC	CAGACACATG	ASAAAAATAG	TCCGAAATGG	120
	GAATCTGAGA	TTAATGTGGA	CTTCACANTT	TCCAGCAGCG	ATAATATCT	AGACACATT	180
	TTCTACCGCT	ATGAGAGAAA	TAATCTTTTG	TGAGTTGAGG	GGTTACAGAA	ATTACTTCAA	240
	AATAAGGCA	TAGATAAGAT	TAAAGRAAT	CATATACACC	ATGACACGGA	CCATCACTCA	300
15	GACACGAGC	ATCACCTGAA	CCATGAGCGT	CACCTAGAGC	ATGAGCATCA	CTGAGACCAAC	360
	GACATCACT	CTGACATGA	CTGACATCC	CACCATATCT	ATGCTGCTTC	TGGTAAAAAT	420
	AGCGGAAAG	CTTTTGTGCC	AGACCATGAC	TGAGATAGTT	CAAGTAAAGA	TCTTAGAAAC	480
	AGCCAGGGGA	AGGAGCTCA	CCGACAGAA	CATCCGATG	GTAGAAGGAA	TGTCAAGGAC	540
20	AGTGTAGTG	CTAGTGAGGT	GACCTCAACT	GTGTACAGCA	CTGTCTCTGA	AGGAACTCAC	600
	TTTCTAGAGA	CAATAGAGC	TCCAGACCT	GGAAAGATCT	TCCCAAGAGA	TGGTAAGGAC	660
	TCTCATCCAC	CGAGTGTAC	ATCAAGAGC	CGGTGAGCC	GGCTGCTGCT	TAGCAAAAAC	720
	AATGAATCTG	TGAGTGAAGC	CCGAAAGGC	TTATGTATT	CGGAAAGAC	AAATGAAAT	780
	CTTCAGAGT	GTTCATATG	ATCAAGATTA	CTGACATCT	ATGGCATGGG	CATCAGGTT	840
25	CGCTGAATG	CAACAGATT	CAACTATCT	TGTCGAGCA	TGATCAACCA	AATGTATCT	900
	AGTCTTGT	TGATCATAC	AACTGAAAG	AAAGCTGAA	TCCCTCGAA	GACCTATTCA	960
	TTCAAAATG	CTTGAGTGG	TGGTTTTATA	GCCATTCCA	TCACTAGTTT	CTGTCTCTG	1020
	CTGGGGATTA	CTCTAGTGCC	TCTCATGAAT	CGGTGTTT	TCAATTTCT	CTGAGTTCT	1080
	CTTGTGACAC	TGGCCTGTGG	GACTTTGAGT	GGTATAGTT	TTTACACCT	TCTTCACAT	1140
	TCTTATGGA	GTAGCATAC	TATGCTAGC	CTAGAGAGC	CACTATGAG	ATGGAAGAA	1200
30	GGACCATTT	CTAGTCACT	GTCTTCTCAA	AACATAGAG	AAAGTGCTTA	TTTGTATTC	1260
	AOTGGGAAGG	GTCTAACAGC	CTAGAGAGC	CTGTATTCA	TGTTTCTGT	TGAACTATC	1320
	CTCATCATTA	TCAAACATT	TAAAGTAG	ANGAAAGAA	ATCGAGAGA	ACCTGAAAT	1380
	GATATAGTG	TGGAGTTAA	GGTGGGTTG	CTTGAGTTT	AATCTCATCT	TTCAAAGAT	1440
	GGAGGAAGG	TAGATACAGA	TGATCGAAT	CAAGCTATT	TACAGCAGA	CTCACAGAG	1500
35	CCCTCCCAT	TTGATCTCA	GCAAGCTGCA	GTCTTGAGG	ANGAGAGGT	CATGATAGT	1560
	TACCTCATC	CACAGAGGT	CTACATGAA	TAATGACCA	GAGGTGCAA	GAATAAATC	1620
	CTCATCACT	TCACAGAGC	ACTGAGCCG	CTATCCACA	CCATCATCA	CTGATGAGC	1680
	CACTCATATA	TTCTCATCA	TCACACAC	CAACACAC	ATCTCCACG	TCACAGCCAG	1740
	CGCATCTCT	GGGAGAGCT	GAAAGATGCC	GGGTGCGCA	CTTGTGCTG	GATGTGATA	1800
40	ATGGGTATG	GCCTGCACA	TCTCAGCAT	GGCTAGGGA	TGTGTGCTC	TTTACTGAA	1860
	GACTATCAA	GTGGTTTAA	TACTCTTCT	GGTGTGCT	GTATCATGTT	GGCTCATGA	1920
	TGAGTGACT	TGCTGTCT	CTAAGAGCT	GGCATGAGC	TTAAGCAGC	TGTCTTTAT	1980
	AATCATGTT	CAGCCTGCT	GGCTATCTT	GGATGGCAA	CAGGAATTT	CATGTGTCAT	2040
	TATGCTAAA	ATGTTCTTAT	GTGATATTT	GCATCTACT	CTGGCTATT	CATGTATGTT	2100
45	GCCTCTGTT	ATATGTACC	TAAAGCTG	CACATATG	CTAGTACCA	TGGATGAGC	2160
	CGCTGGGCT	ATCTCTTTT	ACGAGATCT	GGAGCTTTT	TGGTGTTCG	AATATGTTA	2220
	CTATTTCGA	TATTGAACA	TAAATCGTG	TTTGATATA	ATTTCAG		

Seq ID NO: 177 Protein Sequence
Protein Accession #: XP_084007

	1	11	21	31	41	51	
55	VRKLGVILL	LTPLGVTPH	LHELKAAFP	PTTEKISRW	ESGIVNDLAI	STGYHLQGL	60
	PKYRGNNSL	SVBQFKLLQ	NIQDIKKIR	NIHHCCHHS	DHERHSDBR	HSDHEHSDR	120
	EHSDIHDSH	HNHNAAGK	KIKALCPDH	DSGSKDFPN	SQKGARHRE	HASGRNVKD	180
	SVASBETVT	VHNTSEGTH	PLETIETPR	GLPLFQVSS	STPFVTVSS	RVLRLQJKT	240
	NSVSRIRG	PIRSLTVDN	DDCFMABL	LTRGQGVGV	PLMRTFPLV	CPALINDIA	300
	RCLLITSEK	KAEIPPKTYS	LQIAVVGSI	ALSIISFLSL	LGVLVPLAN	RVFFKFLSP	360
60	LVALAVTSL	GDAFLHLLP	SHASHHSHS	HEEPAMENK	GPLFSLSSQ	NIEESAYDS	420
	TKRSLTGG	LYPMFLVHV	LGLCAFGK	KKNKNGKPN	DDVETKQL	SCESQLSTN	480
	ESYDIDRT	SGILNAGT	NSHNSQQA	HNHNSWTA	HNHNSWTA	YVRSCHMG	540
	HSFPHDTLG	SDLLHSHHD	YHILHHHHH	QNHSHSHSQ	YSRRELKKA	GATLAWNVI	600
	MDGLNRFSD	GLAIGAPTE	GLSSGLSTV	AVFCHLHRE	LDFPVLKKA	MTQVQAVLY	660
65	NALBANLAY	GNATGIFGH	YAHNVSHVF	ALTAGLFTVY	ALVDNVPENL	HNDSHGHGS	720
	RMVFTQLQA	GHLGFGIML	LISIFEHKIV	PRNPF			

Seq ID NO: 178 DNA Sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1790

	1	11	21	31	41	51	
75	CAGACGCTGG	GAGCAGCTC	TGGGGAAGT	CGAGACCTCC	GATCAGCGCT	TCTTGCGGCT	60
	AGCTACGCGT	GGTGTGTAG	AACGGGCGG	GGCTCHSGG	TGGGCTCCCT	AGTGGAGACC	120
	CAGTGGGAG	AGGCAAGAC	TCTCCAGCTT	CCTCGCTTCT	GGGTCACTC	CTTATTCAAG	180
	TCTGAGCGG	GCTCCAGGG	AGATCTCGT	GGACTTCAG	AAA GCTGGG	CAGTCTCGCT	240
	TTCAACCATG	CCCTCTCTCC	TGGGAGCGGA	GATGTGGGGG	CTTGAAGCTT	GGCTCTCTCT	300

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	GCTGCTACTG	CTGGGATCAT	TTACAGGCCG	GTGCCCCGCG	GGTGAGCTGG	AGACCTCAGA	360
	CTGCTTAAC	CTGGTGCTGG	GCCAGGACCG	AAATCTGCC	TGCTCTAC	GAGGGCAGTC	420
	CGGAGAGCA	GTGGGGCAG	TGCGATGGGC	TGGGTGGAG	CGGGCGAAG	GCGCCACAGA	480
	ACTGCGCTA	CTGCTCTCA	AATAGCGGCT	TGATGTGAG	CGGCTTAGC	AGGCCGAGCT	540
5	GGAGCAGCG	CGGCTCCAC	GGAACCTCTT	GGACGCTCA	GTGCTCTGC	CGAACGAGT	600
	CGAGCGGAT	GAGGGCGAGT	ACGAGTGGCG	GGTCAAGACC	TTCCGCCCG	CGAGCTTCA	660
	CGGCGGCTG	CGGCTCGAG	TGCTGTGTGC	TCCGCTGCC	TCACTGAATC	CTGGTCCAGG	720
	ACTAGAGAG	GCGCGGGCC	TGACCTTGGC	AGCTCTCTGC	ACAGCTTAGG	GCGAGCCAG	780
	CGGAGGCTG	ACCTGTGCA	CGAGGTCA	AGGTACAG	TGTACCTCT	CTCTGACGA	840
10	CTGCGCTCT	GCTGGGCTCA	CCTCAGATT	CAACTGTGT	CTTAGGCCCA	GATGAAATG	900
	CGAGCACTG	ACTTGTGTG	TGTCCCATCC	TGGCTGTCT	CAGACGAAA	GGATCACCA	960
	CACTCTCAC	GTGTCTTGC	TTGCTAGGC	CTTGTGAG	GGCTCTTAG	ACCAAAATCT	1020
	CTGCAACTT	GGGAGGAG	GAGTGTGCT	CAATGTGCT	AGTGAAGCT	AGCTGCTTC	1080
	CTCATACAC	TGAGCAGCG	TGGAATGGCC	TCTGCCCAT	GGGTACAG	TGATGTGGG	1140
15	CAGTTGGGC	TTTCCCCCAG	TGACCACTCA	GACAGCGGC	ATCTAGTCT	GCAATGTCA	1200
	CAATGATTC	TGCTCAAAG	ATTCTTAGT	CAGTGTGAT	GTTCCTGAC	CCGAAATAGA	1260
	CTCTGGAG	CAGTGTGAC	TAGTGTGAC	CTCTGGTGT	GTGGTGTGT	TGATGCCCG	1320
	ACTCTGTTC	TGCTTCTG	TGGTGTGTG	GGTGTCTAG	TCCCGATAC	ATCGGCGCA	1380
	GGCCAGCAG	ATGACCCAGA	AATATGAGA	GGAGCTGAC	CTGACCGGG	AGAACTCCAT	1440
	CGGAGGCTG	CATTGCCAT	ACAAGGACC	CAGAGCGAG	CGGAGGAGA	GTGTAGGGCT	1500
	GAGAGCCG	GCGCACCTC	ATAGTTCGA	GGACACAT	AGCTCTCTG	TGATAGTGA	1560
	AGAGCCGAG	GCGCCGAGT	ACTCCAAGT	GACCAAGCT	AGGAGATAG	AAACACAGAC	1620
	TGAACTCTG	TCTCCAGGCT	CTGGGCGGCG	CGAGAGGAG	GAGATCAG	ATGAAAGCAT	1680
	CAAGACGCC	ATGACCAAT	TTGTTGAGA	GAATGGGAC	CTACGGGCA	AGCCCAAGG	1740
20	ATAGGCTC	TACATCTAG	GGCGGGGAGA	CTGCTGTCA	CGAGGCGCT	CTCTCTCTC	1800
	CTGCTCTG	CTCTCTCTG	TGACATGGA	GATTTAGCT	CAGCTTGGG	GCTCTCTTA	1860
	ACAGCCCAT	TTCTTGGA	AGATGCTCCC	ACTCCCACT	ACTGCTTAG	CTTACCTCC	1920
	AACTCTCTG	TTGCTCGGA	GGCTCCACC	AATTAGTCT	CTCCCACT	CGATGCAAGT	1980
	CAGCTGTGT	TTGCATGTG	GCTCTGTGGA	GTGTTGACT	ACTGTGTGT	TGTGGAGG	2040
30	TAGCTGTGT	TGTGTGTG	GCTGTGCTC	TGTTGTGAG	TAGTGTCTA	TACAGAGTC	2100
	AAGTGAACT	TGATGTATGT	GCCAGGGAT	TGAGTGTG	GCTGTGCA	CAGTGTCA	2160
	GTGTTGGCT	TGTGTCAZGT	GCTGTGTGT	GACTCTGCC	TGAAAGACA	GZATTTTCT	2220
	CAGAGCCAG	AGCATATTA	ATGATGAGA	GTTGTGAGA	GAGAGGTGA	CAGTGTGCT	2280
	CAGAGCCAG	TGATGTGAG	TAGTGTGAG	TGATGTGCT	CGCTGTGTC	AGGAAAGCT	2340
35	TCTCTTACA	CTCTCGAGC	ATGCGGCGAA	TGTGGAAGA	GCAATCTCT	GGTTCAGCA	2400
	GAGGCTGGA	CTGTGATGA	AGCCCTCTGC	CCTCTGTGT	CGCTGTGCC	TGCTGTATGT	2460
	ACGATTTTC	TGTAAATATA	ATGCGCGCG	GAGCTTCTG	CAGGAATCT	GCTCGGATC	2520
	ACTTTTAAT	TTTTTTCTT	TTTTTTCTG	CGCTTCTG	TAGTGTCTA	GZATTTTAT	2580
40	TTTTTTT	TTTTTTTTT	AGATTTGAG	TCCGCTCTG	AGATATAGC	CAGACCTGT	2640
	CTGTAAAAA	ACCAAAAAA	AAAAAAAAA	AAAAAAAAA			

Seq ID NO: 179 Protein Sequence

Nucleic Acid Accession #: AAL10423

45	1	11	21	31	41	51	
	NPFLSGAENV	GPFWLLILL	LASSTGTGCT	AGLESTSDV	TVVLGQDAKL	PCFYNGDSGE	60
	QWQVNAHNV	DAGEGAQELA	LHSHKYGLHV	SPAYBQVQ	PPFRNPDLG	SVLLRHAVCA	120
	DBEYECRVG	TPPAGSTQAR	LALRLVFPPL	PSLNGPDALE	EQGLTLAAS	CTABSGPAPB	180
50	VWVGYEYRG	TSSRSFKSR	SAVTSSEPHL	VFSNPMQGL	LCTVYBFPGL	LAQRLTHLL	240
	HYFSLASRY	MLXELQNLH	IGREDAALAC	LSRQPPREY	HWLELDLPL	BOVRVMDZL	300
	GFPLFTTHS	GIYVCEVNE	FSSRDSQVTV	DVLPQDESD	QKVLVBSAV	VWVGVIAALL	360
	FCLLAVVVL	MSRYRRKAG	QWTKYEEEL	TLTKRENSIR	LHSHTDPRS	QPEBSVGLRA	420
	BRPFLSKDN	SGCVMSPEP	SRBYSTLT	VREISTQTEL	LSPGSGRAEE	HEPQDGLIQ	480
55	HNHFVQSG	TLAKRPTGNG	LYVNGRHLV				

Seq ID NO: 180 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482..3067

60	1	11	21	31	41	51	
	AACTAGAGCTA	AGAGGAATA	CTGCAAAAGG	AGGAGGAGA	CAATTGCTGC	AGCTTGGATC	60
	TACACACTAA	GAAGCAACA	GTGATCAATC	TCACTCTGT	TAAACATCTT	TTGACTTAGC	120
65	TCGATTCACC	ACCTTGCAAA	TGGTAACTA	TATCGAAAA	AGTCAGCATA	CGTGTAAAGT	180
	ATCGCGGAA	TTTATATGA	GCGAAAAAG	GACATTTGCT	TGAGATGCT	CTAGATATCA	240
	CTCTCTGTA	AATATATCT	AGGAAATGCA	CAGATATCTA	TGCTGACAA	GAGGTTTAA	300
	CTTATGAGG	CTATGCACT	TGACAAAAG	TGATATTTGA	GAGAAAGTA	CGAGTGGTGT	360
70	GGTGTCTTCT	TTTTTTTAAT	AAAGGAATG	AATTACTTGT	AACAACCTCT	CGAGCTGTGC	420
	ATTACAGATA	ACGTGAGGA	GAGTCTCTGC	TTTACAGAT	CGATTTTCAT	CAGAGACACA	480
	CAATGAGCA	CGATTCATC	TTTTTTATCT	ATCTCCGCTT	GCGCTATAT	CTTTCAGCT	540
	CGAACTTCA	GTCCTCTAT	CGAGAGCTTC	TTGTGATCT	TTCTTCAAT	CTAGGAGAAA	600
	AGATGCGACA	ATGCTAATAA	ATTGTGAGC	AAAGGCTATC	AGATGTGTA	CTGAATATAG	660
75	TGTCGACCA	TGACGACCTT	TCCAACTAAG	CTTATTAAT	AAAGCGCTGA	GAGAGCTTCA	720
	CACAAATAC	TTTCTGGGC	TTCACATGTC	TATTTCAADA	TAAGCTTGAAT	TTTATATAG	780
	TGCAATATCT	GAGATAGGCT	CTTTATATG	CTTGTGATC	CTGAACGAT	TTCAATATAC	840
	TGCAATATCT	TGAGAGGCT	TTPAAGAGGA	TACTTTCCAT	GGACGTGAAA	GGTGTGATTT	900
	CTCGAAGCA	GATACAAATT	TTATACAGAT	GATTGAACCA	AGTGCCTTTA	CGAGCTCTAA	960

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CAGACTCAAA GTGTTAATT TAAATGACAA TGTATTGAG AGTCTCTCT CAAACATCTT 1020
 CGATTTTGT CTTTAAACCC ATTCAGATCT TGTGGGAAT CAATTACAAA CATTGCTTTA 1080
 TGTGTGTTT TGTGACACA TTGCGGAAT ATTGATCTT CAGTGGGAG ACACAAATG 1140
 GGTGTCAAT TGTGATGAA TCGATGGTA TGTGATCTT GAGACATCT CTCACAGATG 1200
 TATAATTGTT GATCTGTCTT GCACAGGCC TCCATCTTTT AAAGAAGA TACTCATGAG 1260
 ACTAAAGAAG GAATCTATT GCCCTACTCC ACCAGTGAT GAAGACATCT AGGATCTCTT 1320
 AGATCATTA CATCTGGCAG CAACATCTTC AATAAATGAT AGTGCATGT CAATATAGAC 1380
 CAGCTGCTT CTAAACATC CCGCAAGAC ACCGATGTT ATCATCTTA TTAACAAGCT 1440
 ATGACATTA CTCTCGGAG CTTCAGGCC TATCTCTGT AACTGCARA GTCATATGCC 1500
 ATGAGACTT CTAAATCTT GTGCGAGCG CAACATGAA AGCTTATGAT ACTCTAGACC 1560
 TCTCTGCGAA AATCTAGAAA AGCTCATCT AGGGGAAAT ATATTTCACA GTTTAATGAA 1620
 GTCTGACTTA GTGGAATAT TCACCTTGG AATGCTTCA TGGGCAACA ACATGATGAA 1680
 KHTTCTGAA GAGATATCT TTAATCACT ACGAGATCT ACTTAAGAT ACTTAAGAT 1740
 TAAACACCTG ACCGAATGAA GTAAAGCAT GTTCTCTGT CTCATAATC TTGAATACTT 1800
 ATATCTTGAA TACAATGCCA TTAAGGAAAT ACTGCGAGA ACCTTTAATC CAGTGCTTAA 1860
 ACTTAAAGTC CTGATTTTAA ATGAACAAT CTCCTAATTT TPGCACACAC ATATTTTTTC 1920
 AGGTGTCTT CTAGATGAG TAACTTTAA AACACACCG TTATCCCATC TACCTGTAA 1980
 TAAATCTTGT GATGATCTTG ATTTACTAAC CAGACTGAC CTGAGGATA ACCCTGGGA 2040
 CTGCTCTGTT GACTCGGTTG GACTCGAGCA ATGATGATA AATTTAAGCA AGACACAGT 2100
 GAGNGATGAC ATCTCTCTGA CTGCCCGGG GATCTTGAC AAAAGGAT TGAAGSCCT 2160
 AAATAGTGA ATTTCTCTG CAGTTTAGT AATAACCA TCAATGCA CAGAGATG 2220
 TTACTTTATG GTACCACTC CTGCAACAAC AACAAATAG CGTATACTA TTTTAGATC 2280
 TCTTAGGAC CTGTGCGAC TGTCTGTTCT AATATTGGA CTCTGATTA TGTTCATCAC 2340
 TATGTTTTC TGTGTCGAG GATATGATG TCTGTGTTCT CACGCGAGA GAAGATACA 2400
 AAKGAACA CTAGATGAG AATGAGAGA CTACATCTCT TGTATCTTC AGTACAGAT 2460
 GTATGCCAT AAAACCATCT ATCACTACT TGAAGAGGCC TGTGCTTCA TCTATGAACA 2520
 GGCATGGTG AGCCCATCT TTCACTGTCA TAAAGATCA TCTTTGTTCT CAAGCATCT 2580
 GAGAGAGGA GAAGAGAGA ATGAAGAAA AGGATAGAT GCAGAACTC TCCAAAGAG 2640
 TCTTTGGA GAGAGAAAT ATTCACATCT CAGAGAGCA AATATGAAT AGAAACACT 2700
 CAGACATCA AGCAATTTT TATCTTCCA AGATGCCAGC TCAATGTACA GAACATCT 2760
 AGRAAAGAA AGGGAATCT AGCAACTGG AATCAAGAA TACCTAAGA AAAAGATTC 2820
 TCGCTCCAG CCGTATATG AGGCACATTA TCTCGAGAC CAGAAAGAG TGAATTAAT 2880
 AATCATTA ATATCTACG GTCAAGAAA GGTGTTATG AATATGATA AATATGATA 2940
 TTTTAACT AAGATTAAT TACTATCTA ACTCATCT TTAGAATCT TGAGACAGA 3000
 AAGATAGAT GAGAGTTGA GGGCTTGGC AGAAATGCT TGATCTGTT TTAAGTCCAT 3060
 ACCTTGTAAA TAASTGCTT AAGTATGAT GTCATCAAT AGAAGCTAAG CACAGAGTA 3120
 AACATGGG AAAAARAAG AAGAAGAAA GAATCTAG GATCACTGG AGAAGCAGT 3180
 GATATCTCT CAGGATTTT AGTCTGTCC AATAAATCT AATCTTCCA TGTAAATC 3240

Seq ID NO: 181 Protein Sequence
 Protein Accession #: Bos sequence

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1 11 21 31 41 51
 MKLNLPLYS SLACISLHS QTPVLSRRGS CDELCHCEK DDTNLHCEA KGRNVSIS 60
 VPRPRPOLB LBNGLTLE TDSPLGVA 19HLSPNT ADIECAWNG KALLAGLIN 120
 ENSLERLKD YHGLNLEF LQADNMFIV 1EPSPFKLN KLVLLINDN AIESLPHIF 180
 RPLVLHLDL RGHQLTLPY VGLLEHIGI LDQLLEDHKN ACNDDLQK TWLENNPPQS 240
 IEDVNVSPS PFFGGLILGR LKESICPTP PVYSEHSDS GSHLLA78S INDSRMSVT 300
 TLEKLPTKA POLIPTTSP FOLTPOLPYC 1PCNGLVPL SOLLHCOER WLESLDAP 360
 PPQMPKLLI AQNIHSLMK SOLVEYFTE LHLGNMRK VLBSGPNEL TRLOKLYNG 420
 NHLTLEKSH FLGLNHLVL YLEYNALKEI LPQTFNMPK LKVLPLANNL LQVLPPLHS 480
 GVPLFVNLK NQPTFLPVS NILDLDGLT GIDLENDPH CSDLVLDLQK WIGLBHVTY 540
 TUDILCTSRG NLEKHEKAL NHELCGLVW TAIKTEIATG YLVYFTTTP TWATITLIR 600
 LITAVLESLV LGLGLLPHIT YVCAAGIVV LVLIHRRVKE KCVQGMQMD KSPHVLQSN 660
 YGKTHHTTT ERFASBLTDQ RMVSPMVHYV RSPFGPIHL ESEERNEKE GSDAHLQRS 720
 LLQENHSPL TBRMKYKTT NQSTSPLSFO DABSLRNIL ENRELEOQLG ITEYLRKHA 780
 QLQPMHARY PGASHELAM ETLMYSPFRK VLVQYKNEY FELKANLHAS PDLVLSQQ 840
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Seq ID NO: 182 DNA Sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 1..1524

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1 11 21 31 41 51
 ATGCGGGGTG CGGGCCGGA GCGGCGGGCG CTACGGGGCG CCGGGGCGGA GAGGAGGAA 60
 GAGCGGGGG AGAAGATGCT GCGCGCGGAG AGCGCGGAG GCTCGGGCG CCGAGCGAG 120
 GCGAGCGCG TACCTGTCA GCGAGACATC ACCTGCTCA ACAGCTGGCG CATCATGCTG 180
 GCGACATTA TCGGCTGCG GAGCTGCGAG CGCTGCTCA GCGGCGGAG GCGGCGGAG 240
 TCGCGCGCG TCGCGCTGCT GCGGCGGCG GCGTGGCGCG TCTTCTCAT CTCTGGCGCG 300
 CTCTGCTACG CCGAGCTCG CACCACTCAT TCCAAATCG GCGGCGACTA CCGCTACATG 360
 CTGAGGCTCT ACAGCTGCT GCGCGCTTTC CTGAGCTCT GAGTGGAGCT GCTCATCATC 420
 GCGCTTCA CCGAGTCAAT GCGGCGGAG GCGGCTGCG GAGTGGAGCT GAGGCTGCT 480
 TCTGCTCAT GCGCGTCTG CCGAGAGCGA GCGGAGCTCG YGCTGCTCT CTGCGTGTCT 540
 CTGCTCAAG CCGTGAACCT CTACAGCTG AAGCGCGCA CCGCGGCTCA GAGTGTCTT 600
 GCGCGCGCA AGCTCTGCG CTGCGCGCTG ATCATCTCT TGGCTTCTG CAGAGTCGA 660

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 10
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M/CCTCATG TGTCAATCT AGATCCCAAC TTCTCATTTG AAGGACCAAA ACTGGATGTG 720
 CGGACATTTG TGCTGGGATT ATACAGACGCC CTCTTTCCTT ATGGAGGATG GAATTACTTG 780
 AATTTCGTCA CAGAGGAATT GATCAACCCC TACAGAAACC TGCCCTTGCC CATCATCATC 840
 TCCCTGCCA TCCATGACCT GGTGTACGTG CTAGACCAAC TGCCCTACTT CACCACTCCG 900
 TCCACACAGC AGATGCTCTG GTCCGAGGCC GTGGCGCTGG ACTTGGGAAA CTATCAACTG 960
 GGCATCATGT CCTGATCATC CCCCCTCTTC GTGGGCGTGT CCGCTCTCGG CCGCTCATAT 1020
 GCGCTCTGTG TCGATCTCTC CAGGCTCTTC TTCTGTTGGT CCGGGAAGAG CCACTTGCCC 1080
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 TGTGTATGA CCGTCACTCA CGCTCTCTCC AAGGACATCT TTCTCCATCA CCACTCTCTC 1200
 AGCTCTTCA CACTGCTCTG CCGGCGCTTG GGCATCATCG GCATATCTG GTGGGCCAC 1260
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 CTGGCTGCCC CTCTCTCAT GTGCGTCTCC TTCTGGAAAG CCGCTGTGA GTGTGGCTAT 1380
 GCTTTCACA TCACTCCGAG GCGCTGCCC GTTCACTCT CTGGGCTCTG GTGGAAAC 1440
 AACCCAGAT GGCCTCCCA GGCATCTTC TCCACACCG TCTGTGTCA GAAGCTCATG 1500
 CAGTCTCCC CCGAGACAC ATAG

Seq ID NO: 183 Protein Sequence
 Protein Accession #: XP_035292.2

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1 11 21 31 41 51
 MAGAGPKERA LAAPAAEKE EAREKMLAAK SADGSAPAGE GBSVTLQRNI TLNMGVAIV 60
 GTIIGGIPV TPTGVLEKAG SPGLALVWA ACGVPSIVGA LCVAELOTTI SKGGGDVAYM 120
 LEVVGSLPAP LKIMLELIL RPSSQIVLVA VPATILLEPL PPTCPVEEA AKVLALCLVL 180
 LTAIVNCTVQ KAATGACGA AAKLLAAL ILLIPVQI KGVSNLDVW PSVSTPLDV 240
 QNIVLALYG LPAVGGNYL NPVTSEHNP VHLPLAII SLPIFSLVIV LTKLAFPTL 300
 STWGLSSEA LVADFGNYL GVNSHNPV VGLSGPSVW GELFVLSRLV FVGSREGLP 360
 SILKMHPL LTPVSLVPT CVHLLYAFS KDIFRVNHF SFPMMLCALV AIGMGLWRH 420
 KPELERPIK VNLALPVFI LALFLIAYS PKITPVBCGI GTTILGLP VIFFGVNKH 480
 KPHLLQIF STVLLCKLM QVVPQST

Seq ID NO: 184 DNA Sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 1..822

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1 11 21 31 41 51
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 GGGGCGATCT GGCTGTCTCT GGTCTTCTAT TTCCGCGTGC TGGGTACTCT GGTGAAGGCC 120
 GAGGTGTGT GGAATGATGA CCAACAAGAC TTGAGTGTGA ATATCTGCCA CCGCGGCTGC 180
 TCCAACTCTT GCTTTGAGA GTTCTTCCCT GTGTCCXNG TGCGGCTCTG GCGGCTCAG 240
 CTATCTCTGG TACAGTCCCG CTACATCTCT GTGGTCTGCG AGTGGGCTCA CCGGAGCTT 300
 CAGGAGAAGA GCGACACAGA AGCCCAATGG GAGAACGTGT GGCCTCTCTA CCGTGAACCC 360
 GGCAGAAGCC GGGGTGGCTC CTGCTGGACA TATCTTCTGA GCTATGTGTT CAAGCGGAC 420
 GTGTGTAAT GCGACAGCA TCGATCTCC ANTPAKTGS ACTCTCTAT CTGCAAGCC 480
 TCAAGAGA ACAATTTTAC CCTCTCTATG GTGGCGACAG CTGCTCTCTG CATCTCTCTC 540
 AACCTCTGG AGCTCATCTA CCGTGTGAGC AAGAGATGCC ACGATGCTCT GCGACAGAG 600
 AAGGCTCAG CCAATGTGCA AGGTCAATAC CCGCAAGTTC CCACTCTCTC CTGCAAGAA 660
 GAGACCTCT TTTCGGGAGA CCTCATCTTT CTGGCTGCG CAGTCTATCC TCTCTCTCTA 720
 CAGACCGCC CCGCAAGCA TGTAAAGAA ACCATCTGT GA TCTCTCTCTA 780

Seq ID NO: 185 Protein Sequence
 Protein Accession #: NP_005259.1

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1 11 21 31 41 51
 MNSIFBOLL SGNKYSTAP GRIMLELVP FRVLVLYTA EYNSDHDH FCHTRQDGC 60
 SYVCTEPFF VSVILWALG LILVTPPELL VNMVAREV QSKREHAEK ENGRILYNP 120
 GKRGSLWFT YVCSLVFRA VDIAFLVFN SFYPKYLFP VVKHADPCP NIVDCPISKP 180
 SEKIMILPM VATAICILL NLVELLYVS KRCEHLAAR KAQMCTGSH PRHTTSSCKQ 240
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Seq ID NO: 186 DNA Sequence
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 CCGCGAAGC GAGTACCGCT AGTGGCGTTC GGGGCGCTGC ACCCGACAGA CGAGAGATG 180
 GCGCTGGGT TTCCCGCAGG GCACTTGCGG GCGCGAGACC CAGCGATCCG GGTGAGGGT 240
 GCGCTGACAC TGGAGAGAG AGTTTGAGC CAGCTCAGAG TACAGTTTGG AGAACGAGG 300
 TCGGTGATG GAGGAGAGC GCAACAAAT CTGCGCAAGT CCGCAAGTCC AGGCGCTGAG 360
 GATCTTGG TCGCGAGAG CACTCTGTT CACCAAGTCT TCGACCCCA AGACCAAGC 420
 AAGGCTCANA CCGCAAGAG GGAAGGANA GAGCTAGAC CAGGCGTGG ATGCGAAGA 480
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5 CACCACTGCC TTCTGTCTGC TOSTTAGCTT TAATCAATCA TGCCTTGCCY TGTCCCTCTC 600
ACTTCCCGAC CCACACCCCTA AGTACCACAA GTGGGAGAGC ACACGGATCT CTGGAGAGCT 610
TGAAGCTGCC CCAAGACCAT GTGA GTCCCA GAGCCGCTCT TTGTCTCTCC CCAACATGCT 720
ATTACTAAGA AACACATCA ATAACATGAC TTTTTCCTCC CATATAAGC TCTCTCTTTT 780
TAATAT

Seq ID NO: 187 Protein Sequence
Protein Accession #: NP_002382.1

10 1 11 21 31 41 51
MQHGRFLILT LLALLALTS VAKKKDKVKK GSPGSRCAEM AKGQCTPSSK DGVGPRBHT 60
GGAQTGRIRC RVPNCNKKRP GADCKYKFPN WGACDGGTGT KVRQGTLEKA RYNAQQQETI 120
RVTKCPKPKT KAKAKAKKKK GKD

15 Seq ID NO: 188 DNA Sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241-1902

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CCGACAGAGA GCGTGGGCGA GGTAGCCGAG GGGGCCCCCA GCGCCTCCCC AGGCGCGGAG 60
CGCCCTCTGC GGGTGGCTGT GCGTCCCTCT CCGAGACTCGA GGGACGAGAC CGGTGAACTG 120
CGAGTGGAGC GGGGAGCCCG AGCGGCTGAG GAGAGAGAGG GCGGCGGCTT ACGTGTCAZO 180
GGGTCCGCGC GCGCCGCTCC CCGAGGGGGG CACAGAGGAG GAGAGGAGAC CGGTGCGAGA 240
ATGCGCTTGC CCGTAGAGCT TGCAGTCCCG CTGCTGCTCT CCGTGGTGGC AGTGGTPTTC 300
GGGAGACCGG GCGATGACAG GCTATCAOAG TTGTTAGCAT CGGACCTCA CCGTGGGGTC 360
TGTCTCATAT GAACTAAACT GCGATGCTGC TAGCGCTGGA GAGAAAGAGC CAGTGGAGCT 420
TGTGAGCTCA CATGGAAGC TGGATGTAA GGTGTGTGAT GGTGTGGACG AAACAATGTC 480
AGATGCTTTC CAGGATGACG GCGGAAACCC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCGCGGC CATCGCAACA CAGATGTGTG AATACACAGC GAGCTACAGA GTGCTTTTTC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGGA GACTCTGAG ACTCTGAGAC ATGTGCCATG 660
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GOTAAATGA TCTGTCCCTA CAATGGAAAG TGTGTGAACA CATTTGAGG CTACTACTUC 840
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Seq ID NO: 189 Protein Sequence
Protein Accession #: NP_056322.2

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LCHPLAGCA KCVNISTGCM INQVNSCEDT BEBQGLCFPS SGLRIARNGR DCLDIDECAS 180
GKVIQPVNR CVNTGGSYV KCEIAPGLAY IGGVYCDITF NCTWDSHTC SHUAKPNQ 240
CSFKKCKGGY YKNGILRCSA IPENSVEKVL RAQPTIKRI KCLLAHNSM KKKAKIKQVT 300
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70	<p> 160 180 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480 500 520 540 560 580 600 </p>
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PCT/US02/21338

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5 Seq ID NO: 192 DNA Sequence
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NIVPVPFBSR QNRSPFGGVY AALLAGRLAG GLSLRLSLRN HPLFLPRLVY AQLPFLRLD 240
LBNISLVSIL YVSFRLTHL ESLALEDNAL KVLBNGLTAR LQGLMTRVF LDNPNWVDC 300
RWADYHVLXK ETEVYQKDR LTCAYPEIKR NRVLLELSNA DLDCPILPFL SLGTSYVFLG 360
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60 Seq ID NO: 194 DNA Sequence
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Coding sequence: 86..1126

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WO 03/003906

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 AANVTSLPV RGCYQDEFCT RDGVTGSRF LSGSCQQGRS CYNASLHKTY FSPRFPVLVR
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GDUKLELH PTVSLELHSH HSALGESAHA PHELESLRST HSEKTFYED KSNWINDIAP 480
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CAACAGCTGT CCTCGAAAAA GATUCAGTTT CGAGTCTTCT ACCCTCGGTC GTTCTCTCGC 1620
CTAGACACCT GAATATAGTA TACACTGGCC CCTATACATT TGCATCGAAA GATCAACTGT 1680

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Protein Accession #: NP_001935

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 ATDADEFML NSKIAFKIVS QSPATPMFL LNSRTGVRT LNSLDRQEA SSYRLVYSGA 240
 DRDGEGLSTQ CSCHIKVDV IDNPFMPRDS QYSARIEHI LSSELLAFQV TDLDEEYTN 300
 WLAIFYFTTS MECHNEFIQT DPTNMEGILK VVIALDVQL QSVLSIAVK NAEFLISVI 360
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 NMTKLGAITE SGAAGFATC TVSGAAGCFO AATGVICSS QGSGMTBTH TGTQNKDYA 780
 DQALSNFLD SYFSQAFAK ASBBDGJAN DCLLYINRG ADATGSPVGS VOCCSPIAD 840
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 GCGACTCGG GTCCCTAAG TCTGATTCT TTCTCCCTA CTGAGACGC CCGGACACAC 240
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1 11 21 31 41 51
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GATTCAGAGA AATTCACAGA AACTCTTCAT AGATCCATG TCAGAGGAGT TATTTATTTG 240
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CATCTCAGAG ATCGACAGAT GATTACATCA CTTATAGTTC TAGTAAATTT ATTAAATATA 360
AACTCAGAGA GATTCTCAATA TCACATCTGC TTACACCAAT AGCATAGAT TCAATGTTCAG 420
CTATGCAAT TGAATATGAG CTGTTTGTG ATTTAAAGGT TPAATTTCT CTACCAAGAC 480
TGCTGTATCC AGATGCAAGA CTCGAAATGT TAATATTGTG TCTGGAGAGA CAATCAAAATA 540
AGACTTAAGA GGAAGAGGAA TGGCCACAAT CCACCTGAAA TTTTTCCTTA AAAAGTGTGC 600
AGCCTACTAA ATCGAATGA AAATAGAGAT ACAGATTAT AAACAAATAG CAATCAAACT 660
TTTCTAAGC TTACTTAAG ATATTTCATC TGAAGATTTC AAGACATTTT GTTCAACATT 720
AAATGACAAA TCTAACTAAA CAGTCTTTT GAATTTATGC ATGTGTATGA ACATCTCTCC 780
TATTAACTTT ATTACCTAAG GCTAAACCTA AAATTTTAAA GCAAATTAG AAAAATAGTC 840
TTCACTCATC AAAAATATAA GTTTGTTTACA TTTAGTATTT TCCCAATAA ATGTGTCGTC 900
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CGGAAACCCG CTATCCCGCA CAGCCCACTG TGGTCCCGAC TGTCTAGAGG GTGCATCCGG 180
CTCATACTAA CCGGTCCCGC GTGCCCCAGT AGCCCCCGAG GTCTCTGAGC CAGGCTTCCA 240
ACCCCTCTGT CTGCGGAG AGCAANTCC CATCCCGGAG AGTGTGTAC TCAAGAGTA 300
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CTGCGCTACT CTGGAGTTC ATGGCGAGCA AGTGTCCAA CTCTGGGATA GAGTGGGACT 420
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CATCTCAGAG GAACTCTGCG CACCCTGTGT GCCAAGAGCA TGTGAAAGAG AACTCAAGGC 600
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AACAGCATGT TCTGCCCAAC CACGGCATGA TGTCTGACGC AGAACACGCT TGTGTGATTT 1200
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Protein Accession #: NP_005647.1

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5  SNPVYCTPKP  SPGGFVCTSK  TKCALCTILT  LGPLVLGAAL  ANGLLMRHP  SKCSNIGIRC  120
    DSGSTCNPS  NMCDDGSHCP  GGRDENRCVR  LGPNPILQM  YSSRSXMHF  VQDDKNNBY  180
    GRAACRMAG  KNIPIYSQGI  VDDSGSTSPH  KMFPSAGNDV  IYKRLYBDA  CSKXAVSLR  240
    CLAGCGRLMS  SRSRIRVGG  SALSPPAPMP  CGSLIIPFN  LTVKALPVEK  300
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10  VKFVCLPHFG  MHLQFQLQM  ISGNGATBKK  GKTSEVLMA  KVLILSTQRC  NSRYVYDNL  420
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 Protein Accession #: XP_044533.6

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 15 GKGRCDFDRN FKSTALVVDG ELVTOTVSSF QMDPAISRS QSLRPTKTS SLAMMLQDPAP 240
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 20 PRVHIIEELQ IFSSQDPON LLLDTHRGLL YAASHGVVQ VPMANCLYR SQDCLLARD 540
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 FGRVYNTLA CPLSLHATR LALRQAPVN ASAQSVLFT GLLLVCTQY GRTQCHELE 660
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 25 NCLDFVLAVL LPVLFLLYRH RSNKVFLLQ CBCASVHPKT CPVVLPPETR PLMLGPPST 780
 PLDRGYQSL SDSPFGSRVP TSEKRLPLG QDEPVEVSDV CPRPRVLGS EIRDGVV

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a bladder cancer-associated transcript in a cell from a patient,
5 the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.
2. The method of Claim 1, wherein the biological sample comprises isolated nucleic
10 acids.
3. The method of Claim 2:
 - a) wherein the nucleic acids are mRNA; or
 - b) further comprising the step of amplifying nucleic acids before the step of contacting
15 the biological sample with the polynucleotide.
4. The method of Claim 1, wherein the polynucleotide:
 - a) comprises a sequence as shown in Tables 1A-13; or
 - b) is immobilized on a solid surface.
20
5. The method of Claim 1, wherein the patient is:
 - a) undergoing a therapeutic regimen to treat bladder cancer; or
 - b) suspected of having bladder cancer.
- 25 6. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.
7. The nucleic acid molecule of Claim 6, which is labeled.
- 30 8. An expression vector comprising the nucleic acid of Claim 7.

9. A host cell comprising the expression vector of Claim 8.
10. An isolated polypeptide which is encoded by a nucleic acid molecule having
5 polynucleotide sequence as shown in Tables 1A-13.
11. An antibody that specifically binds a polypeptide of Claim 10.
12. The antibody of Claim 11, further conjugated to an effector component.
- 10 13. The antibody of Claim 12, wherein the effector component is a fluorescent label.
14. The antibody of Claim 12, wherein the effector component is a radioisotope or a
cytotoxic chemical.
- 15 15. The antibody of Claim 11, which is
a) an antibody fragment; or
b) a humanized antibody
- 20 16. A method of detecting a bladder cancer cell in a biological sample from a patient, the
method comprising contacting the biological sample with an antibody of Claim 11.
17. The method of Claim 16, wherein the antibody is further conjugated to an effector
component.
- 25 18. The method of Claim 17, wherein the effector component is a fluorescent label.
19. A method for identifying a compound that modulates a bladder cancer-associated
polypeptide, the method comprising the steps of:

- a) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and
- b) determining the functional effect of the compound upon the polypeptide.

5

20. A drug screening assay comprising the steps of

- a) administering a test compound to a mammal having bladder cancer or a cell isolated therefrom;
- b) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

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